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|-----|-------|------|--------|-----------|-----------|-----------|-----|-------|------|-------|-----------|
| 98 | 565.2 | 38.1 | 582.5 | BP098937 | BP098937 | BP098937 | 171 | 393.6 | 26.5 | 505.7 | CK322957 |
| 99 | 564.6 | 38.0 | 921.4 | BP1547056 | BP1547056 | BP1547056 | 172 | 393.4 | 26.5 | 511.6 | CK552855 |
| 100 | 563.4 | 37.9 | 620.4 | BM016283 | BM016283 | BM016283 | 173 | 391.8 | 26.4 | 514.1 | AI050501 |
| 101 | 554.8 | 37.4 | 558.5 | BP338657 | BP338657 | BP338657 | 174 | 391.6 | 26.3 | 503.3 | BE048740 |
| 102 | 553.8 | 37.3 | 557.4 | BI063664 | BI063664 | BI063664 | 175 | 390.6 | 26.3 | 833.4 | BI6590860 |
| 103 | 551.4 | 36.9 | 581.5 | BP314951 | BP314951 | BP314951 | 176 | 389.8 | 26.2 | 712.2 | BI413660 |
| 104 | 547.8 | 36.9 | 564.5 | BP276942 | BP276942 | BP276942 | 177 | 388.4 | 26.2 | 502.1 | AA771125 |
| 105 | 546.4 | 36.8 | 574.5 | BP981070 | BP981070 | BP981070 | 178 | 382.4 | 25.8 | 566.2 | BP782251 |
| 106 | 545.2 | 36.7 | 581.5 | BP276312 | BP276312 | BP276312 | 179 | 381.4 | 25.7 | 595.2 | BP307809 |
| 107 | 545 | 36.7 | 582.5 | BP201409 | BP201409 | BP201409 | 180 | 381.4 | 25.7 | 734.5 | BK659268 |
| 108 | 541.2 | 36.4 | 582.5 | BP200472 | BP200472 | BP200472 | 181 | 380 | 25.6 | 466.6 | CD555983 |
| 109 | 536.4 | 35.8 | 535.4 | CN389163 | CN389163 | CN389163 | 182 | 378.6 | 25.5 | 483.3 | CG061538 |
| 110 | 531.6 | 35.8 | 535.4 | BI828549 | BI828549 | BI828549 | 183 | 376.8 | 25.4 | 448.1 | AI991465 |
| 111 | 531.6 | 35.8 | 572.7 | CR769410 | CR769410 | CR769410 | 184 | 376.6 | 25.4 | 745.5 | CN317425 |
| 112 | 530.8 | 35.7 | 859.4 | BI859273 | BI859273 | BI859273 | 185 | 376.6 | 25.4 | 509.7 | H38402 |
| 113 | 527.4 | 35.5 | 583.5 | BP210065 | BP210065 | BP210065 | 186 | 376.2 | 25.3 | 765.5 | CA492190 |
| 114 | 526.4 | 35.4 | 762.4 | BI759941 | BI759941 | BI759941 | 187 | 374.6 | 25.2 | 437.7 | BF971521 |
| 115 | 521.4 | 35.1 | 762.5 | BP455530 | BP455530 | BP455530 | 188 | 370 | 24.9 | 450.5 | BQ209404 |
| 116 | 519.8 | 35.0 | 886.4 | BI522778 | BI522778 | BI522778 | 189 | 369.2 | 24.9 | 582.5 | BP256865 |
| 117 | 516.4 | 34.8 | 519.4 | BM712632 | BM712632 | BM712632 | 190 | 368 | 24.8 | 582.5 | BP256865 |
| 118 | 515.8 | 34.7 | 786.5 | BK390052 | BK390052 | BK390052 | 191 | 366 | 24.6 | 356.2 | BE048014 |
| 119 | 512 | 34.5 | 582.5 | BP360443 | BP360443 | BP360443 | 192 | 364 | 24.5 | 929.4 | BI765220 |
| 120 | 511 | 34.4 | 582.5 | BP310036 | BP310036 | BP310036 | 193 | 362.8 | 24.4 | 935.4 | BI835577 |
| 121 | 506.4 | 34.1 | 508.2 | BF593274 | BF593274 | BF593274 | 194 | 357.4 | 24.1 | 325.4 | AI923506 |
| 122 | 502.6 | 33.8 | 789.4 | BI838884 | BI838884 | BI838884 | 195 | 357 | 24.0 | 358.1 | AI1202519 |
| 123 | 501.4 | 33.8 | 505.7 | CN389161 | CN389161 | CN389161 | 196 | 357 | 24.0 | 358.1 | AI1202563 |
| 124 | 501 | 33.7 | 501.4 | BM797230 | BM797230 | BM797230 | 197 | 357 | 24.0 | 856.4 | BI769105 |
| 125 | 490.8 | 33.1 | 494.7 | CN389162 | CN389162 | CN389162 | 198 | 353 | 23.8 | 354.1 | AI650570 |
| 126 | 479 | 32.3 | 674.2 | BP528522 | BP528522 | BP528522 | 199 | 349 | 23.5 | 602.5 | BP194456 |
| 127 | 472.4 | 31.8 | 528.5 | AA205873 | AA205873 | AA205873 | 200 | 348 | 23.4 | 437.7 | H48148 |
| 128 | 457.2 | 30.8 | 579.4 | BM015437 | BM015437 | BM015437 | 201 | 346.8 | 23.4 | 447.7 | AA016174 |
| 129 | 451.6 | 30.4 | 641.5 | BQ34450 | BQ34450 | BQ34450 | 202 | 346.2 | 23.3 | 771.4 | BI103185 |
| 130 | 450.2 | 30.3 | 477.1 | AU127177 | AU127177 | AU127177 | 203 | 345.8 | 22 | | |
| 131 | 449.2 | 30.2 | 452.1 | BP48656 | BP48656 | BP48656 | 204 | 344.2 | 22.8 | | |
| 132 | 448.8 | 30.2 | 452.1 | AA743902 | AA743902 | AA743902 | 205 | 338.8 | 22.8 | | |
| 133 | 443.6 | 29.9 | 577.5 | BQ323938 | BQ323938 | BQ323938 | 206 | 338 | 22.8 | | |
| 134 | 443 | 29.8 | 572.5 | BQ235058 | BQ235058 | BQ235058 | 207 | 336.6 | 22.7 | | |
| 135 | 441 | 29.7 | 441.4 | BI523405 | BI523405 | BI523405 | 208 | 337 | 22.7 | | |
| 136 | 441 | 29.7 | 547.5 | BQ233997 | BQ233997 | BQ233997 | 209 | 335.2 | 22.5 | | |
| 137 | 438.2 | 29.5 | 457.1 | AI826065 | AI826065 | AI826065 | 210 | 334.4 | 22.5 | | |
| 138 | 437.4 | 29.5 | 2427.3 | CP952132 | CP952132 | CP952132 | 211 | 334.4 | 22.5 | | |
| 139 | 435.8 | 29.3 | 828.7 | AK045539 | AK045539 | AK045539 | 212 | 334.4 | 22.5 | | |
| 140 | 435.8 | 29.3 | 931.5 | BUS16181 | BUS16181 | BUS16181 | 213 | 327.2 | 22.0 | | |
| 141 | 428.6 | 28.9 | 210.3 | AK028955 | AK028955 | AK028955 | 214 | 322.2 | 21.7 | | |
| 142 | 428.4 | 28.8 | 882.6 | CA977847 | CA977847 | CA977847 | 215 | 322 | 21.7 | | |
| 143 | 427.2 | 28.8 | 763.5 | BUS58976 | BUS58976 | BUS58976 | 216 | 322 | 21.7 | | |
| 144 | 425.6 | 28.7 | 875.6 | CA462133 | CA462133 | CA462133 | 217 | 321.8 | 21.7 | | |
| 145 | 424.4 | 28.6 | 426.1 | AI1244708 | AI1244708 | AI1244708 | 218 | 321.4 | 21.6 | | |
| 146 | 421.4 | 28.4 | 844.6 | CA481096 | CA481096 | CA481096 | 219 | 321 | 21.6 | | |
| 147 | 421.2 | 28.4 | 862.6 | CA94764 | CA94764 | CA94764 | 220 | 318 | 21.4 | | |
| 148 | 420 | 28.3 | 847.6 | CB575856 | CB575856 | CB575856 | 221 | 307 | 20.7 | | |
| 149 | 419.4 | 28.2 | 574.5 | BP339377 | BP339377 | BP339377 | 222 | 305.8 | 20.6 | | |
| 150 | 419.2 | 28.2 | 747.6 | CB599384 | CB599384 | CB599384 | 223 | 301.8 | 20.3 | | |
| 151 | 417.8 | 28.1 | 649.6 | BY737042 | BY737042 | BY737042 | 224 | 301.4 | 20.3 | | |
| 152 | 417.8 | 28.1 | 653.2 | BB643983 | BB643983 | BB643983 | 225 | 299 | 20.1 | | |
| 153 | 417.8 | 28.1 | 666.2 | BB611100 | BB611100 | BB611100 | 226 | 298.2 | 20.1 | | |
| 154 | 417.8 | 28.1 | 744.5 | BQ746584 | BQ746584 | BQ746584 | 227 | 297 | 20.0 | | |
| 155 | 417.8 | 28.1 | 807.6 | CA468685 | CA468685 | CA468685 | 228 | 294 | 19.8 | | |
| 156 | 417.8 | 28.1 | 849.7 | CK789647 | CK789647 | CK789647 | 229 | 293 | 19.7 | | |
| 157 | 417.2 | 28.1 | 686.7 | CF168745 | CF168745 | CF168745 | 230 | 291.6 | 19.6 | | |
| 158 | 417.2 | 28.1 | 689.7 | CF168755 | CF168755 | CF168755 | 231 | 291 | 19.6 | | |
| 159 | 415.8 | 28.0 | 588.5 | BQ057760 | BQ057760 | BQ057760 | 232 | 289.6 | 19.5 | | |
| 160 | 415.8 | 28.0 | 591.4 | BO808095 | BO808095 | BO808095 | 233 | 287.2 | 19.5 | | |
| 161 | 412.4 | 27.8 | 708.2 | BE779745 | BE779745 | BE779745 | 234 | 285.2 | 19.2 | | |
| 162 | 410.8 | 27.7 | 594.6 | CB545546 | CB545546 | CB545546 | 235 | 280.8 | 18.9 | | |
| 163 | 409.4 | 27.6 | 505.2 | BP723284 | BP723284 | BP723284 | 236 | 280.8 | 18.9 | | |
| 164 | 405.8 | 27.5 | 608.2 | CB613347 | CB613347 | CB613347 | 237 | 277.4 | 18.7 | | |
| 165 | 404.8 | 27.3 | 526.6 | CB719919 | CB719919 | CB719919 | 238 | 277.2 | 18.7 | | |
| 166 | 404.6 | 27.2 | 780.5 | BDU08166 | BDU08166 | BDU08166 | 239 | 277.2 | 18.7 | | |
| 167 | 404.6 | 27.2 | 517.6 | CD561266 | CD561266 | CD561266 | 240 | 275.8 | 18.6 | | |
| 168 | 403.2 | 27.2 | 527.7 | H41343 | H41343 | H41343 | 241 | 274.8 | 18.5 | | |
| 169 | 400.4 | 27.0 | 513.2 | N28515 | N28515 | N28515 | 242 | 272 | 18.3 | | |
| 170 | 395.2 | 26.6 | 722.2 | BB980311 | BB980311 | BB980311 | 243 | 271.8 | 18.3 | | |
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|-----|-------|------|------|---|----------|---------------------|-----|-------|------|-----|---|-----------|---------------------|
| 244 | 271.8 | 18.3 | 640 | 4 | B1390073 | B1390073 ppp1c.pk0 | 317 | 228.6 | 15.4 | 442 | 4 | B1875973 | B1875973 f165903.y |
| 245 | 271.8 | 18.3 | 672 | 5 | B0277862 | B0277862 603577269 | 318 | 228.2 | 15.4 | 619 | 4 | B1876510 | B1876510 f185c09.y |
| 246 | 270.6 | 18.2 | 669 | 4 | B1103099 | B1103099 602889328 | 319 | 224.8 | 15.1 | 516 | 7 | C0799071 | C0799071 AGENCOURT |
| 247 | 270.2 | 18.2 | 542 | 4 | BG709745 | BG709745 pgl1n.pk0 | 320 | 224 | 15.1 | 265 | 1 | A1527943 | A1527943 u138a12.y |
| 248 | 270.2 | 18.2 | 667 | 5 | B0280025 | B0280025 603599847 | 321 | 222.8 | 15.0 | 928 | 4 | B1090937 | B1090937 602859175 |
| 249 | 270 | 18.2 | 378 | 2 | B8847268 | B8847268 BB847268 | 322 | 218.2 | 14.7 | 771 | 7 | CV111128 | CV111128 AGENCOURT |
| 250 | 268.8 | 18.1 | 313 | 1 | A1527941 | A1527941 u138a10.y | 323 | 216.8 | 14.6 | 433 | 3 | H49932 | H49932 y025a02.r1 |
| 251 | 267.8 | 18.0 | 839 | 5 | B0107229 | B0107229 603110585 | 324 | 213.4 | 14.4 | 710 | 2 | BF937885 | BF937885 fme9h08.y |
| 252 | 267.6 | 18.0 | 511 | 1 | AA821445 | AA821445 v625f01.r | 325 | 210.4 | 14.2 | 685 | 9 | CC519350 | CC519350 CH240.366 |
| 253 | 267.2 | 18.0 | 365 | 5 | BY230544 | BY230544 BY230544 | 326 | 210.2 | 14.2 | 302 | 2 | BB565259 | BB565259 BB565259 |
| 254 | 266.2 | 17.9 | 395 | 5 | BY025499 | BY025499 BY025499 | 327 | 209 | 14.1 | 727 | 6 | CB593062 | CB593062 AGENCOURT |
| 255 | 265.4 | 17.9 | 363 | 5 | BY036259 | BY036259 BY036259 | 328 | 209 | 14.1 | 860 | 6 | CD253668 | CD253668 AGENCOURT |
| 256 | 263.2 | 17.7 | 1217 | 2 | B8535866 | B8535866 601060567 | 329 | 209 | 14.1 | 881 | 7 | CF591853 | CF591853 AGENCOURT |
| 257 | 263.2 | 17.7 | 383 | 5 | BY023280 | BY023280 BY023280 | 330 | 209 | 14.1 | 892 | 6 | CB198304 | CB198304 AGENCOURT |
| 258 | 262 | 17.6 | 375 | 1 | AA110032 | AA110032 mp10b11.r | 331 | 207.4 | 14.0 | 653 | 7 | CN084451 | CN084451 EC2BBA24A |
| 259 | 260.8 | 17.6 | 704 | 7 | CO505714 | CO505714 GGEZEB1.02 | 332 | 207.4 | 14.0 | 756 | 7 | CN075936 | CN075936 EC2BBA11A |
| 260 | 260 | 17.5 | 456 | 1 | AA657100 | AA657100 v823e12.r | 333 | 207.4 | 14.0 | 927 | 7 | CK441905 | CK441905 CR441905 |
| 261 | 259.2 | 17.5 | 391 | 5 | BY126248 | BY126248 BY126248 | 334 | 207 | 13.9 | 799 | 7 | CK363543 | CK363543 AGENCOURT |
| 262 | 258.8 | 17.4 | 377 | 5 | BY025812 | BY025812 BY025812 | 335 | 206.6 | 13.9 | 764 | 7 | CF271342 | CF271342 AGENCOURT |
| 263 | 257.8 | 17.4 | 293 | 9 | AY414947 | AY414947 Mus_muscu | 336 | 206.6 | 13.9 | 942 | 7 | CK803918 | CK803918 AGENCOURT |
| 264 | 257.8 | 17.4 | 691 | 5 | B0302599 | B0302599 603737887 | 337 | 205.8 | 13.9 | 909 | 7 | CO801966 | CO801966 AGENCOURT |
| 265 | 256.8 | 17.3 | 356 | 5 | BY235679 | BY235679 BY235679 | 338 | 205.2 | 13.8 | 264 | 2 | BB864814 | BB864814 BB864814 |
| 266 | 255.8 | 17.2 | 285 | 1 | AA339850 | AA339850 EST14971 | 339 | 205 | 13.8 | 832 | 7 | CK797080 | CK797080 AGENCOURT |
| 267 | 254.2 | 17.1 | 680 | 5 | B0454572 | B0454572 603767910 | 340 | 201.8 | 13.6 | 929 | 7 | CN325880 | CN325880 AGENCOURT |
| 268 | 251 | 16.9 | 379 | 5 | B0029649 | B0029649 UI-H-DT0- | 341 | 197 | 13.3 | 737 | 7 | CO581559 | CO581559 ILLUMIGEN |
| 269 | 248 | 16.7 | 360 | 1 | A1358973 | A1358973 GY19f08.x | 342 | 196.2 | 13.2 | 803 | 2 | BF106155 | BF106155 ILUMIGEN |
| 270 | 245 | 16.5 | 718 | 7 | CV118715 | CV118715 AGENCOURT | 343 | 196 | 13.2 | 410 | 1 | A1263238 | A1263238 g236h07.x |
| 271 | 245 | 16.5 | 772 | 7 | CF347849 | CF347849 AGENCOURT | 344 | 195.6 | 13.2 | 388 | 6 | C88427 | C88427 C88427 Carp |
| 272 | 244.2 | 16.4 | 354 | 5 | BY232254 | BY232254 BY232254 | 345 | 195.2 | 13.1 | 760 | 7 | CN057491 | CN057491 Salmande |
| 273 | 243.8 | 16.4 | 302 | 6 | BY783751 | BY783751 BY783751 | 346 | 193.8 | 13.1 | 554 | 1 | AJ709348 | AJ709348 AJ709348 |
| 274 | 243.4 | 16.4 | 670 | 7 | CV490080 | CV490080 AGENCOURT | 347 | 193.8 | 13.1 | 558 | 2 | BE856263 | BE856263 7E91e02.x |
| 275 | 243.4 | 16.4 | 708 | 7 | CN512587 | CN512587 AGENCOURT | 348 | 193.8 | 13.1 | 647 | 1 | AV715206 | AV715206 AV715206 |
| 276 | 243.4 | 16.4 | 784 | 7 | CP998223 | CP998223 AGENCOURT | 349 | 192.8 | 13.0 | 638 | 4 | BG435747 | BG435747 602506851 |
| 277 | 243.4 | 16.4 | 790 | 7 | CK017959 | CK017959 AGENCOURT | 350 | 192.8 | 13.0 | 647 | 6 | CD521600 | CD521600 AGENCOURT |
| 278 | 243.4 | 16.4 | 844 | 7 | CK363313 | CK363313 AGENCOURT | 351 | 192.6 | 13.0 | 819 | 6 | CD521694 | CD521694 AGENCOURT |
| 279 | 242.4 | 16.4 | 853 | 7 | CN176901 | CN176901 AGENCOURT | 352 | 192.2 | 12.9 | 519 | 1 | AA482171 | AA482171 aa53d12.r |
| 280 | 242.4 | 16.3 | 583 | 5 | BP349530 | BP349530 BP349530 | 353 | 192.2 | 12.9 | 535 | 4 | BF439336 | BF439336 UI-E-C01- |
| 281 | 241.8 | 16.3 | 566 | 4 | BI876477 | BI876477 f172h06.y | 354 | 192.2 | 12.9 | 549 | 2 | BF438657 | BF438657 nab89e05 |
| 282 | 241.8 | 16.3 | 567 | 4 | BI875861 | BI875861 f164a03.y | 355 | 192.2 | 12.9 | 560 | 5 | B0198346 | B0198346 DCBGMF07 |
| 283 | 241.8 | 16.3 | 575 | 1 | A1722021 | A1722021 f618d09.y | 356 | 192.2 | 12.9 | 574 | 6 | CA307834 | CA307834 UI-H-FT1- |
| 284 | 241.8 | 16.3 | 579 | 2 | BF157393 | BF157393 f149g06.y | 357 | 192.2 | 12.9 | 604 | 2 | AM951219 | AM951219 EST363289 |
| 285 | 241.8 | 16.3 | 602 | 4 | BM315713 | BM315713 f6w4c03.y | 358 | 192.2 | 12.9 | 647 | 7 | CK004698 | CK004698 AGENCOURT |
| 286 | 241.8 | 16.3 | 622 | 2 | AW343367 | AW343367 f176f12.y | 359 | 192.2 | 12.9 | 649 | 5 | B0929744 | B0929744 AGENCOURT |
| 287 | 241.8 | 16.3 | 637 | 2 | AW343018 | AW343018 f172c03.y | 360 | 192.2 | 12.9 | 653 | 1 | AV735265 | AV735265 AV735265 |
| 288 | 241.8 | 16.3 | 655 | 5 | BM889951 | BM889951 f6y3c06.y | 361 | 192.2 | 12.9 | 660 | 6 | CD522794 | CD522794 AGENCOURT |
| 289 | 241.8 | 16.3 | 680 | 4 | BM777661 | BM777661 f6y3f09.y | 362 | 192.2 | 12.9 | 676 | 1 | AV733822 | AV733822 AGENCOURT |
| 290 | 241.8 | 16.3 | 733 | 4 | BI888826 | BI888826 ZF637-2-0 | 363 | 192.2 | 12.9 | 692 | 5 | B0929850 | B0929850 AGENCOURT |
| 291 | 241.8 | 16.3 | 747 | 7 | CV490839 | CV490839 AGENCOURT | 364 | 192.2 | 12.9 | 705 | 1 | AV714777 | AV714777 AGENCOURT |
| 292 | 241.8 | 16.3 | 791 | 7 | CV120378 | CV120378 AGENCOURT | 365 | 192.2 | 12.9 | 710 | 1 | AV714667 | AV714667 AGENCOURT |
| 293 | 241.8 | 16.3 | 819 | 7 | CN020307 | CN020307 AGENCOURT | 366 | 192.2 | 12.9 | 736 | 1 | AV714455 | AV714455 AGENCOURT |
| 294 | 241.8 | 16.3 | 841 | 7 | CO814959 | CO814959 AGENCOURT | 367 | 191.8 | 12.9 | 642 | 1 | AV715253 | AV715253 AGENCOURT |
| 295 | 241.8 | 16.3 | 855 | 7 | CO824858 | CO824858 AGENCOURT | 368 | 191.4 | 12.9 | 732 | 2 | BF527057 | BF527057 602039969 |
| 296 | 241.8 | 16.3 | 918 | 7 | CO925434 | CO925434 AGENCOURT | 369 | 191.2 | 12.9 | 566 | 1 | A1147216 | A1147216 g489C10.x |
| 297 | 241.8 | 16.3 | 982 | 7 | CN832815 | CN832815 AGENCOURT | 370 | 190.6 | 12.8 | 556 | 5 | B0198397 | B0198397 DCBGMAL2 |
| 298 | 241.4 | 16.3 | 541 | 5 | B0285026 | B0285026 faa17e08 | 371 | 190.6 | 12.8 | 593 | 8 | BU199056 | BU199056 DCBVC09 |
| 299 | 241.4 | 16.3 | 597 | 4 | BM755975 | BM755975 f6y19d07.y | 372 | 190.6 | 12.8 | 638 | 6 | CD521795 | CD521795 AGENCOURT |
| 300 | 241.2 | 16.2 | 791 | 7 | CN021410 | CN021410 AGENCOURT | 373 | 190.6 | 12.8 | 639 | 1 | AV717067 | AV717067 AGENCOURT |
| 301 | 241 | 16.2 | 936 | 7 | CN179527 | CN179527 AGENCOURT | 374 | 190.6 | 12.8 | 659 | 1 | AV717298 | AV717298 AGENCOURT |
| 302 | 240.4 | 16.2 | 551 | 2 | AM174473 | AM174473 f143f04.y | 375 | 190.6 | 12.8 | 665 | 1 | AV715034 | AV715034 AGENCOURT |
| 303 | 240.2 | 16.2 | 554 | 2 | AM422967 | AM422967 f166f01.y | 376 | 190.6 | 12.8 | 697 | 1 | AV717754 | AV717754 AGENCOURT |
| 304 | 240.2 | 16.2 | 612 | 2 | AM134031 | AM134031 f114f08.y | 377 | 190.6 | 12.8 | 698 | 7 | CN094476 | CN094476 EC2BBA3DC |
| 305 | 240.2 | 16.2 | 647 | 7 | BM776472 | BM776472 f6y25b12.y | 378 | 190.6 | 12.8 | 700 | 6 | CD641977 | CD641977 AGENCOURT |
| 306 | 238.2 | 16.0 | 742 | 7 | CV119794 | CV119794 AGENCOURT | 379 | 190.6 | 12.8 | 710 | 1 | AV713498 | AV713498 AGENCOURT |
| 307 | 236.4 | 15.9 | 448 | 1 | AA206236 | AA206236 Zq54c06.r | 380 | 190.2 | 12.8 | 534 | 1 | AV716954 | AV716954 AGENCOURT |
| 308 | 235.8 | 15.9 | 859 | 7 | CO916637 | CO916637 AGENCOURT | 381 | 190.2 | 12.8 | 549 | 1 | AV707768 | AV707768 a635c03.x |
| 309 | 235 | 15.8 | 590 | 1 | A0176996 | A0176996 AU176996 | 382 | 189.4 | 12.8 | 707 | 1 | A17076847 | A17076847 AGENCOURT |
| 310 | 234.4 | 15.8 | 417 | 5 | BY061227 | BY061227 BU061227 | 383 | 189.4 | 12.8 | 534 | 1 | A1707931 | A1707931 a634f01.x |
| 311 | 234.4 | 15.7 | 323 | 4 | BG062669 | BG062669 L0956807- | 384 | 189.4 | 12.8 | 558 | 6 | CB053926 | CB053926 NISC_gm01 |
| 312 | 233.6 | 15.7 | 709 | 5 | BX082727 | BX082727 BX082727 | 385 | 189.4 | 12.8 | 596 | 6 | CB053925 | CB053925 NISC_gm01 |
| 313 | 233.2 | 15.7 | 727 | 5 | B0042180 | B0042180 UI-M-E00- | 386 | 189.4 | 12.8 | 598 | 6 | CD521003 | CD521003 AGENCOURT |
| 314 | 231.4 | 15.6 | 685 | 5 | B0279023 | B0279023 603601345 | 387 | 189.4 | 12.8 | 603 | 1 | AV715633 | AV715633 AGENCOURT |
| 315 | 231.2 | 15.6 | 494 | 4 | BG062759 | BG062759 L0957E03- | 388 | 189.4 | 12.8 | 648 | 1 | AV714479 | AV714479 AGENCOURT |
| 316 | 229.6 | 15.5 | 527 | 4 | BG738554 | BG738554 f6p0a07.y | 389 | 189.4 | 12.8 | 654 | 1 | AV715129 | AV715129 AGENCOURT |

| | | | | | | | | | | | | | |
|-----|-------|------|------|---|----------|-----------|-----------|-----|-------|------|------|---|-----------|
| 390 | 189.4 | 12.8 | 721 | 1 | AV716806 | AV716806 | AV716806 | 463 | 177.2 | 11.9 | 401 | 2 | BF039286 |
| 391 | 189 | 12.7 | 584 | 1 | AV713748 | AV713748 | AV713748 | 464 | 177 | 11.9 | 613 | 1 | AV735626 |
| 392 | 189 | 12.7 | 590 | 1 | AV715528 | AV715528 | AV715528 | 465 | 176.8 | 11.9 | 457 | 4 | BI244719 |
| 393 | 189 | 12.7 | 706 | 1 | AV716279 | AV716279 | AV716279 | 466 | 175.6 | 11.8 | 557 | 4 | AA854452 |
| 394 | 189 | 12.7 | 707 | 1 | AV716933 | AV716933 | AV716933 | 467 | 173.4 | 11.7 | 474 | 5 | BO037559 |
| 395 | 188.4 | 12.7 | 419 | 9 | AV421431 | Homo sapi | AV421431 | 468 | 173.4 | 11.7 | 594 | 5 | BI9198503 |
| 396 | 188.4 | 12.7 | 588 | 5 | BU198551 | DCBVCV04 | CEP271352 | 469 | 173.2 | 11.7 | 580 | 5 | BP331936 |
| 397 | 188.2 | 12.7 | 759 | 7 | BI555766 | AV714543 | AV714543 | 470 | 172.6 | 11.6 | 672 | 7 | CN834368 |
| 398 | 188 | 12.7 | 528 | 4 | BI555766 | AV714543 | AV714543 | 471 | 171.6 | 11.6 | 619 | 5 | BU199128 |
| 399 | 188 | 12.7 | 731 | 1 | BU198757 | DCBVC06 | CEP271352 | 472 | 170.8 | 11.5 | 386 | 1 | AA372010 |
| 400 | 187.6 | 12.6 | 935 | 5 | BU198757 | AV714543 | AV714543 | 473 | 170.8 | 11.5 | 529 | 1 | AA372010 |
| 401 | 187.6 | 12.6 | 886 | 6 | CEB97534 | AGENCOURT | CEB97534 | 474 | 170.6 | 11.5 | 531 | 4 | BM366826 |
| 402 | 187.4 | 12.6 | 558 | 2 | BE855886 | AGENCOURT | BE855886 | 475 | 170.6 | 11.5 | 627 | 5 | BM366826 |
| 403 | 187.4 | 12.6 | 648 | 1 | AV715393 | AA256092 | AA256092 | 476 | 170.6 | 11.5 | 631 | 5 | BM366826 |
| 404 | 186.6 | 12.6 | 501 | 1 | AA256092 | AA256092 | AA256092 | 477 | 170.6 | 11.5 | 631 | 5 | BM366826 |
| 405 | 186.4 | 12.6 | 451 | 1 | AV713104 | AV713104 | AV713104 | 478 | 168.2 | 11.3 | 376 | 4 | BO711587 |
| 406 | 186 | 12.5 | 186 | 1 | AA782827 | AV713104 | AV713104 | 479 | 168.2 | 11.3 | 881 | 7 | CN978034 |
| 407 | 185.8 | 12.5 | 186 | 1 | AA782827 | AV713104 | AV713104 | 480 | 167.4 | 11.3 | 449 | 5 | WE69953 |
| 408 | 185.8 | 12.5 | 438 | 1 | AL916193 | AL916193 | AL916193 | 481 | 166 | 11.2 | 586 | 5 | BP112693 |
| 409 | 185.8 | 12.5 | 437 | 1 | AV706038 | AV706038 | AV706038 | 482 | 165.8 | 11.2 | 719 | 6 | CA465342 |
| 410 | 185.6 | 12.5 | 1020 | 6 | CD521829 | AV715156 | AV715156 | 483 | 165 | 11.2 | 492 | 1 | AI133670 |
| 411 | 185.2 | 12.5 | 600 | 6 | CA529800 | CA529800 | CA529800 | 484 | 164.6 | 11.1 | 547 | 6 | CB489425 |
| 412 | 185.2 | 12.5 | 735 | 1 | AV046029 | AV046029 | AV046029 | 485 | 164.6 | 11.1 | 547 | 6 | CB489425 |
| 413 | 185.2 | 12.5 | 874 | 3 | AK006562 | AK006562 | AK006562 | 486 | 163.6 | 11.0 | 528 | 4 | BI290741 |
| 414 | 185.2 | 12.5 | 875 | 3 | AK006562 | AK006562 | AK006562 | 487 | 163.6 | 11.0 | 389 | 5 | BY088751 |
| 415 | 184.8 | 12.4 | 395 | 2 | CF124786 | CF124786 | CF124786 | 488 | 163.6 | 10.9 | 528 | 4 | BI290741 |
| 416 | 184.8 | 12.4 | 469 | 2 | BF921332 | MR2-NT013 | BF921332 | 489 | 163.6 | 10.9 | 823 | 2 | AY421432 |
| 417 | 184.6 | 12.4 | 555 | 2 | AW951231 | AW951231 | AW951231 | 490 | 160.8 | 10.8 | 795 | 7 | CO805806 |
| 418 | 184.2 | 12.4 | 467 | 4 | BM432904 | LOE7EB3.A | BM432904 | 491 | 160.6 | 10.8 | 543 | 7 | N32605 |
| 419 | 184.2 | 12.4 | 482 | 5 | BU198959 | BU198959 | BU198959 | 492 | 159.8 | 10.7 | 769 | 7 | WE8116 |
| 420 | 184.2 | 12.4 | 524 | 1 | AV662884 | AV662884 | AV662884 | 493 | 159 | 10.7 | 864 | 3 | CE271197 |
| 421 | 184.2 | 12.4 | 544 | 2 | AV652741 | AA653147 | AA653147 | 494 | 158.6 | 10.7 | 780 | 3 | CR720427 |
| 422 | 184.2 | 12.4 | 559 | 7 | CO880878 | BOVgen.09 | CO880878 | 495 | 157.6 | 10.6 | 1218 | 3 | CR723168 |
| 423 | 184.2 | 12.4 | 590 | 7 | CO880878 | BOVgen.09 | CO880878 | 496 | 157.6 | 10.6 | 421 | 1 | AA045718 |
| 424 | 184.2 | 12.4 | 595 | 7 | CR451547 | CR451547 | CR451547 | 497 | 157 | 10.6 | 803 | 7 | CO549829 |
| 425 | 184.2 | 12.4 | 669 | 7 | CO886811 | BOVgen.15 | CO886811 | 498 | 156.4 | 10.5 | 911 | 7 | CO549829 |
| 426 | 183.6 | 12.4 | 765 | 4 | BI685218 | BI685218 | BI685218 | 499 | 155.4 | 10.5 | 440 | 1 | AA041906 |
| 427 | 183.6 | 12.4 | 772 | 6 | CB601178 | AA754746 | AA754746 | 500 | 154.6 | 10.4 | 649 | 7 | AA046385 |
| 428 | 183.6 | 12.4 | 772 | 6 | CB601178 | AA754746 | AA754746 | 501 | 154.6 | 10.4 | 649 | 7 | AA046385 |
| 429 | 183.4 | 12.4 | 220 | 1 | AA740657 | AA740657 | AA740657 | 502 | 154 | 10.4 | 487 | 1 | AA946905 |
| 430 | 182.8 | 12.3 | 563 | 1 | AV713775 | AV713775 | AV713775 | 503 | 153.6 | 10.3 | 566 | 1 | AI566824 |
| 431 | 182.8 | 12.3 | 920 | 1 | AV713775 | AV713775 | AV713775 | 504 | 153.2 | 10.3 | 408 | 1 | AA245272 |
| 432 | 182.6 | 12.3 | 918 | 6 | CB997566 | AGENCOURT | CB997566 | 505 | 152.8 | 10.3 | 207 | 5 | BO369020 |
| 433 | 182.6 | 12.3 | 546 | 1 | AV712111 | AV712111 | AV712111 | 506 | 152.4 | 10.3 | 207 | 5 | BO369020 |
| 434 | 182.6 | 12.3 | 713 | 6 | CB529249 | UI-H-FP2- | CB529249 | 507 | 152.4 | 10.3 | 207 | 5 | BO369020 |
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| 436 | 182.2 | 12.3 | 495 | 4 | BM432904 | LOE7EB3.A | BM432904 | 509 | 150.8 | 10.2 | 187 | 2 | AW743164 |
| 437 | 182.2 | 12.3 | 527 | 4 | BM432904 | LOE7EB3.A | BM432904 | 510 | 150.8 | 10.2 | 538 | 4 | BI325080 |
| 438 | 182.2 | 12.3 | 531 | 4 | BM432904 | LOE7EB3.A | BM432904 | 511 | 150.6 | 10.1 | 470 | 1 | AI147271 |
| 439 | 182.2 | 12.3 | 531 | 4 | BM432904 | LOE7EB3.A | BM432904 | 512 | 150.2 | 10.1 | 612 | 7 | CV027982 |
| 440 | 182 | 12.3 | 647 | 4 | BI278279 | UI-R-CY0- | BI278279 | 513 | 149.6 | 10.1 | 413 | 4 | BM287376 |
| 441 | 181.6 | 12.2 | 461 | 1 | AV734963 | AV734963 | AV734963 | 514 | 149.6 | 10.1 | 569 | 1 | AI308997 |
| 442 | 181.6 | 12.2 | 835 | 5 | BU963161 | AGENCOURT | BU963161 | 515 | 148.4 | 10.0 | 480 | 4 | BM672323 |
| 443 | 181.4 | 12.2 | 594 | 1 | AV714476 | AV714476 | AV714476 | 516 | 148.4 | 10.0 | 480 | 4 | BM672323 |
| 444 | 181.2 | 12.2 | 565 | 2 | BF940967 | BF940967 | BF940967 | 517 | 147.7 | 9.9 | 440 | 6 | CD285051 |
| 445 | 181 | 12.2 | 454 | 2 | BF600660 | 265408.MA | BF600660 | 518 | 147 | 9.9 | 451 | 1 | AA169646 |
| 446 | 181 | 12.2 | 476 | 4 | BM636675 | BM636675 | BM636675 | 519 | 146.6 | 9.9 | 485 | 1 | AA169646 |
| 447 | 181 | 12.2 | 630 | 6 | CB480047 | CB480047 | CB480047 | 520 | 145.6 | 9.8 | 470 | 1 | AI057299 |
| 448 | 181 | 12.2 | 633 | 6 | CB480047 | CB480047 | CB480047 | 521 | 145.6 | 9.8 | 470 | 1 | AI057299 |
| 449 | 180.4 | 12.1 | 419 | 9 | AV421433 | Mus muscu | AV421433 | 522 | 145.4 | 9.8 | 444 | 1 | AI052165 |
| 450 | 180 | 12.1 | 439 | 1 | AA878897 | AA878897 | AA878897 | 523 | 145.4 | 9.8 | 450 | 1 | AI094373 |
| 451 | 180 | 12.1 | 446 | 1 | AV734741 | AV734741 | AV734741 | 524 | 144.8 | 9.8 | 477 | 5 | BY447302 |
| 452 | 179.6 | 12.1 | 996 | 6 | BY706281 | BY706281 | BY706281 | 525 | 144.4 | 9.7 | 513 | 1 | AV756012 |
| 453 | 179.6 | 12.1 | 785 | 5 | BU962218 | AGENCOURT | BU962218 | 526 | 143.6 | 9.7 | 726 | 7 | CN441830 |
| 454 | 178.6 | 12.0 | 640 | 1 | AV715059 | AV715059 | AV715059 | 527 | 143.6 | 9.7 | 371 | 5 | BY172067 |
| 455 | 178.6 | 12.0 | 753 | 6 | CH591949 | AGENCOURT | CH591949 | 528 | 143.6 | 9.7 | 726 | 7 | CN441830 |
| 456 | 178.4 | 12.0 | 520 | 2 | AW028268 | AW028268 | AW028268 | 529 | 143 | 9.6 | 338 | 5 | BO708258 |
| 457 | 178.4 | 12.0 | 560 | 2 | BF472539 | BF472539 | BF472539 | 530 | 143 | 9.6 | 957 | 5 | BY102285 |
| 458 | 178 | 12.0 | 563 | 1 | AA923155 | AA923155 | AA923155 | 531 | 142.4 | 9.6 | 338 | 5 | BY102285 |
| 459 | 177.8 | 12.0 | 536 | 7 | N32593 | N32593 | N32593 | 532 | 142 | 9.6 | 449 | 1 | AI083862 |
| 460 | 177.6 | 12.0 | 655 | 7 | CN984526 | CN984526 | CN984526 | 533 | 141.4 | 9.5 | 449 | 1 | AI083862 |
| 461 | 177.6 | 12.0 | 787 | 7 | CN977704 | CN977704 | CN977704 | 534 | 140.6 | 9.5 | 418 | 5 | BY277446 |
| 462 | 177.4 | 11.9 | 531 | 1 | AI423895 | AI423895 | AI423895 | 535 | 140.6 | 9.5 | 418 | 5 | BY277446 |

| | | | | | | | | | | | | |
|-------|-------|-----|------|---|----------|----------------------|-----|-------|-----|-----|---|------------|
| 536 | 140.6 | 9.5 | 737 | 4 | BI690781 | BI690781 603312104 | 609 | 119.4 | 8.0 | 373 | 7 | H94792 |
| C 537 | 140.4 | 9.5 | 180 | 5 | BQ368640 | BQ368640 PM3-GN051 | 610 | 119.4 | 8.0 | 526 | 4 | BG500722 |
| C 538 | 139.6 | 9.4 | 447 | 7 | W57975 | W57975 zdl18905..81 | 611 | 119.2 | 8.0 | 386 | 7 | CN082453 |
| 539 | 139.4 | 9.4 | 352 | 5 | BY283333 | BY283333 BX283333 | 612 | 119 | 8.0 | 464 | 1 | AV712779 |
| 540 | 139.2 | 9.4 | 369 | 7 | FJ36997 | FJ36997 HSPD35004 H | 613 | 118.8 | 8.0 | 633 | 7 | CK988879 |
| 541 | 138.8 | 9.3 | 455 | 7 | H78962 | H78962 yu123c06..r1 | 614 | 118.8 | 8.0 | 633 | 7 | CK988911 |
| C 542 | 137.8 | 9.3 | 422 | 1 | AA255894 | AA255894 z829b06..8 | 615 | 118.8 | 8.0 | 633 | 7 | CK989205 |
| 543 | 137.6 | 9.3 | 351 | 7 | F25751 | F25751 HSPD12943 | 616 | 118 | 7.9 | 199 | 2 | BB565425 |
| C 544 | 137.6 | 9.3 | 444 | 1 | AI081516 | AI081516 on04e06..x | 617 | 117.6 | 7.9 | 669 | 6 | CB500992 |
| C 545 | 137.6 | 9.3 | 867 | 5 | BU938900 | BU938900 AGENCOURT | 618 | 117.4 | 7.9 | 217 | 2 | AW795992 |
| C 546 | 137.4 | 9.3 | 262 | 5 | BU074012 | BU074012 fz34c01..x | 619 | 116 | 7.8 | 717 | 7 | CN837729 |
| C 547 | 136.6 | 9.2 | 417 | 1 | AA688011 | AA688011 nv16d03..8 | 620 | 115.2 | 7.8 | 403 | 2 | BB689241 |
| C 548 | 136.4 | 9.2 | 421 | 5 | BY260254 | BY260254 BY260254 | 621 | 115 | 7.7 | 422 | 2 | BF712127 |
| C 549 | 136.2 | 9.2 | 380 | 2 | BE702457 | BE702457 RCL-NN106 | 622 | 114.2 | 7.7 | 423 | 2 | BE947563 |
| C 550 | 136 | 9.2 | 438 | 1 | AI031523 | AI031523 gm27a07..x | 623 | 114.2 | 7.7 | 709 | 1 | AI046602 |
| C 551 | 135.6 | 9.1 | 297 | 1 | AI597484 | AI597484 v167c08..x | 624 | 113.8 | 7.7 | 536 | 1 | AV735697 |
| C 552 | 135.6 | 9.1 | 462 | 7 | W67362 | W67362 z40c011..r1 | 625 | 113.2 | 7.6 | 391 | 1 | AA862940 |
| C 553 | 134.4 | 9.1 | 445 | 1 | AI860218 | AI860218 wk98f01..x | 626 | 113.2 | 7.6 | 489 | 7 | H91762 |
| 554 | 134.2 | 9.0 | 297 | 1 | AA348982 | AA348982 EST15526 | 627 | 112.6 | 7.6 | 417 | 5 | BY453236 |
| 555 | 133.8 | 9.0 | 786 | 6 | CD299124 | CD299124 AGENCOURT | 628 | 111.4 | 7.5 | 325 | 7 | CO818216 |
| 556 | 133.6 | 9.0 | 362 | 2 | BF522081 | BF522081 UI-R-YO-a | 629 | 111.2 | 7.5 | 252 | 2 | BB600459 |
| 557 | 133.2 | 9.0 | 851 | 2 | BE677828 | BE677828 602085342 | 630 | 111 | 7.5 | 427 | 2 | BE702461 |
| C 558 | 133 | 9.0 | 436 | 1 | AI336788 | AI336788 qh47d10..x | 631 | 110.8 | 7.5 | 416 | 2 | BB67981 |
| 559 | 131.6 | 8.9 | 1100 | 5 | BG827770 | BG827770 602751875 | 632 | 110.4 | 7.4 | 426 | 7 | W69954 |
| C 560 | 131.4 | 8.8 | 409 | 5 | BP430759 | BP430759 BP430759 | 633 | 110 | 7.4 | 110 | 7 | T12552 |
| C 561 | 131.4 | 8.8 | 441 | 1 | AI472171 | AI472171 t186d08..x | 634 | 109.6 | 7.4 | 274 | 2 | BB608708 |
| C 562 | 131.4 | 8.8 | 457 | 2 | AM001967 | AM001967 wt82d05..x | 635 | 109.4 | 7.4 | 672 | 6 | CD292736 |
| 563 | 131.4 | 8.8 | 510 | 1 | AV739645 | AV739645 AV739645 | 636 | 108.6 | 7.3 | 479 | 7 | W67118 |
| 564 | 131.4 | 8.8 | 556 | 5 | BU198266 | BU198266 DCBCOF2 | 637 | 107.2 | 7.2 | 419 | 6 | CD727031 |
| 565 | 131.4 | 8.8 | 571 | 1 | AV714391 | AV714391 AV714391 | 638 | 107.2 | 7.2 | 435 | 6 | CD727179 |
| 566 | 131.4 | 8.8 | 572 | 6 | CD249922 | CD249922 AGENCOURT | 639 | 107.2 | 7.2 | 460 | 6 | CD731805 |
| 567 | 131.4 | 8.8 | 714 | 1 | AV717839 | AV717839 AV717839 | 640 | 106.8 | 7.2 | 711 | 6 | CD323422 |
| 568 | 131.4 | 8.8 | 763 | 1 | AV757157 | AV757157 AV757157 | 641 | 106.6 | 7.2 | 309 | 2 | BB600132 |
| 569 | 131.4 | 8.8 | 790 | 4 | BG777669 | BG777669 602665283 | 642 | 106.4 | 7.2 | 381 | 5 | BU198849 |
| 570 | 131.4 | 8.8 | 858 | 6 | CD049027 | CD049027 AGENCOURT | 643 | 106 | 7.1 | 585 | 4 | BM842172 |
| 571 | 130.2 | 8.8 | 495 | 1 | AV713156 | AV713156 AV713156 | 644 | 105.8 | 7.1 | 245 | 1 | AI914826 |
| 572 | 130 | 8.8 | 436 | 7 | CF384688 | CF384688 caa09h05.. | 645 | 105.6 | 7.1 | 296 | 7 | W67117 |
| 573 | 129.8 | 8.7 | 331 | 5 | BY346874 | BY346874 BY346874 | 646 | 105.6 | 7.1 | 386 | 1 | AA618511 |
| 574 | 129.8 | 8.7 | 464 | 2 | AM315225 | AM315225 12360 MAR | 647 | 105.6 | 7.1 | 711 | 1 | AV712188 |
| 575 | 129.8 | 8.7 | 592 | 1 | AV717608 | AV717608 AV717608 | 648 | 105.4 | 7.1 | 295 | 2 | AA421829 |
| C 576 | 129.6 | 8.7 | 431 | 7 | CF106360 | CF106360 ma106a08.. | 649 | 104.4 | 7.0 | 497 | 1 | AA857142 |
| 577 | 129 | 8.7 | 462 | 7 | CO613989 | CO613989 DG9-13002 | 650 | 104.4 | 7.0 | 519 | 4 | BM840025 |
| 578 | 128.8 | 8.6 | 375 | 1 | AI836903 | AI836903 y183f05..r1 | 651 | 104.4 | 7.0 | 536 | 4 | BM761792 |
| 579 | 128.4 | 8.6 | 657 | 2 | BG612433 | BG612433 602640203 | 652 | 104.4 | 7.0 | 596 | 4 | BM842904 |
| 580 | 128.4 | 8.6 | 293 | 2 | BB601345 | BB601345 BB601345 | 653 | 104.2 | 7.0 | 299 | 5 | BY345636 |
| 581 | 127.2 | 8.6 | 869 | 4 | BG501051 | BG501051 602846459 | 654 | 103.2 | 6.9 | 393 | 1 | AV716687 |
| 582 | 127 | 8.6 | 265 | 7 | CN264069 | CN264069 170004243 | 655 | 103.2 | 6.9 | 720 | 6 | CB591084 |
| C 583 | 126.8 | 8.5 | 744 | 7 | CN075935 | CN075935 EC2BBA11A | 656 | 103 | 6.9 | 238 | 7 | W21034 |
| 584 | 125.8 | 8.5 | 265 | 7 | CN264069 | CN264069 170004243 | 657 | 102.6 | 6.9 | 269 | 2 | BB308721 |
| 585 | 125.6 | 8.5 | 210 | 5 | BY130246 | BY130246 BY130246 | 658 | 102.6 | 6.9 | 501 | 5 | BQ427081 |
| C 586 | 125.6 | 8.5 | 792 | 2 | BM924843 | BM924843 BX924843 | 659 | 101.6 | 6.8 | 769 | 7 | CN840497 |
| 587 | 125.4 | 8.4 | 418 | 2 | AM057565 | AM057565 wy60h01..x | 660 | 100.2 | 6.7 | 392 | 5 | BY419579 |
| C 588 | 125 | 8.4 | 405 | 1 | AA171641 | AA171641 z094c03..x | 661 | 100 | 6.7 | 243 | 1 | AU059421 |
| 589 | 124.4 | 8.4 | 346 | 6 | CA383795 | CA383795 6640404 NC | 662 | 99.8 | 6.7 | 297 | 1 | AA339879 |
| C 590 | 124.2 | 8.4 | 410 | 1 | AA046323 | AA046323 zfi2h01..8 | 663 | 99.8 | 6.7 | 323 | 6 | CD334756 |
| C 591 | 124.2 | 8.4 | 411 | 7 | CK771111 | CK771111 959349 MA | 664 | 99.2 | 6.7 | 145 | 2 | BE171454 |
| C 592 | 124.2 | 8.4 | 772 | 7 | CK771110 | CK771110 959348 MA | 665 | 98.4 | 6.6 | 357 | 1 | AA954019 |
| C 593 | 123.8 | 8.3 | 428 | 1 | AI712935 | AI712935 UI-R-YO-a | 666 | 98.2 | 6.6 | 656 | 5 | BP515858 |
| C 594 | 123.4 | 8.3 | 513 | 5 | BO598626 | BO598626 MI-P-E4-a | 667 | 98 | 6.6 | 659 | 8 | AA2970400 |
| C 595 | 123.2 | 8.2 | 331 | 5 | BY346080 | BY346080 BY346080 | 668 | 97.8 | 6.6 | 211 | 2 | BF126F04.Y |
| 596 | 122.4 | 8.2 | 431 | 1 | BB848284 | BB848284 BB848284 | 669 | 97 | 6.5 | 685 | 7 | T79448 |
| 597 | 122.2 | 8.2 | 328 | 1 | AA495202 | AA495202 fz04b11..x | 670 | 97 | 6.5 | 405 | 7 | CN094475 |
| 598 | 122 | 8.2 | 267 | 2 | BB608654 | BB608654 BB608654 | 671 | 96.6 | 6.5 | 822 | 5 | BU962740 |
| 599 | 121.8 | 8.2 | 716 | 7 | CN833424 | CN833424 AGENCOURT | 672 | 96.4 | 6.5 | 822 | 5 | BU962740 |
| C 600 | 121.8 | 8.2 | 463 | 1 | AI607846 | AI607846 ub60a05..x | 673 | 95.8 | 6.5 | 304 | 6 | CD728766 |
| C 601 | 120.6 | 8.1 | 794 | 2 | BF213829 | BF213829 601848003 | 674 | 94.8 | 6.4 | 353 | 1 | AV735632 |
| 602 | 120.4 | 8.1 | 845 | 1 | AV755892 | AV755892 AV755892 | 675 | 94.2 | 6.3 | 451 | 7 | CN777509 |
| 603 | 120.4 | 8.1 | 338 | 5 | BY345789 | BY345789 BY345789 | 676 | 93.4 | 6.3 | 378 | 6 | BY620420 |
| 604 | 120.2 | 8.1 | 336 | 1 | AI129208 | AI129208 qf08e05..x | 677 | 92 | 6.2 | 398 | 4 | BF709612 |
| C 605 | 120.2 | 8.1 | 423 | 1 | AI206818 | AI206818 qf08e05..x | 678 | 91.8 | 6.2 | 325 | 2 | BI538912 |
| C 606 | 120.2 | 8.1 | 393 | 1 | AA045719 | AA045719 zk81e12..8 | 679 | 91.6 | 6.2 | 345 | 1 | AA977870 |
| C 607 | 120 | 8.1 | 426 | 1 | AI717269 | AI717269 UI-R-YO-a | 680 | 91 | 6.1 | 997 | 9 | CNS02X04 |
| C 608 | 119.8 | 8.1 | 426 | 1 | AI717269 | AI717269 UI-R-YO-a | 681 | 90.6 | 6.1 | 997 | 9 | CNS02X04 |
| 536 | 140.6 | 9.5 | 737 | 4 | BI690781 | BI690781 603312104 | 609 | 119.4 | 8.0 | 373 | 7 | H94792 |
| C 537 | 140.4 | 9.5 | 180 | 5 | BQ368640 | BQ368640 PM3-GN051 | 610 | 119.4 | 8.0 | 526 | 4 | BG500722 |
| C 538 | 139.6 | 9.4 | 447 | 7 | W57975 | W57975 zdl18905..81 | 611 | 119.2 | 8.0 | 386 | 7 | CN082453 |
| 539 | 139.4 | 9.4 | 352 | 5 | BY283333 | BY283333 BX283333 | 612 | 119 | 8.0 | 464 | 1 | AV712779 |
| 540 | 139.2 | 9.4 | 369 | 7 | FJ36997 | FJ36997 HSPD35004 H | 613 | 118.8 | 8.0 | 633 | 7 | CK988879 |
| 541 | 138.8 | 9.3 | 455 | 7 | H78962 | H78962 yu123c06..r1 | 614 | 118.8 | 8.0 | 633 | 7 | CK988911 |
| C 542 | 137.8 | 9.3 | 422 | 1 | AA255894 | AA255894 z829b06..8 | 615 | 118.8 | 8.0 | 633 | 7 | CK989205 |
| 543 | 137.6 | 9.3 | 351 | 7 | F25751 | F25751 HSPD12943 | 616 | 118 | 7.9 | 199 | 2 | BB565425 |
| C 544 | 137.6 | 9.3 | 444 | 1 | AI081516 | AI081516 on04e06..x | 617 | 117.6 | 7.9 | 669 | 6 | CB500992 |
| C 545 | 137.6 | 9.3 | 867 | 5 | BU938900 | BU938900 AGENCOURT | 618 | 117.4 | 7.9 | 217 | 2 | AW795992 |
| C 546 | 137.4 | 9.3 | 262 | 5 | BU074012 | BU074012 fz34c01..x | 619 | 116 | 7.8 | 717 | 7 | CN837729 |
| C 547 | 136.6 | 9.2 | 417 | 1 | AA688011 | AA688011 nv16d03..8 | 620 | 115.2 | 7.8 | 403 | 2 | BB689241 |
| C 548 | 136.4 | 9.2 | 421 | 5 | BY260254 | BY260254 BY260254 | 621 | 115 | 7.7 | 422 | 2 | BF712127 |
| C 549 | 136.2 | 9.2 | 380 | 2 | BE702457 | BE702457 RCL-NN106 | 622 | 114.2 | 7.7 | 423 | 2 | BE947563 |
| C 550 | 136 | 9.2 | 438 | 1 | AI031523 | AI031523 gm27a07..x | 623 | 114.2 | 7.7 | 709 | 1 | AI046602 |
| C 551 | 135.6 | 9.1 | 297 | 1 | AI597484 | AI597484 v167c08..x | 624 | 113.8 | 7.7 | 536 | 1 | AV735697 |
| C 552 | 135.6 | 9.1 | 462 | 7 | W67362 | W67362 z40c011..r1 | 625 | 113.2 | 7.6 | 391 | 1 | AA862940 |
| C 553 | 134.4 | 9.1 | 445 | 1 | AI860218 | AI860218 wk98f01..x | 626 | 113.2 | 7.6 | 489 | 7 | H91762 |
| 554 | 134.2 | 9.0 | 297 | 1 | AA348982 | AA348982 EST15526 | 627 | 112.6 | 7.6 | 417 | 5 | BY453236 |
| 555 | 133.8 | 9.0 | 786 | 6 | CD299124 | CD299124 AGENCOURT | 628 | 111.4 | 7.5 | 325 | 7 | CO818216 |
| 556 | 133.6 | 9.0 | 362 | 2 | BF522081 | BF522081 UI-R-YO-a | 629 | 111.2 | 7.5 | 252 | 2 | BB600459 |
| 557 | 133.2 | 9.0 | 851 | 2 | BE677828 | BE677828 602085342 | 630 | 111 | 7.5 | 427 | 2 | BE702461 |
| C 558 | 133 | 9.0 | 436 | 1 | AI336788 | AI336788 qh47d10..x | 631 | 110.8 | 7.5 | 416 | 2 | BB67981 |
| 559 | 131.6 | 8.9 | 1100 | 5 | | | | | | | | |

| | | | | | | | | | | | | |
|-------|------|-----|------|---|----------|------------|-----|------|-----|------|---|-----------|
| C 682 | 90.6 | 6.1 | 1029 | 4 | BF67777 | 602287670 | 755 | 70.6 | 4.8 | 747 | 7 | CK363896 |
| C 683 | 90.2 | 6.1 | 223 | 1 | AA742490 | mx20906.8 | 756 | 70.6 | 4.8 | 765 | 7 | CY073847 |
| C 684 | 90 | 6.1 | 407 | 1 | AI311729 | qo92908.x | 757 | 70.6 | 4.8 | 869 | 7 | COS56098 |
| C 685 | 89.4 | 6.0 | 345 | 1 | AI335182 | qo85f12.x | 758 | 69.4 | 4.7 | 725 | 4 | BI597567 |
| C 686 | 89.2 | 6.0 | 423 | 2 | AM153547 | f122h11.y | 759 | 69.4 | 4.7 | 740 | 7 | CY102637 |
| C 687 | 89 | 6.0 | 408 | 1 | AI648598 | tz56h07.x | 760 | 69.2 | 4.7 | 172 | 7 | R28847 |
| C 688 | 89 | 6.0 | 472 | 9 | CC598998 | OST265164 | 761 | 69.2 | 4.7 | 312 | 7 | CN028954 |
| C 689 | 89 | 6.0 | 477 | 6 | CD333918 | StPn536. | 762 | 69.2 | 4.7 | 645 | 1 | AUI39545 |
| C 690 | 88.8 | 6.0 | 318 | 7 | CN555613 | tae14g09. | 763 | 69 | 4.6 | 163 | 1 | AA216197 |
| C 691 | 87.6 | 5.9 | 329 | 2 | AM794442 | RC6-UM001 | 764 | 69 | 4.6 | 383 | 5 | BP195948 |
| C 692 | 87 | 5.9 | 288 | 2 | BB566814 | BB566814 | 765 | 69 | 4.6 | 654 | 5 | BP147700 |
| C 693 | 86.6 | 5.8 | 303 | 1 | AA046284 | 2k77d05.x | 766 | 69 | 4.6 | 673 | 7 | CN788776 |
| C 694 | 86.6 | 5.8 | 531 | 7 | CK988762 | BgHC-10.8 | 767 | 69 | 4.6 | 863 | 1 | AI545843 |
| C 695 | 86.6 | 5.8 | 362 | 2 | CF675310 | tac99a01. | 768 | 68.8 | 4.6 | 444 | 4 | BG688875 |
| C 696 | 86 | 5.8 | 529 | 2 | AM794640 | RC6-UM001 | 769 | 68.8 | 4.6 | 447 | 6 | CI69651 |
| C 697 | 86 | 5.8 | 374 | 1 | AI763751 | UI-R-Y0-a | 770 | 68.8 | 4.6 | 348 | 4 | BI596284 |
| C 698 | 85.6 | 5.8 | 416 | 7 | CN770263 | tad66g11. | 771 | 68.8 | 4.6 | 583 | 5 | BE211992 |
| C 699 | 85.6 | 5.8 | 495 | 7 | CN555282 | laci4g09. | 772 | 68.8 | 4.6 | 586 | 2 | BE299401 |
| C 700 | 85.6 | 5.8 | 938 | 5 | BK355822 | BK355822 | 773 | 68.8 | 4.6 | 607 | 2 | AM411072 |
| C 701 | 85.4 | 5.8 | 362 | 2 | BF190380 | 236897.MA | 774 | 68.8 | 4.6 | 629 | 2 | AM410900 |
| C 702 | 85.2 | 5.7 | 686 | 9 | CC541655 | CH240.422 | 775 | 68.8 | 4.6 | 641 | 4 | BG826674 |
| C 703 | 85 | 5.7 | 498 | 2 | AM838647 | RC5-LT005 | 776 | 68.8 | 4.6 | 671 | 2 | BE264542 |
| C 704 | 84.6 | 5.7 | 848 | 2 | BF529243 | 602041673 | 777 | 68.8 | 4.6 | 693 | 4 | BM718744 |
| C 705 | 84.4 | 5.7 | 569 | 1 | AV714854 | AV714854 | 778 | 68.8 | 4.6 | 737 | 2 | BE298457 |
| C 706 | 84 | 5.7 | 932 | 5 | BU171702 | AGENCOURT | 779 | 68.8 | 4.6 | 884 | 1 | AL551444 |
| C 707 | 83 | 5.6 | 336 | 2 | BF602955 | 268335.MA | 780 | 68.8 | 4.6 | 894 | 5 | BUB49635 |
| C 708 | 83 | 5.6 | 457 | 2 | BF651777 | 274644.MA | 781 | 68.8 | 4.6 | 910 | 6 | CA487350 |
| C 709 | 82.6 | 5.5 | 520 | 7 | CK989616 | BgHC-19.5 | 782 | 68.8 | 4.6 | 916 | 5 | BO681872 |
| C 710 | 82.4 | 5.5 | 466 | 5 | BK669266 | BK669266 | 783 | 68.8 | 4.6 | 917 | 1 | AL544055 |
| C 711 | 81.4 | 5.5 | 363 | 1 | AA492947 | VI67C08.x | 784 | 68.8 | 4.6 | 922 | 5 | BO929825 |
| C 712 | 80.6 | 5.4 | 245 | 1 | AA380326 | EST193278 | 785 | 68.8 | 4.6 | 941 | 5 | BK453804 |
| C 713 | 80.6 | 5.4 | 337 | 2 | AM214766 | up01f07.y | 786 | 68.8 | 4.6 | 985 | 5 | BK399814 |
| C 714 | 80.2 | 5.4 | 440 | 1 | AA491303 | aa53d12.8 | 787 | 68.8 | 4.6 | 1004 | 1 | AL546572 |
| C 715 | 80.2 | 5.4 | 317 | 4 | BM255927 | 518155.MA | 788 | 68.8 | 4.6 | 1005 | 1 | AL548946 |
| C 716 | 78.6 | 5.3 | 1694 | 4 | BG336860 | 602404528 | 789 | 68.8 | 4.6 | 1012 | 5 | BO722957 |
| C 717 | 77.2 | 5.2 | 329 | 6 | CS808938 | ssal1c028 | 790 | 68.8 | 4.6 | 1021 | 5 | BK417423 |
| C 718 | 76.8 | 5.2 | 458 | 7 | T79402 | y4f5a05.a1 | 791 | 68.8 | 4.6 | 1058 | 4 | BG037157 |
| C 719 | 76.6 | 5.2 | 643 | 1 | AI645493 | vt90f10.x | 792 | 68.8 | 4.6 | 1061 | 4 | BM560630 |
| C 720 | 76.6 | 5.2 | 382 | 7 | CN082452 | EC2BBA21A | 793 | 68.8 | 4.6 | 1064 | 5 | BM923206 |
| C 721 | 76.4 | 5.1 | 832 | 7 | CK188608 | EST777823 | 794 | 68.8 | 4.6 | 1074 | 1 | AL551936 |
| C 722 | 75.8 | 5.1 | 408 | 7 | CN267263 | 170004708 | 795 | 68.8 | 4.6 | 1076 | 2 | BF203295 |
| C 723 | 75.8 | 5.1 | 417 | 7 | W67363 | z4d0c11.s1 | 796 | 68.8 | 4.6 | 1083 | 1 | AL545414 |
| C 724 | 75.4 | 5.1 | 546 | 4 | BI708855 | fp93c11.y | 797 | 68.8 | 4.6 | 1114 | 2 | BE793016 |
| C 725 | 75.4 | 5.1 | 581 | 4 | BI845516 | fb98c04.y | 798 | 68.8 | 4.6 | 1179 | 5 | BM924255 |
| C 726 | 75.4 | 5.1 | 672 | 4 | BJ003659 | BJ003659 | 799 | 68.8 | 4.6 | 1188 | 5 | BM925699 |
| C 727 | 75.4 | 5.1 | 673 | 2 | AM280732 | fi45a09.y | 800 | 68.8 | 4.6 | 1544 | 4 | AP176923 |
| C 728 | 75.4 | 5.1 | 699 | 4 | BI891222 | ZF6373-0 | 801 | 68.8 | 4.6 | 1778 | 3 | CR624361 |
| C 729 | 75.4 | 5.1 | 782 | 7 | CN506945 | AGENCOURT | 802 | 68.8 | 4.6 | 1831 | 3 | CR599516 |
| C 730 | 75.4 | 5.1 | 833 | 7 | CK016721 | AGENCOURT | 803 | 68.8 | 4.6 | 1833 | 3 | CR597707 |
| C 731 | 75.4 | 5.1 | 861 | 7 | CO914049 | AGENCOURT | 804 | 68.8 | 4.6 | 1834 | 3 | CR603402 |
| C 732 | 75.4 | 5.1 | 876 | 7 | CK395467 | AGENCOURT | 805 | 68.8 | 4.6 | 1894 | 3 | CR620373 |
| C 733 | 75.4 | 5.1 | 946 | 7 | CN023023 | AGENCOURT | 806 | 68.8 | 4.6 | 1998 | 8 | BC035476 |
| C 734 | 75.2 | 5.1 | 500 | 6 | CD604091 | R2151A3EO | 807 | 68.8 | 4.6 | 2227 | 3 | CR599551 |
| C 735 | 75.2 | 5.1 | 563 | 4 | BI706206 | lq02g01.y | 808 | 68.8 | 4.6 | 695 | 4 | BG829306 |
| C 736 | 74.2 | 5.0 | 329 | 2 | AM009539 | w884b02.x | 809 | 68.6 | 4.6 | 1097 | 7 | BI5397591 |
| C 737 | 74.2 | 5.0 | 557 | 7 | CK890315 | SGP150543 | 810 | 68.4 | 4.6 | 784 | 7 | CN502422 |
| C 738 | 74 | 5.0 | 328 | 2 | AM794441 | RC6-UM001 | 811 | 68 | 4.6 | 546 | 6 | CB517420 |
| C 739 | 74 | 5.0 | 631 | 4 | BM781995 | K-EST0058 | 812 | 67.8 | 4.6 | 225 | 4 | BI038199 |
| C 740 | 73.8 | 5.0 | 482 | 7 | CK989768 | BgHC-22.4 | 813 | 67.8 | 4.6 | 868 | 6 | CD519669 |
| C 741 | 73.8 | 5.0 | 569 | 4 | BI845563 | fb99d12.y | 814 | 67.2 | 4.5 | 461 | 3 | CN80949M |
| C 742 | 73.8 | 5.0 | 584 | 4 | BI845474 | fb97d05.y | 815 | 67.2 | 4.5 | 638 | 4 | BG707999 |
| C 743 | 73.4 | 5.0 | 837 | 7 | CN832603 | AGENCOURT | 816 | 67.2 | 4.5 | 744 | 4 | BG702116 |
| C 744 | 73.4 | 4.9 | 325 | 7 | T69387 | YC37h11.r1 | 817 | 67.2 | 4.5 | 773 | 6 | CB988040 |
| C 745 | 72.8 | 4.9 | 391 | 2 | BF156959 | fi59a11.y | 818 | 67.2 | 4.5 | 884 | 5 | BK427985 |
| C 746 | 72.6 | 4.9 | 479 | 2 | BB862177 | UI-M-BHO- | 819 | 67.2 | 4.5 | 921 | 4 | BI600392 |
| C 747 | 72.6 | 4.9 | 590 | 3 | CN809AOK | Single.re | 820 | 67.2 | 4.5 | 938 | 4 | BG394370 |
| C 748 | 72.6 | 4.9 | 1240 | 6 | CD497710 | CD429-D07 | 821 | 67 | 4.5 | 477 | 1 | AA797956 |
| C 749 | 72.4 | 4.9 | 304 | 4 | BI867753 | fb63c06.y | 822 | 67 | 4.5 | 666 | 4 | BI553529 |
| C 750 | 71.4 | 4.8 | 752 | 4 | BI669979 | 603294491 | 823 | 66.8 | 4.5 | 550 | 4 | BG898800 |
| C 751 | 71.4 | 4.8 | 1037 | 1 | AL533084 | AL533084 | 824 | 66.6 | 4.5 | 182 | 7 | NS4755 |
| C 752 | 70.6 | 4.8 | 572 | 6 | CB615310 | AMGNNUC:N | 825 | 66.4 | 4.5 | 545 | 6 | CD730522 |
| C 753 | 70.6 | 4.8 | 700 | 6 | AG092733 | Pan.ctogl | 826 | 66.4 | 4.5 | 571 | 4 | BG710682 |
| C 754 | 70.6 | 4.8 | 742 | 7 | CK367504 | AGENCOURT | 827 | 66.4 | 4.5 | 585 | 5 | BP257027 |

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|-----|------|-----|------|---|-----------|-----|------|-----|------|---|----------|
| 828 | 66.4 | 4.5 | 646 | 4 | B1392555 | 901 | 64.4 | 4.3 | 869 | 6 | CA987481 |
| 829 | 66.4 | 4.5 | 804 | 7 | CN219157 | 902 | 64.4 | 4.3 | 901 | 5 | BUB99794 |
| 830 | 66.4 | 4.5 | 848 | 4 | B1460146 | 903 | 64.4 | 4.3 | 910 | 6 | CA792351 |
| 831 | 66.4 | 4.5 | 853 | 4 | BUI107470 | 904 | 64.4 | 4.3 | 916 | 6 | CA788575 |
| 832 | 66.4 | 4.5 | 861 | 1 | AL544229 | 905 | 64.4 | 4.3 | 926 | 6 | CA984841 |
| 833 | 66.4 | 4.5 | 871 | 1 | AL540364 | 906 | 64.4 | 4.3 | 992 | 6 | CA983119 |
| 834 | 66.4 | 4.5 | 1490 | 3 | CR611215 | 907 | 64.2 | 4.3 | 308 | 7 | T30350 |
| 835 | 66.4 | 4.5 | 1529 | 3 | CR616869 | 908 | 64.2 | 4.3 | 446 | 5 | BX486916 |
| 836 | 66.4 | 4.5 | 1836 | 3 | CR627385 | 909 | 64.2 | 4.3 | 505 | 4 | BM497075 |
| 837 | 66.2 | 4.5 | 321 | 2 | BP093306 | 910 | 64.2 | 4.3 | 526 | 4 | BM443390 |
| 838 | 66.2 | 4.5 | 474 | 5 | BY257579 | 911 | 64.2 | 4.3 | 537 | 2 | AM410192 |
| 839 | 66.2 | 4.5 | 1049 | 2 | BF205499 | 912 | 64.2 | 4.3 | 549 | 2 | BM719552 |
| 840 | 65.8 | 4.4 | 427 | 7 | CK883885 | 913 | 64.2 | 4.3 | 556 | 2 | AM673424 |
| 841 | 65.8 | 4.4 | 503 | 1 | AI605719 | 914 | 64.2 | 4.3 | 562 | 4 | BM021900 |
| 842 | 65.8 | 4.4 | 632 | 7 | CK620135 | 915 | 64.2 | 4.3 | 582 | 6 | CD675109 |
| 843 | 65.8 | 4.4 | 647 | 6 | BY707612 | 916 | 64.2 | 4.3 | 585 | 5 | BX357454 |
| 844 | 65.8 | 4.4 | 673 | 2 | BB649238 | 917 | 64.2 | 4.3 | 586 | 4 | BM023210 |
| 845 | 65.8 | 4.4 | 678 | 2 | BB649239 | 918 | 64.2 | 4.3 | 586 | 4 | BM023312 |
| 846 | 65.8 | 4.4 | 688 | 6 | BY753713 | 919 | 64.2 | 4.3 | 595 | 1 | AL776367 |
| 847 | 65.8 | 4.4 | 744 | 6 | BY736698 | 920 | 64.2 | 4.3 | 603 | 6 | CS528447 |
| 848 | 65.8 | 4.4 | 770 | 4 | BI656335 | 921 | 64.2 | 4.3 | 609 | 6 | CD365628 |
| 849 | 65.8 | 4.4 | 858 | 2 | BP138444 | 922 | 64.2 | 4.3 | 614 | 6 | CA431118 |
| 850 | 65.8 | 4.4 | 864 | 7 | CF617205 | 923 | 64.2 | 4.3 | 620 | 5 | BQ575162 |
| 851 | 65.8 | 4.4 | 882 | 4 | BI410683 | 924 | 64.2 | 4.3 | 625 | 4 | BM742136 |
| 852 | 65.8 | 4.4 | 891 | 2 | BF584891 | 925 | 64.2 | 4.3 | 651 | 4 | BI829555 |
| 853 | 65.8 | 4.4 | 926 | 5 | BQ925890 | 926 | 64.2 | 4.3 | 657 | 1 | AL882958 |
| 854 | 65.8 | 4.4 | 930 | 5 | BQ947300 | 927 | 64.2 | 4.3 | 668 | 4 | BI085428 |
| 855 | 65.8 | 4.4 | 943 | 5 | BQ897301 | 928 | 64.2 | 4.3 | 701 | 6 | CD366973 |
| 856 | 65.8 | 4.4 | 947 | 5 | CF585383 | 929 | 64.2 | 4.3 | 706 | 4 | BM682862 |
| 857 | 65.8 | 4.4 | 1032 | 5 | BQ686354 | 930 | 64.2 | 4.3 | 732 | 5 | BX462778 |
| 858 | 65.8 | 4.4 | 2049 | 3 | AK007560 | 931 | 64.2 | 4.3 | 739 | 5 | BI460106 |
| 859 | 65.8 | 4.4 | 2123 | 3 | AK011219 | 932 | 64.2 | 4.3 | 752 | 5 | BUI65459 |
| 860 | 65.8 | 4.4 | 2382 | 3 | AK048475 | 933 | 64.2 | 4.3 | 758 | 5 | BX341939 |
| 861 | 65.6 | 4.4 | 351 | 5 | BX357453 | 934 | 64.2 | 4.3 | 760 | 6 | CB240768 |
| 862 | 65.6 | 4.4 | 635 | 6 | CA332916 | 935 | 64.2 | 4.3 | 795 | 4 | BI753983 |
| 863 | 65.6 | 4.4 | 635 | 4 | CK598261 | 936 | 64.2 | 4.3 | 813 | 7 | CF222019 |
| 864 | 65.6 | 4.4 | 688 | 4 | BUI738800 | 937 | 64.2 | 4.3 | 823 | 4 | BG748791 |
| 865 | 65.6 | 4.4 | 690 | 6 | CB8420 | 938 | 64.2 | 4.3 | 838 | 5 | BX362459 |
| 866 | 65.6 | 4.4 | 746 | 7 | CK474032 | 939 | 64.2 | 4.3 | 867 | 7 | BE531131 |
| 867 | 65.6 | 4.4 | 752 | 7 | CK482038 | 940 | 64.2 | 4.3 | 870 | 7 | CF593217 |
| 868 | 65.6 | 4.4 | 755 | 7 | CK469333 | 941 | 64.2 | 4.3 | 870 | 7 | CR424943 |
| 869 | 65.6 | 4.4 | 757 | 7 | CV107376 | 942 | 64.2 | 4.3 | 871 | 5 | BI148475 |
| 870 | 65.6 | 4.4 | 760 | 7 | CK474093 | 943 | 64.2 | 4.3 | 878 | 7 | CR435674 |
| 871 | 65.6 | 4.4 | 801 | 7 | CK602945 | 944 | 64.2 | 4.3 | 885 | 5 | BUI55199 |
| 872 | 65.6 | 4.4 | 817 | 7 | CK470702 | 945 | 64.2 | 4.3 | 889 | 5 | BQ881044 |
| 873 | 65.6 | 4.4 | 819 | 7 | CK602625 | 946 | 64.2 | 4.3 | 897 | 7 | CF377547 |
| 874 | 65.6 | 4.4 | 827 | 7 | CK597533 | 947 | 64.2 | 4.3 | 923 | 5 | BUI45649 |
| 875 | 65.6 | 4.4 | 836 | 7 | CK652925 | 948 | 64.2 | 4.3 | 932 | 5 | BX712713 |
| 876 | 65.6 | 4.4 | 1005 | 5 | BQ678462 | 949 | 64.2 | 4.3 | 940 | 5 | BQ941943 |
| 877 | 65.4 | 4.4 | 479 | 2 | BF286638 | 950 | 64.2 | 4.3 | 942 | 5 | BO219478 |
| 878 | 65.4 | 4.4 | 599 | 7 | CK835564 | 951 | 64.2 | 4.3 | 983 | 5 | BX401762 |
| 879 | 65.4 | 4.4 | 960 | 5 | BQ844837 | 952 | 64.2 | 4.3 | 1012 | 5 | BQ712614 |
| 880 | 65 | 4.4 | 271 | 2 | AM128286 | 953 | 64.2 | 4.3 | 1016 | 5 | BX421204 |
| 881 | 65 | 4.4 | 294 | 4 | BG706326 | 954 | 64.2 | 4.3 | 1021 | 5 | BQ934215 |
| 882 | 65 | 4.4 | 1217 | 5 | BM909152 | 955 | 64.2 | 4.3 | 1039 | 5 | BX362886 |
| 883 | 64.6 | 4.4 | 1217 | 7 | TE69310 | 956 | 64.2 | 4.3 | 1046 | 5 | BX396406 |
| 884 | 64.6 | 4.4 | 506 | 2 | BE514790 | 957 | 64.2 | 4.3 | 1055 | 5 | BX363513 |
| 885 | 64.4 | 4.3 | 433 | 4 | BI349433 | 958 | 64.2 | 4.3 | 1062 | 5 | BQ056222 |
| 886 | 64.4 | 4.3 | 444 | 4 | BUI072850 | 959 | 64.2 | 4.3 | 1136 | 4 | BM544927 |
| 887 | 64.4 | 4.3 | 514 | 5 | BX925677 | 960 | 64.2 | 4.3 | 1151 | 1 | AL534927 |
| 888 | 64.4 | 4.3 | 544 | 4 | BQ069518 | 961 | 64.2 | 4.3 | 1300 | 5 | BM919262 |
| 889 | 64.4 | 4.3 | 549 | 4 | BUI039077 | 962 | 64.2 | 4.3 | 2210 | 3 | CR616014 |
| 890 | 64.4 | 4.3 | 573 | 4 | BUI059508 | 963 | 64.2 | 4.3 | 228 | 1 | AA718055 |
| 891 | 64.4 | 4.3 | 574 | 4 | BI477519 | 964 | 64.2 | 4.3 | 389 | 1 | AL837900 |
| 892 | 64.4 | 4.3 | 577 | 4 | BQ072660 | 965 | 64.2 | 4.3 | 604 | 5 | BUB05770 |
| 893 | 64.4 | 4.3 | 592 | 5 | BO383510 | 966 | 64.2 | 4.3 | 609 | 6 | CA589719 |
| 894 | 64.4 | 4.3 | 592 | 5 | CK654220 | 967 | 64.2 | 4.3 | 611 | 5 | BUB06039 |
| 895 | 64.4 | 4.3 | 731 | 7 | CK804649 | 968 | 64.2 | 4.3 | 652 | 6 | CA589027 |
| 896 | 64.4 | 4.3 | 755 | 7 | CF287392 | 969 | 64.2 | 4.3 | 655 | 5 | BUB07595 |
| 897 | 64.4 | 4.3 | 784 | 7 | CF286348 | 970 | 64.2 | 4.3 | 673 | 5 | BX885152 |
| 898 | 64.4 | 4.3 | 790 | 7 | CF270916 | 971 | 64.2 | 4.3 | 674 | 5 | BUB07896 |
| 899 | 64.4 | 4.3 | 855 | 6 | CA971881 | 972 | 64.2 | 4.3 | 818 | 6 | CA846215 |
| 900 | 64.4 | 4.3 | 866 | 6 | CA985745 | 973 | 64.2 | 4.3 | 880 | 5 | BQ951778 |

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| CA987481 | AGENCOURT |
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| CA792351 | AGENCOURT |
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| CA984841 | AGENCOURT |
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| BM719552 | UI-B-EJ1- |
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| BM021900 | 1e73e03.y |
| CD675109 | feh9b02.y |
| BX357454 | BX357454 |
| BM023210 | 1e61b07.x |
| BM023312 | 1e62g05.x |
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| CD365628 | UI-H-FT2- |
| CA431118 | UI-H-FT1- |
| BQ575162 | UI-H-EJ1- |
| BM742136 | K-BST0014 |
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| BM682862 | UI-B-EJ1- |
| BX462778 | BX462778 |
| BI460106 | 603201672 |
| BUI65459 | UI-H-FG0- |
| BX341939 | BX341939 |
| CB240768 | UI-CF-FN0 |
| BI753983 | 603027415 |
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| BI148475 | AGENCOURT |
| CR435674 | CR435674 |
| BUI55199 | AGENCOURT |
| BO881044 | AGENCOURT |
| CF377547 | AGENCOURT |
| BUI45649 | AGENCOURT |
| BX712713 | BX712713 |
| BO941943 | AGENCOURT |
| BO219478 | AGENCOURT |
| BX401762 | BX401762 |
| BQ712614 | AGENCOURT |
| BQ421204 | BQ421204 |
| BO934215 | AGENCOURT |
| BX362886 | BX362886 |
| BX396406 | BX396406 |
| BX363513 | BX363513 |
| BO056222 | AGENCOURT |
| BM544927 | AGENCOURT |
| AL534927 | AL534927 |
| BM919262 | AGENCOURT |
| CR616014 | full - leng |
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| AL837900 | AL837900 |
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| BUB06039 | haa26a03. |
| CA589027 | haa25h05. |
| BUB07595 | haa62h01. |
| BX885152 | BX885152 |
| BUB07896 | haa18h08. |
| CA846215 | haa11a06. |
| BQ951778 | AGENCOURT |

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|------|------|-----|------|---|----------|--------------------|------|------|-----|------|---|----------|--------------------|
| 974 | 64 | 4.3 | 1729 | 3 | AK045911 | AK045911 Mus muscu | 1047 | 61.4 | 4.1 | 856 | 2 | BF309230 | BF309230 601890171 |
| 975 | 64 | 4.3 | 1805 | 3 | AK016491 | AK016491 Mus muscu | 1048 | 61 | 4.1 | 61 | 7 | T12612 | T12612 CHR90132 Ch |
| 976 | 63.8 | 4.3 | 1460 | 7 | CK608216 | CK608216 ITN B06 I | 1049 | 61 | 4.1 | 574 | 4 | B1115218 | B1115218 602861671 |
| 977 | 63.8 | 4.3 | 591 | 7 | CK307425 | CK307425 SB02043B1 | 1050 | 61 | 4.1 | 580 | 2 | AM664179 | AM664179 h105e10.x |
| 978 | 63.8 | 4.3 | 649 | 2 | AM321637 | AM321637 U036611.Y | 1051 | 61 | 4.1 | 652 | 5 | BX371495 | BX371495 BX371495 |
| 979 | 63.6 | 4.3 | 400 | 7 | AM220122 | AM220122 RA062B02 | 1052 | 61 | 4.1 | 1017 | 5 | BO865792 | BO865792 AGENCOURT |
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| 981 | 63.6 | 4.3 | 422 | 5 | CN234377 | CN234377 RA094C04 | 1054 | 61 | 4.1 | 514 | 4 | BM151565 | BM151565 TCBA1E04 |
| 982 | 63.6 | 4.3 | 550 | 5 | BP213919 | BP213919 BP213919 | 1055 | 60.8 | 4.1 | 442 | 7 | CN959409 | CN959409 6909.1001 |
| 983 | 63.6 | 4.3 | 556 | 4 | BM490119 | BM490119 P9P2n.PK0 | 1056 | 60.6 | 4.1 | 567 | 7 | BM827267 | BM827267 K-EST0099 |
| 984 | 63.6 | 4.3 | 616 | 4 | BI392159 | BI392159 P9P1n.PK0 | 1057 | 60.6 | 4.1 | 617 | 7 | CF723843 | CF723843 UI-M-G20 |
| 985 | 63.6 | 4.3 | 636 | 4 | BU231422 | BU231422 603800637 | 1058 | 60.6 | 4.1 | 947 | 7 | CN455679 | CN455679 UI-M-HP0 |
| 986 | 63.6 | 4.3 | 656 | 4 | BG488856 | BG488856 602534848 | 1059 | 60.6 | 4.1 | 825 | 5 | BO958968 | BO958968 AGENCOURT |
| 987 | 63.6 | 4.3 | 727 | 5 | BU211470 | BU211470 604152150 | 1060 | 60.6 | 4.1 | 671 | 4 | BM044488 | BM044488 603622007 |
| 988 | 63.6 | 4.3 | 766 | 5 | BU368992 | BU368992 603598513 | 1061 | 60.6 | 4.1 | 806 | 4 | BG775636 | BG775636 603626913 |
| 989 | 63.6 | 4.3 | 776 | 5 | BU255007 | BU255007 603747266 | 1062 | 60.6 | 4.1 | 947 | 7 | CN455679 | CN455679 UI-M-HP0 |
| 990 | 63.6 | 4.3 | 781 | 7 | CN221062 | CN221062 WLA029G03 | 1063 | 60.4 | 4.1 | 331 | 7 | CR522276 | CR522276 |
| 991 | 63.6 | 4.3 | 809 | 5 | BU132109 | BU132109 603117794 | 1064 | 60.4 | 4.1 | 505 | 2 | BE258279 | BE258279 |
| 992 | 63.6 | 4.3 | 827 | 5 | BU277250 | BU277250 WLA110D09 | 1065 | 60.4 | 4.1 | 858 | 1 | AI533024 | AI533024 |
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| 995 | 63.6 | 4.3 | 893 | 5 | BU327241 | BU327241 603492096 | 1068 | 60.2 | 4.1 | 412 | 2 | AM961315 | AM961315 |
| 996 | 63.6 | 4.3 | 894 | 5 | BU433641 | BU433641 603221461 | 1069 | 60.2 | 4.0 | 929 | 5 | AM012274 | AM012274 |
| 997 | 63.6 | 4.3 | 895 | 5 | BB643629 | BB643629 BB643629 | 1070 | 60 | 4.0 | 523 | 2 | BB611133 | BB611133 |
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| 999 | 63.2 | 4.3 | 671 | 7 | CR415574 | CR415574 RC2BBA14B | 1072 | 59.8 | 4.0 | 523 | 2 | AM012274 | AM012274 |
| 1000 | 63.2 | 4.3 | 671 | 7 | CR415574 | CR415574 RC2BBA14B | 1073 | 59.8 | 4.0 | 523 | 2 | AM012274 | AM012274 |
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| 1003 | 63.2 | 4.3 | 963 | 7 | CR573735 | CR573735 | 1076 | 59.4 | 4.0 | 946 | 5 | BO959396 | BO959396 |
| 1004 | 63 | 4.2 | 598 | 1 | AA544785 | AA544785 | 1077 | 59.4 | 4.0 | 611 | 7 | T24722 | T24722 |
| 1005 | 63 | 4.2 | 598 | 1 | AA544785 | AA544785 | 1078 | 59.4 | 4.0 | 611 | 7 | T24722 | T24722 |
| 1006 | 63 | 4.2 | 165 | 2 | BE563649 | BE563649 601334785 | 1079 | 59.2 | 4.0 | 656 | 4 | BI548144 | BI548144 |
| 1007 | 62.8 | 4.2 | 165 | 2 | BE563649 | BE563649 601334785 | 1080 | 59.2 | 4.0 | 656 | 4 | BI548144 | BI548144 |
| 1008 | 62.6 | 4.2 | 581 | 5 | BI966097 | BI966097 601508152 | 1081 | 59.2 | 4.0 | 735 | 7 | CO196389 | CO196389 |
| 1009 | 62.6 | 4.2 | 601 | 5 | BO520975 | BO520975 NISC n108 | 1082 | 59 | 4.0 | 356 | 2 | AM841732 | AM841732 |
| 1010 | 62.6 | 4.2 | 638 | 1 | AL848424 | AL848424 AL848424 | 1083 | 58.8 | 4.0 | 290 | 4 | BG062118 | BG062118 |
| 1011 | 62.6 | 4.2 | 651 | 1 | AL867994 | AL867994 | 1084 | 58.8 | 4.0 | 340 | 2 | BF720256 | BF720256 |
| 1012 | 62.6 | 4.2 | 659 | 7 | CR577323 | CR577323 | 1085 | 58.8 | 4.0 | 340 | 2 | BF720256 | BF720256 |
| 1013 | 62.6 | 4.2 | 758 | 7 | CF149892 | CF149892 | 1086 | 58.8 | 4.0 | 340 | 2 | BF720256 | BF720256 |
| 1014 | 62.6 | 4.2 | 787 | 5 | BK723292 | BK723292 | 1087 | 58.8 | 4.0 | 340 | 2 | BF720256 | BF720256 |
| 1015 | 62.6 | 4.2 | 847 | 7 | CR433581 | CR433581 | 1088 | 58.8 | 4.0 | 340 | 2 | BF720256 | BF720256 |
| 1016 | 62.6 | 4.2 | 865 | 7 | CR433581 | CR433581 | 1089 | 58.8 | 4.0 | 340 | 2 | BF720256 | BF720256 |
| 1017 | 62.6 | 4.2 | 865 | 7 | CR433581 | CR433581 | 1090 | 58.8 | 4.0 | 340 | 2 | BF720256 | BF720256 |
| 1018 | 62.6 | 4.2 | 915 | 7 | CR433581 | CR433581 | 1091 | 58.8 | 4.0 | 340 | 2 | BF720256 | BF720256 |
| 1019 | 62.6 | 4.2 | 983 | 5 | BO924405 | BO924405 | 1092 | 58.8 | 4.0 | 457 | 2 | BM751438 | BM751438 |
| 1020 | 62.6 | 4.2 | 538 | 5 | BO924405 | BO924405 | 1093 | 58.8 | 4.0 | 457 | 2 | BM751438 | BM751438 |
| 1021 | 62.4 | 4.2 | 538 | 5 | BO924405 | BO924405 | 1094 | 58.8 | 4.0 | 457 | 2 | BM751438 | BM751438 |
| 1022 | 62.4 | 4.2 | 566 | 7 | CF104721 | CF104721 | 1095 | 58.8 | 4.0 | 457 | 2 | BM751438 | BM751438 |
| 1023 | 62.4 | 4.2 | 575 | 7 | CF197822 | CF197822 | 1096 | 58.8 | 4.0 | 457 | 2 | BM751438 | BM751438 |
| 1024 | 62.4 | 4.2 | 588 | 4 | BI477647 | BI477647 | 1097 | 58.8 | 4.0 | 457 | 2 | BM751438 | BM751438 |
| 1025 | 62.4 | 4.2 | 614 | 5 | BQ399256 | BQ399256 NISC mp02 | 1098 | 58.8 | 4.0 | 457 | 2 | BM751438 | BM751438 |
| 1026 | 62.4 | 4.2 | 616 | 7 | CV074265 | CV074265 | 1099 | 58.8 | 4.0 | 457 | 2 | BM751438 | BM751438 |
| 1027 | 62.4 | 4.2 | 642 | 4 | BJ057809 | BJ057809 | 1100 | 58.8 | 4.0 | 457 | 2 | BM751438 | BM751438 |
| 1028 | 62.4 | 4.2 | 691 | 5 | BX849635 | BX849635 | 1101 | 58.8 | 4.0 | 457 | 2 | BM751438 | BM751438 |
| 1029 | 62.4 | 4.2 | 724 | 7 | CN832945 | CN832945 | 1102 | 58.6 | 3.9 | 1165 | 4 | BM462345 | BM462345 |
| 1030 | 62.4 | 4.2 | 796 | 7 | CN217052 | CN217052 | 1103 | 58.4 | 3.9 | 592 | 4 | BM462345 | BM462345 |
| 1031 | 62.4 | 4.2 | 829 | 7 | CV074535 | CV074535 | 1104 | 58.4 | 3.9 | 637 | 2 | BF309494 | BF309494 |
| 1032 | 62.4 | 4.2 | 850 | 5 | BU274575 | BU274575 | 1105 | 58.4 | 3.9 | 668 | 5 | BX660019 | BX660019 |
| 1033 | 62.4 | 4.2 | 865 | 5 | BU290552 | BU290552 | 1106 | 58.4 | 3.9 | 753 | 5 | BX660019 | BX660019 |
| 1034 | 62.4 | 4.2 | 871 | 6 | CB558697 | CB558697 | 1107 | 58.4 | 3.9 | 784 | 5 | BX660019 | BX660019 |
| 1035 | 62.2 | 4.2 | 762 | 7 | BX879898 | BX879898 | 1108 | 58.4 | 3.9 | 796 | 5 | BX660019 | BX660019 |
| 1036 | 62 | 4.2 | 612 | 7 | CN084450 | CN084450 | 1109 | 58.4 | 3.9 | 803 | 5 | BX660019 | BX660019 |
| 1037 | 62 | 4.2 | 1328 | 4 | AL843094 | AL843094 | 1110 | 58.4 | 3.9 | 487 | 4 | BM306330 | BM306330 |
| 1038 | 61.8 | 4.2 | 417 | 1 | AL843094 | AL843094 | 1111 | 58.2 | 3.9 | 487 | 4 | BM306330 | BM306330 |
| 1039 | 61.6 | 4.1 | 612 | 7 | CN084258 | CN084258 | 1112 | 58.2 | 3.9 | 517 | 4 | BM792003 | BM792003 |
| 1040 | 61.6 | 4.1 | 618 | 7 | CN084258 | CN084258 | 1113 | 58.2 | 3.9 | 780 | 4 | BG775636 | BG775636 |
| 1041 | 61.6 | 4.1 | 889 | 5 | BU147032 | BU147032 | 1114 | 58.2 | 3.9 | 810 | 6 | CD752612 | CD752612 |
| 1042 | 61.4 | 4.1 | 614 | 5 | CB215777 | CB215777 | 1115 | 58.2 | 3.9 | 856 | 4 | BI647230 | BI647230 |
| 1043 | 61.4 | 4.1 | 732 | 2 | BF304475 | BF304475 | 1116 | 58 | 3.9 | 307 | 2 | BF093126 | BF093126 |
| 1044 | 61.4 | 4.1 | 803 | 4 | BF667128 | BF667128 | 1117 | 58 | 3.9 | 498 | 7 | R26367 | R26367 |
| 1045 | 61.4 | 4.1 | 820 | 4 | BI667411 | BI667411 | 1118 | 57.8 | 3.9 | 728 | 7 | CN389160 | CN389160 |
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| B1115218 | 602861671 |
| AM664179 | h105e10.x |
| BX371495 | BX371495 |
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| CF723843 | UI-M-G20 |
| BM044488 | 603622007 |
| BM047568 | 603626913 |
| BM775636 | 602650573 |
| CN455679 | UI-M-HP0 |
| BO958968 | AGENCOURT |
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| BE258279 | BE258279 |
| BM258279 | 601106373 |
| CN094528 | EC2BBA9Df |
| AI533024 | S004693.5 |
| BM921410 | AGENCOURT |
| BY724416 | BY724416 |
| BU525991 | AGENCOURT |
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| AM012274 | un06511.Y |
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| BG708540 | 602670438 |
| CG517489 | OST77927 |
| BO959396 | AGENCOURT |
| T24722 | EST97 Huma |
| EG270782 | 1899003.Y |
| BI548144 | 603189484 |
| CO196389 | EKO04024. |
| BI261399 | 603003383 |
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| BQ033911 | UI-1-CF0- |
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| CF751563 | UI-M-HK0- |
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| BM951957 | UI-M-EH0- |
| CA751143 | UI-M-FD0- |
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| BX660019 | BX660019 |
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| R26367 | Yn40a05.81 |
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|------|------|-----|------|---|-----------|-------------|-------|------|-----|------|---|----------|
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| 1124 | 57.2 | 3.9 | 392 | 2 | BB837430 | BB837430 | 1197 | 52 | 3.5 | 881 | 4 | BB699656 |
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| 1127 | 57.2 | 3.9 | 442 | 5 | BB834887 | BB834887 | 1200 | 51.8 | 3.5 | 1342 | 5 | BB905941 |
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| 1134 | 57 | 3.8 | 435 | 6 | CB8366 | CB8366 | 1207 | 50.8 | 3.4 | 316 | 2 | BB501029 |
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| 1137 | 56.8 | 3.8 | 696 | 4 | BI546531 | BI546531 | 1210 | 50.8 | 3.4 | 503 | 4 | BI846300 |
| 1138 | 56.8 | 3.8 | 908 | 5 | BU179913 | BU179913 | 1211 | 50.8 | 3.4 | 570 | 4 | BI845458 |
| 1139 | 56.4 | 3.8 | 327 | 1 | AI849272 | AI849272 | 1212 | 50.8 | 3.4 | 701 | 7 | CK172514 |
| 1140 | 56.4 | 3.8 | 517 | 7 | CK137373 | CK137373 | 1213 | 50.8 | 3.4 | 701 | 7 | CK172515 |
| 1141 | 56.2 | 3.8 | 390 | 5 | BY380023 | BY380023 | 1214 | 50.8 | 3.4 | 711 | 6 | CD492738 |
| 1142 | 56.2 | 3.8 | 1091 | 5 | CL648805 | CL648805 | 1215 | 50.8 | 3.4 | 1101 | 9 | CNS017RP |
| 1143 | 56 | 3.8 | 441 | 5 | BO221449 | BO221449 | 1216 | 50.8 | 3.4 | 1174 | 5 | BO671970 |
| 1144 | 56 | 3.8 | 930 | 5 | BO940582 | BO940582 | 1217 | 50.6 | 3.4 | 246 | 2 | BF896928 |
| 1145 | 55.8 | 3.8 | 561 | 9 | AV039984 | AV039984 | 1218 | 50.6 | 3.4 | 401 | 2 | AM188794 |
| 1146 | 55.8 | 3.8 | 310 | 9 | CE603961 | CE603961 | 1219 | 50.6 | 3.4 | 653 | 5 | BM436126 |
| 1147 | 55.6 | 3.7 | 275 | 1 | AI118784 | AI118784 | 1220 | 50.6 | 3.4 | 704 | 5 | BM436127 |
| 1148 | 55.6 | 3.7 | 348 | 9 | AY412711 | AY412711 | 1221 | 50.6 | 3.4 | 764 | 5 | BU258414 |
| 1149 | 55.6 | 3.7 | 365 | 5 | BY415990 | BY415990 | 1222 | 50.6 | 3.4 | 765 | 5 | BM429595 |
| 1150 | 55.6 | 3.7 | 385 | 4 | BM852501 | BM852501 | 1223 | 50.6 | 3.4 | 1051 | 5 | BX464372 |
| 1151 | 55.6 | 3.7 | 415 | 9 | AY412710 | AY412710 | 1224 | 50.4 | 3.4 | 514 | 2 | AM337550 |
| 1152 | 55.6 | 3.7 | 591 | 2 | AM500528 | AM500528 | 1225 | 50.4 | 3.4 | 601 | 5 | BM341587 |
| 1153 | 55.6 | 3.7 | 700 | 2 | BE296236 | BE296236 | 1226 | 50.4 | 3.4 | 675 | 5 | BM248558 |
| 1154 | 55.6 | 3.7 | 839 | 4 | BI820066 | BI820066 | 1227 | 50.4 | 3.4 | 686 | 5 | BM056869 |
| 1155 | 55.6 | 3.7 | 931 | 6 | CD359314 | CD359314 | 1228 | 50.4 | 3.4 | 687 | 5 | BM250225 |
| 1156 | 55.6 | 3.7 | 932 | 2 | BE735129 | BE735129 | 1229 | 50.4 | 3.4 | 699 | 5 | BM047661 |
| 1157 | 55.6 | 3.7 | 1154 | 5 | BO054990 | BO054990 | 1230 | 50.4 | 3.4 | 707 | 5 | BM478438 |
| 1158 | 55.6 | 3.7 | 127 | 6 | CB7647 | CB7647 | 1231 | 50.4 | 3.4 | 712 | 5 | BM041956 |
| 1159 | 55.4 | 3.7 | 427 | 6 | CO378095 | CO378095 | 1232 | 50.4 | 3.4 | 806 | 5 | BU301036 |
| 1160 | 55.2 | 3.7 | 725 | 7 | BE705925 | BE705925 | 1233 | 50.2 | 3.4 | 308 | 1 | AV040523 |
| 1161 | 54.6 | 3.7 | 763 | 4 | BE377559 | BE377559 | 1234 | 50.2 | 3.4 | 325 | 7 | CO966620 |
| 1162 | 54.6 | 3.7 | 759 | 8 | AO743375 | AO743375 | 1235 | 50.2 | 3.4 | 444 | 2 | AM087991 |
| 1163 | 54.4 | 3.7 | 781 | 7 | CN756232 | CN756232 | 1236 | 50.2 | 3.4 | 491 | 7 | CP157964 |
| 1164 | 54.4 | 3.7 | 950 | 8 | AO743722 | AO743722 | 1237 | 50.2 | 3.4 | 574 | 5 | BO422142 |
| 1165 | 54.4 | 3.7 | 986 | 8 | BM909681 | BM909681 | 1238 | 50.2 | 3.4 | 707 | 1 | AO081289 |
| 1166 | 54.4 | 3.7 | 950 | 8 | BM909681 | BM909681 | 1239 | 50 | 3.4 | 281 | 1 | AV082140 |
| 1167 | 54.2 | 3.6 | 426 | 4 | BM821451 | BM821451 | 1240 | 50 | 3.4 | 660 | 2 | BF046772 |
| 1168 | 54.2 | 3.6 | 493 | 4 | BG745652 | BG745652 | 1241 | 50 | 3.4 | 819 | 4 | BI647605 |
| 1169 | 54.2 | 3.6 | 531 | 4 | BG745918 | BG745918 | 1242 | 49.8 | 3.4 | 590 | 4 | BI455815 |
| 1170 | 54 | 3.6 | 415 | 9 | AY412712 | AY412712 | 1243 | 49.8 | 3.4 | 793 | 6 | CA141250 |
| 1171 | 54 | 3.6 | 465 | 2 | BB830143 | BB830143 | 1244 | 49.8 | 3.4 | 793 | 7 | CN053475 |
| 1172 | 54 | 3.6 | 632 | 7 | BU055145 | BU055145 | 1245 | 49.8 | 3.4 | 999 | 5 | BO918433 |
| 1173 | 53.8 | 3.6 | 281 | 7 | FI9347 | FI9347 | 1246 | 49.6 | 3.3 | 484 | 6 | CB639653 |
| 1174 | 53.6 | 3.6 | 964 | 5 | BO686539 | BO686539 | 1247 | 49.6 | 3.3 | 543 | 7 | CF340723 |
| 1175 | 53.6 | 3.6 | 287 | 4 | BM854652 | BM854652 | 1248 | 49.6 | 3.3 | 585 | 1 | AU225865 |
| 1176 | 53.6 | 3.6 | 387 | 6 | CB806010 | CB806010 | 1249 | 49.6 | 3.3 | 631 | 6 | CB653047 |
| 1177 | 53.6 | 3.6 | 493 | 1 | AI592398 | AI592398 | 1250 | 49.6 | 3.3 | 720 | 6 | CB659405 |
| 1178 | 53.6 | 3.6 | 1404 | 5 | BM907186 | BM907186 | 1251 | 49.6 | 3.3 | 722 | 6 | CB659406 |
| 1179 | 53.4 | 3.6 | 156 | 9 | CG516394 | CG516394 | 1252 | 49.6 | 3.3 | 842 | 7 | CO435891 |
| 1180 | 53.4 | 3.6 | 229 | 2 | AM422685 | AM422685 | 1253 | 49.4 | 3.3 | 357 | 5 | BO696623 |
| 1181 | 53.4 | 3.6 | 988 | 5 | BO897984 | BO897984 | 1254 | 49.2 | 3.3 | 372 | 5 | BY050439 |
| 1182 | 53.2 | 3.6 | 458 | 1 | BF151139 | BF151139 | 1255 | 49.2 | 3.3 | 372 | 5 | BY050439 |
| 1183 | 53.2 | 3.6 | 933 | 2 | ALU559613 | ALU559613 | 1256 | 49.2 | 3.3 | 383 | 5 | BY059594 |
| 1184 | 52.2 | 3.6 | 1247 | 6 | BU542112 | BU542112 | 1257 | 49.2 | 3.3 | 393 | 5 | CB773777 |
| 1185 | 52.6 | 3.5 | 343 | 6 | CD102272 | CD102272 | 1258 | 49.2 | 3.3 | 410 | 5 | BY313404 |
| 1186 | 52.6 | 3.5 | 482 | 5 | BY255020 | BY255020 | 1259 | 49.2 | 3.3 | 415 | 6 | CB799926 |
| 1187 | 52.6 | 3.5 | 662 | 2 | AM097140 | AM097140 | 1260 | 49.2 | 3.3 | 422 | 6 | CB763144 |
| 1188 | 52.4 | 3.5 | 423 | 4 | BG146767 | BG146767 | 1261 | 49.2 | 3.3 | 430 | 6 | CB758592 |
| 1189 | 52.4 | 3.5 | 473 | 7 | CK689936 | CK689936 | 1262 | 49.2 | 3.3 | 432 | 7 | DI5295 |
| 1190 | 52.4 | 3.5 | 514 | 4 | BM681050 | BM681050 | 1263 | 49.2 | 3.3 | 440 | 6 | CB749636 |
| 1191 | 52.4 | 3.5 | 658 | 7 | CK189556 | CK189556 | 1264 | 49.2 | 3.3 | 444 | 6 | CI7719 |
| 1192 | 52.4 | 3.5 | 791 | 7 | CK189557 | CK189557 | 1265 | 49.2 | 3.3 | 446 | 6 | CB747532 |

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| AA919092 | 0178d06.b |
| AW188838 | xk88h08.x |
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| BB509232 | dc08a01.y |
| BB756029 | 603030372 |
| BM905941 | AGENCYCOURT |
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| AU261278 | AU261278 |
| CB741222 | AMGNNUC:N |
| BM781979 | K-EST0058 |
| AI300999 | gn61e06.x |
| BB501029 | BB501029 |
| BT841846 | BT841846 |
| CB729237 | AMGNNUC:N |
| BI846300 | BI846300 |
| BI845458 | f897a07.y |
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| CK172515 | EST761835 |
| CD492738 | CDA01-B07 |
| CNS017RP | Drosoph11 |
| BO671970 | AGENCYCOURT |
| BF896928 | CM2-MT015 |
| AM188794 | xk88d12.x |
| BM436126 | BM436126 |
| BM436127 | BM436127 |
| BU258414 | 603413304 |
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| BX464372 | BX464372 |
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| BM248558 | BM248558 |
| BM056869 | BM056869 |
| BM250225 | BM250225 |
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| BM478438 | BM478438 |
| BM041956 | BM041956 |
| BU301036 | 603738947 |
| AV040523 | AV040523 |
| CO966620 | aa001-2m8 |
| AM087991 | xb47a04.x |
| CP157964 | B0654C12-x |
| BO422142 | Cyhem-027 |
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| AV082140 | AV082140 |
| BF046772 | EST857.MA |
| BI647605 | 603278186 |
| BI455815 | 603171030 |
| CA141250 | SCJFRT205 |
| CN053475 | Salamande |
| BO918433 | AGENCYCOURT |
| CB639653 | OSJNEAL1H |
| CF340723 | RCL1--08- |
| AU225865 | AU225865 |
| CB653047 | OSJNEC01L |
| CB659405 | OSJNEC16F |
| CB659406 | OSJNEC16F |
| CO435891 | OSJNEC16F |
| BO696623 | BO696623 |
| BY071779 | BY071779 |
| BY050439 | BY050439 |
| BY059594 | BY059594 |
| CB773777 | AMGNNUC:T |
| BY313404 | BY313404 |
| CB799926 | AMGNNUC:C |
| CB763144 | AMGNNUC:C |
| CB758592 | AMGNNUC:N |
| DI5295 | RICCO419A.R |
| CB749636 | AMGNNUC:N |
| CI7719 | C17719.Huma |
| CB747532 | AMGNNUC:N |

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|------|------|-----|------|---|----------|----------|-----------|------|------|-----|------|---|----------|-----------|
| 1266 | 49.2 | 3.3 | 484 | 6 | CB727526 | CB727526 | AMGNNUC:N | 1339 | 49 | 3.3 | 688 | 5 | EX917412 | EX917412 |
| 1267 | 49.2 | 3.3 | 498 | 6 | CB712568 | CB712568 | AMGNNUC:C | 1340 | 49 | 3.3 | 690 | 5 | EX916400 | EX916400 |
| 1268 | 49.2 | 3.3 | 505 | 6 | CB783529 | CB783529 | AMGNNUC:N | 1341 | 49 | 3.3 | 692 | 5 | EX918886 | EX918886 |
| 1269 | 49.2 | 3.3 | 510 | 4 | BG307340 | BG307340 | fmo3a02.y | 1342 | 49 | 3.3 | 693 | 5 | EX673594 | EX673594 |
| 1270 | 49.2 | 3.3 | 515 | 6 | CB274539 | CB274539 | mai70d07. | 1343 | 49 | 3.3 | 699 | 7 | CN166011 | CN166011 |
| 1271 | 49.2 | 3.3 | 517 | 6 | CB716226 | CB716226 | AMGNNUC:N | 1344 | 49 | 3.3 | 700 | 5 | BQ598574 | MI-P-E3-a |
| 1272 | 49.2 | 3.3 | 525 | 6 | CB720233 | CB720233 | AMGNNUC:N | 1345 | 49 | 3.3 | 711 | 7 | CK467154 | CK465055 |
| 1273 | 49.2 | 3.3 | 526 | 1 | AL913377 | AL913377 | AMGNNUC:N | 1346 | 49 | 3.3 | 711 | 7 | CK467154 | CK467154 |
| 1274 | 49.2 | 3.3 | 529 | 6 | CB719410 | CB719410 | AMGNNUC:N | 1347 | 49 | 3.3 | 879 | 6 | CB996556 | CB996556 |
| 1275 | 49.2 | 3.3 | 535 | 6 | CB718099 | CB718099 | AMGNNUC:N | 1348 | 49 | 3.3 | 359 | 5 | BY099449 | BY099449 |
| 1276 | 49.2 | 3.3 | 541 | 6 | CB612601 | CB612601 | AMGNNUC:C | 1349 | 48.8 | 3.3 | 365 | 2 | BE543216 | BE543216 |
| 1277 | 49.2 | 3.3 | 572 | 6 | CB058793 | CB058793 | Li_PACHE | 1350 | 48.8 | 3.3 | 948 | 4 | BC331194 | BC331194 |
| 1278 | 49.2 | 3.3 | 576 | 6 | CB608302 | CB608302 | AMGNNUC:N | 1351 | 48.8 | 3.3 | 954 | 5 | EX465059 | EX465059 |
| 1279 | 49.2 | 3.3 | 580 | 7 | CN049803 | CN049803 | DR_AOV_FU | 1352 | 48.6 | 3.3 | 174 | 7 | NA7817 | NA7817 |
| 1280 | 49.2 | 3.3 | 584 | 7 | CN020383 | CN020383 | ToF3513_G | 1353 | 48.6 | 3.3 | 536 | 7 | CK898109 | CK898109 |
| 1281 | 49.2 | 3.3 | 586 | 2 | AM127954 | AM127954 | f105b08.y | 1354 | 48.4 | 3.3 | 353 | 5 | BY074771 | BY074771 |
| 1282 | 49.2 | 3.3 | 586 | 2 | CB585582 | CB585582 | AMGNNUC:N | 1355 | 48.4 | 3.3 | 506 | 6 | CD297210 | CD297210 |
| 1283 | 49.2 | 3.3 | 593 | 6 | CB584475 | CB584475 | AMGNNUC:N | 1356 | 48.4 | 3.3 | 785 | 5 | AG594701 | AG594701 |
| 1284 | 49.2 | 3.3 | 593 | 7 | CO552415 | CO552415 | AcLy525.S | 1357 | 48.2 | 3.2 | 367 | 5 | BY072752 | BY072752 |
| 1285 | 49.2 | 3.3 | 596 | 7 | CO551644 | CO551644 | AcLy1243 | 1358 | 48.2 | 3.2 | 370 | 5 | BY054236 | BY054236 |
| 1286 | 49.2 | 3.3 | 600 | 7 | CO552474 | CO552474 | AcLy595.S | 1359 | 48.2 | 3.2 | 543 | 7 | CO506808 | CO506808 |
| 1287 | 49.2 | 3.3 | 601 | 6 | CB588235 | CB588235 | AMGNNUC:N | 1360 | 48.2 | 3.2 | 568 | 7 | CO507234 | CO507234 |
| 1288 | 49.2 | 3.3 | 621 | 7 | CV005712 | CV005712 | aaMO1-1ms | 1361 | 48.2 | 3.2 | 579 | 6 | CD307605 | CD307605 |
| 1289 | 49.2 | 3.3 | 644 | 7 | CO552741 | CO552741 | AcLy936.S | 1362 | 48.2 | 3.2 | 612 | 4 | BI104905 | BI104905 |
| 1290 | 49.2 | 3.3 | 645 | 7 | CO551959 | CO551959 | AcLy1687 | 1363 | 48.2 | 3.2 | 769 | 7 | CN034157 | CN034157 |
| 1291 | 49.2 | 3.3 | 646 | 7 | CO552414 | CO552414 | AcLy523.S | 1364 | 48.2 | 3.2 | 988 | 2 | BF582689 | BF582689 |
| 1292 | 49.2 | 3.3 | 663 | 6 | CD371813 | CD371813 | UI-R-G00- | 1365 | 48.2 | 3.2 | 1069 | 5 | BU938599 | BU938599 |
| 1293 | 49.2 | 3.3 | 761 | 7 | CK693057 | CK693057 | ZF101-P00 | 1366 | 48.2 | 3.2 | 442 | 7 | CF279790 | CF279790 |
| 1294 | 49.2 | 3.3 | 773 | 7 | CO402421 | CO402421 | AGENCOURT | 1367 | 48 | 3.2 | 443 | 3 | BB862264 | BB862264 |
| 1295 | 49.2 | 3.3 | 775 | 7 | CK396848 | CK396848 | AGENCOURT | 1368 | 48 | 3.2 | 871 | 6 | CB565614 | CB565614 |
| 1296 | 49.2 | 3.3 | 801 | 7 | CO399070 | CO399070 | AGENCOURT | 1369 | 48 | 3.2 | 1004 | 1 | AL513914 | AL513914 |
| 1297 | 49.2 | 3.3 | 833 | 4 | BG666609 | BG666609 | DRAPE10 | 1370 | 48 | 3.2 | 894 | 5 | BY082428 | BY082428 |
| 1298 | 49.2 | 3.3 | 855 | 5 | BU962765 | BU962765 | AGENCOURT | 1371 | 47.8 | 3.2 | 357 | 5 | EX669589 | EX669589 |
| 1299 | 49.2 | 3.3 | 871 | 7 | CN331855 | CN331855 | AGENCOURT | 1372 | 47.8 | 3.2 | 404 | 5 | BM670310 | BM670310 |
| 1300 | 49.2 | 3.3 | 884 | 7 | CN832504 | CN832504 | AGENCOURT | 1373 | 47.8 | 3.2 | 459 | 2 | AM670310 | AM670310 |
| 1301 | 49.2 | 3.3 | 890 | 7 | CO927200 | CO927200 | AGENCOURT | 1374 | 47.8 | 3.2 | 528 | 4 | BS704681 | BS704681 |
| 1302 | 49.2 | 3.3 | 946 | 1 | AU079142 | AU079142 | AGENCOURT | 1375 | 47.8 | 3.2 | 1276 | 5 | BQ944424 | BQ944424 |
| 1303 | 49.2 | 3.3 | 949 | 7 | CO546392 | CO546392 | LYEST1665 | 1376 | 47.6 | 3.2 | 240 | 2 | BF896937 | BF896937 |
| 1304 | 49.2 | 3.3 | 1000 | 7 | CO543382 | CO543382 | LYEST1093 | 1377 | 47.6 | 3.2 | 346 | 5 | BY099872 | BY099872 |
| 1305 | 49.2 | 3.3 | 385 | 1 | AJ604640 | AJ604640 | AMGNNUC:M | 1378 | 47.6 | 3.2 | 352 | 5 | BY208732 | BY208732 |
| 1306 | 49.2 | 3.3 | 391 | 6 | CB775169 | CB775169 | AMGNNUC:M | 1379 | 47.6 | 3.2 | 352 | 5 | BY208990 | BY208990 |
| 1307 | 49.2 | 3.3 | 504 | 1 | AJ604900 | AJ604900 | AMGNNUC:M | 1380 | 47.6 | 3.2 | 355 | 5 | BI128100 | BI128100 |
| 1308 | 49.2 | 3.3 | 518 | 4 | BM023619 | BM023619 | 1e82905.y | 1381 | 47.6 | 3.2 | 355 | 5 | BY293965 | BY293965 |
| 1309 | 49.2 | 3.3 | 536 | 5 | BM688559 | BM688559 | AMGNNUC:M | 1382 | 47.6 | 3.2 | 357 | 5 | BY294461 | BY294461 |
| 1310 | 49.2 | 3.3 | 586 | 1 | AJ604693 | AJ604693 | AMGNNUC:M | 1383 | 47.6 | 3.2 | 359 | 5 | BY310127 | BY310127 |
| 1311 | 49.2 | 3.3 | 610 | 7 | CP365146 | CP365146 | 835753.MA | 1384 | 47.6 | 3.2 | 361 | 5 | BY090356 | BY090356 |
| 1312 | 49.2 | 3.3 | 610 | 7 | CP365146 | CP365146 | 835753.MA | 1385 | 47.6 | 3.2 | 362 | 5 | BY074115 | BY074115 |
| 1313 | 49.2 | 3.3 | 611 | 5 | BP016648 | BP016648 | AMGNNUC:M | 1386 | 47.6 | 3.2 | 365 | 5 | BI163806 | BI163806 |
| 1314 | 49.2 | 3.3 | 614 | 1 | AJ604742 | AJ604742 | AMGNNUC:M | 1387 | 47.6 | 3.2 | 366 | 7 | CF585782 | CF585782 |
| 1315 | 49.2 | 3.3 | 622 | 5 | BP016648 | BP016648 | AMGNNUC:M | 1388 | 47.6 | 3.2 | 368 | 5 | BY060827 | BY060827 |
| 1316 | 49.2 | 3.3 | 636 | 5 | BP016648 | BP016648 | AMGNNUC:M | 1389 | 47.6 | 3.2 | 371 | 5 | BY054153 | BY054153 |
| 1317 | 49.2 | 3.3 | 637 | 1 | AJ604861 | AJ604861 | AMGNNUC:M | 1390 | 47.6 | 3.2 | 373 | 5 | BY088761 | BY088761 |
| 1318 | 49.2 | 3.3 | 640 | 5 | BP016648 | BP016648 | AMGNNUC:M | 1391 | 47.6 | 3.2 | 374 | 5 | BY146384 | BY146384 |
| 1319 | 49.2 | 3.3 | 644 | 7 | CK459540 | CK459540 | 929734.MA | 1392 | 47.6 | 3.2 | 375 | 5 | BI204723 | BI204723 |
| 1320 | 49.2 | 3.3 | 652 | 1 | AJ604884 | AJ604884 | AMGNNUC:M | 1393 | 47.6 | 3.2 | 377 | 5 | BY105886 | BY105886 |
| 1321 | 49.2 | 3.3 | 655 | 1 | BM668104 | BM668104 | AMGNNUC:M | 1394 | 47.6 | 3.2 | 379 | 5 | BY165606 | BY165606 |
| 1322 | 49.2 | 3.3 | 673 | 4 | BM190123 | BM190123 | POSMO1000 | 1395 | 47.6 | 3.2 | 378 | 5 | BY038667 | BY038667 |
| 1323 | 49.2 | 3.3 | 674 | 5 | BM190123 | BM190123 | POSMO1000 | 1396 | 47.6 | 3.2 | 385 | 5 | BY099594 | BY099594 |
| 1324 | 49.2 | 3.3 | 674 | 5 | BM190123 | BM190123 | POSMO1000 | 1397 | 47.6 | 3.2 | 389 | 5 | BY307826 | BY307826 |
| 1325 | 49.2 | 3.3 | 676 | 5 | BM190123 | BM190123 | POSMO1000 | 1398 | 47.6 | 3.2 | 401 | 5 | BY086900 | BY086900 |
| 1326 | 49.2 | 3.3 | 677 | 5 | BM190123 | BM190123 | POSMO1000 | 1399 | 47.6 | 3.2 | 407 | 5 | BY059226 | BY059226 |
| 1327 | 49.2 | 3.3 | 677 | 5 | BM190123 | BM190123 | POSMO1000 | 1400 | 47.6 | 3.2 | 407 | 5 | BY272980 | BY272980 |
| 1328 | 49.2 | 3.3 | 680 | 5 | BM190123 | BM190123 | POSMO1000 | 1401 | 47.6 | 3.2 | 407 | 6 | CD546668 | CD546668 |
| 1329 | 49.2 | 3.3 | 680 | 5 | BM190123 | BM190123 | POSMO1000 | 1402 | 47.6 | 3.2 | 413 | 5 | BY155577 | BY155577 |
| 1330 | 49.2 | 3.3 | 680 | 5 | BM190123 | BM190123 | POSMO1000 | 1403 | 47.6 | 3.2 | 425 | 5 | BY260637 | BY260637 |
| 1331 | 49.2 | 3.3 | 680 | 5 | BM190123 | BM190123 | POSMO1000 | 1404 | 47.6 | 3.2 | 437 | 5 | BY041490 | BY041490 |
| 1332 | 49.2 | 3.3 | 681 | 5 | BM190123 | BM190123 | POSMO1000 | 1405 | 47.6 | 3.2 | 439 | 5 | CD552435 | CD552435 |
| 1333 | 49.2 | 3.3 | 682 | 5 | BM190123 | BM190123 | POSMO1000 | 1406 | 47.6 | 3.2 | 448 | 5 | BY081002 | BY081002 |
| 1334 | 49.2 | 3.3 | 682 | 5 | BM190123 | BM190123 | POSMO1000 | 1407 | 47.6 | 3.2 | 455 | 6 | CB741218 | CB741218 |
| 1335 | 49.2 | 3.3 | 683 | 5 | BM190123 | BM190123 | POSMO1000 | 1408 | 47.6 | 3.2 | 457 | 6 | CB356292 | CB356292 |
| 1336 | 49.2 | 3.3 | 683 | 5 | BM190123 | BM190123 | POSMO1000 | 1409 | 47.6 | 3.2 | 468 | 5 | BY244998 | BY244998 |
| 1337 | 49.2 | 3.3 | 686 | 5 | BM190123 | BM190123 | POSMO1000 | 1410 | 47.6 | 3.2 | 469 | 5 | BE495028 | BE495028 |
| 1338 | 49.2 | 3.3 | 686 | 5 | BM190123 | BM190123 | POSMO1000 | 1411 | 47.6 | 3.2 | 474 | 2 | BE653343 | BE653343 |

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|------|------|-----|-----|----------|----------|------------|-----------|------|-----|-----|---|----------|----------|-----------|
| 1412 | 47.6 | 3.2 | 484 | BE266466 | BE266466 | 6010899298 | 1485 | 47.6 | 3.2 | 780 | 5 | BU945837 | BU945837 | AGENCOURT |
| 1413 | 47.6 | 3.2 | 501 | BI845502 | BI845502 | EE97808.Y | 1486 | 47.6 | 3.2 | 783 | 6 | CA463011 | CA463011 | AGENCOURT |
| 1414 | 47.6 | 3.2 | 502 | BI181836 | BI181836 | EP69607.Y | 1487 | 47.6 | 3.2 | 784 | 5 | BU938817 | BU938817 | AGENCOURT |
| 1415 | 47.6 | 3.2 | 502 | BI846253 | BI846253 | EQ79809.Y | 1488 | 47.6 | 3.2 | 788 | 6 | CA463010 | CA463010 | AGENCOURT |
| 1416 | 47.6 | 3.2 | 506 | BQ840062 | BQ840062 | MAH73E12. | 1489 | 47.6 | 3.2 | 789 | 1 | AU080330 | AU080330 | AGENCOURT |
| 1417 | 47.6 | 3.2 | 513 | CB361178 | CB361178 | ZF001.-P00 | 1490 | 47.6 | 3.2 | 800 | 4 | BI158465 | BI158465 | AGENCOURT |
| 1418 | 47.6 | 3.2 | 525 | 4 | BI842193 | FGB3P03.X | 1491 | 47.6 | 3.2 | 800 | 4 | BI066881 | BI066881 | AGENCOURT |
| 1419 | 47.6 | 3.2 | 525 | 4 | BI846611 | FG80N05.X | 1492 | 47.6 | 3.2 | 802 | 1 | AU066841 | AU066841 | AGENCOURT |
| 1420 | 47.6 | 3.2 | 529 | 1 | BF721886 | MAB22G04. | 1493 | 47.6 | 3.2 | 807 | 5 | BU07589 | BU07589 | AGENCOURT |
| 1421 | 47.6 | 3.2 | 530 | 2 | AL913376 | AL913376 | 1494 | 47.6 | 3.2 | 807 | 6 | CA46524 | CA46524 | AGENCOURT |
| 1422 | 47.6 | 3.2 | 531 | 4 | BI845797 | FE97808.X | 1495 | 47.6 | 3.2 | 808 | 1 | AU051621 | AU051621 | AGENCOURT |
| 1423 | 47.6 | 3.2 | 534 | 4 | BI846582 | FGB0B09.X | 1496 | 47.6 | 3.2 | 814 | 5 | BU526317 | BU526317 | AGENCOURT |
| 1424 | 47.6 | 3.2 | 543 | 7 | CO552707 | ACLY890.S | 1497 | 47.6 | 3.2 | 820 | 5 | BU604400 | BU604400 | AGENCOURT |
| 1425 | 47.6 | 3.2 | 547 | 7 | CO552086 | ACLY1871 | 1498 | 47.6 | 3.2 | 821 | 5 | BU525907 | BU525907 | AGENCOURT |
| 1426 | 47.6 | 3.2 | 547 | 7 | CO552554 | ACLY698.S | 1499 | 47.6 | 3.2 | 824 | 5 | BU07958 | BU07958 | AGENCOURT |
| 1427 | 47.6 | 3.2 | 552 | 4 | BO748121 | FM13B02.Y | 1500 | 47.6 | 3.2 | 824 | 5 | BU938947 | BU938947 | AGENCOURT |
| 1428 | 47.6 | 3.2 | 556 | 5 | BO748121 | FM13B02.Y | | | | | | | | |
| 1429 | 47.6 | 3.2 | 562 | 7 | CK137814 | MAJ97F08. | | | | | | | | |
| 1430 | 47.6 | 3.2 | 567 | 6 | CK137814 | MAJ97F08. | | | | | | | | |
| 1431 | 47.6 | 3.2 | 572 | 4 | BI715547 | IC34D09.Y | | | | | | | | |
| 1432 | 47.6 | 3.2 | 573 | 4 | BG307019 | FM12A11.Y | | | | | | | | |
| 1433 | 47.6 | 3.2 | 576 | 7 | CF198113 | MAJ44C12. | | | | | | | | |
| 1434 | 47.6 | 3.2 | 581 | 2 | BF789438 | FM12A11.Y | | | | | | | | |
| 1435 | 47.6 | 3.2 | 586 | 6 | CB585581 | AMGNNUC.N | | | | | | | | |
| 1436 | 47.6 | 3.2 | 589 | 6 | CB272369 | MAJ57E12. | | | | | | | | |
| 1437 | 47.6 | 3.2 | 599 | 7 | CO551668 | ACLY1276 | | | | | | | | |
| 1438 | 47.6 | 3.2 | 602 | 2 | BB615796 | BB615796 | | | | | | | | |
| 1439 | 47.6 | 3.2 | 603 | 5 | BM947339 | UI-M-EGDP | | | | | | | | |
| 1440 | 47.6 | 3.2 | 606 | 7 | CO552280 | ACLY1.S | | | | | | | | |
| 1441 | 47.6 | 3.2 | 609 | 1 | AU251229 | AU251229 | | | | | | | | |
| 1442 | 47.6 | 3.2 | 613 | 7 | CK624281 | ML19C11.Y | | | | | | | | |
| 1443 | 47.6 | 3.2 | 615 | 7 | CO355177 | DR_AYE.NR | | | | | | | | |
| 1444 | 47.6 | 3.2 | 619 | 6 | CA050185 | SSALIRK0 | | | | | | | | |
| 1445 | 47.6 | 3.2 | 620 | 1 | AU051513 | AU051513 | | | | | | | | |
| 1446 | 47.6 | 3.2 | 620 | 2 | BB652381 | BB652381 | | | | | | | | |
| 1447 | 47.6 | 3.2 | 625 | 5 | BU057251 | UI-M-FRO- | | | | | | | | |
| 1448 | 47.6 | 3.2 | 629 | 6 | CA325957 | UI-M-FRO- | | | | | | | | |
| 1449 | 47.6 | 3.2 | 630 | 6 | BY738809 | BY738809 | | | | | | | | |
| 1450 | 47.6 | 3.2 | 631 | 5 | BQ266402 | NISC_FF12 | | | | | | | | |
| 1451 | 47.6 | 3.2 | 637 | 7 | CK602795 | CK602795 | AGENCOURT | | | | | | | |
| 1452 | 47.6 | 3.2 | 638 | 7 | CV054728 | AGENCOURT | | | | | | | | |
| 1453 | 47.6 | 3.2 | 648 | 2 | BE853985 | UX25C06.Y | | | | | | | | |
| 1454 | 47.6 | 3.2 | 650 | 6 | BY745290 | BY745290 | | | | | | | | |
| 1455 | 47.6 | 3.2 | 658 | 7 | CF978120 | 2-4-E02.F | | | | | | | | |
| 1456 | 47.6 | 3.2 | 661 | 6 | CB723954 | UI-M-GKO- | | | | | | | | |
| 1457 | 47.6 | 3.2 | 665 | 6 | CB522726 | UI-M-GKO- | | | | | | | | |
| 1458 | 47.6 | 3.2 | 666 | 5 | BU705072 | UI-M-FPO- | | | | | | | | |
| 1459 | 47.6 | 3.2 | 667 | 7 | CK398964 | AGENCOURT | | | | | | | | |
| 1460 | 47.6 | 3.2 | 677 | 7 | CN839865 | AGENCOURT | | | | | | | | |
| 1461 | 47.6 | 3.2 | 678 | 4 | BM049940 | 603624431 | | | | | | | | |
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| 1465 | 47.6 | 3.2 | 691 | 7 | CK706956 | ZF101.-P00 | | | | | | | | |
| 1466 | 47.6 | 3.2 | 702 | 7 | CN838256 | AGENCOURT | | | | | | | | |
| 1467 | 47.6 | 3.2 | 704 | 7 | CK363019 | AGENCOURT | | | | | | | | |
| 1468 | 47.6 | 3.2 | 715 | 7 | CN840793 | AGENCOURT | | | | | | | | |
| 1469 | 47.6 | 3.2 | 718 | 7 | CN838917 | AGENCOURT | | | | | | | | |
| 1470 | 47.6 | 3.2 | 719 | 7 | CN841960 | AGENCOURT | | | | | | | | |
| 1471 | 47.6 | 3.2 | 729 | 7 | BU962676 | AGENCOURT | | | | | | | | |
| 1472 | 47.6 | 3.2 | 732 | 7 | CN838050 | AGENCOURT | | | | | | | | |
| 1473 | 47.6 | 3.2 | 742 | 7 | CK695109 | ZF101.-P00 | | | | | | | | |
| 1474 | 47.6 | 3.2 | 744 | 6 | CA945720 | UI-M-FPO- | | | | | | | | |
| 1475 | 47.6 | 3.2 | 749 | 5 | BU562334 | AGENCOURT | | | | | | | | |
| 1476 | 47.6 | 3.2 | 749 | 7 | CN840954 | AGENCOURT | | | | | | | | |
| 1477 | 47.6 | 3.2 | 755 | 5 | BU937374 | AGENCOURT | | | | | | | | |
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| 1479 | 47.6 | 3.2 | 769 | 5 | BU945665 | AGENCOURT | | | | | | | | |
| 1480 | 47.6 | 3.2 | 771 | 5 | BU937075 | AGENCOURT | | | | | | | | |
| 1481 | 47.6 | 3.2 | 773 | 5 | BU612543 | UI-M-FRO- | | | | | | | | |
| 1482 | 47.6 | 3.2 | 776 | 1 | AU080211 | AU080211 | | | | | | | | |
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| 1484 | 47.6 | 3.2 | 777 | 1 | AU080507 | AU080507 | | | | | | | | |

| | | | | | | | |
|------|------|-----|-----|---|----------|----------|-----------|
| 1485 | 47.6 | 3.2 | 780 | 5 | BU945837 | BU945837 | AGENCOURT |
| 1486 | 47.6 | 3.2 | 783 | 6 | CA463011 | CA463011 | AGENCOURT |
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| 1489 | 47.6 | 3.2 | 789 | 1 | AU080330 | AU080330 | AGENCOURT |
| 1490 | 47.6 | 3.2 | 800 | 4 | BI158465 | BI158465 | AGENCOURT |
| 1491 | 47.6 | 3.2 | 800 | 4 | BI066881 | BI066881 | AGENCOURT |
| 1492 | 47.6 | 3.2 | 802 | 1 | AU066841 | AU066841 | AGENCOURT |
| 1493 | 47.6 | 3.2 | 807 | 5 | BU07589 | BU07589 | AGENCOURT |
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| 1495 | 47.6 | 3.2 | 808 | 1 | AU051621 | AU051621 | AGENCOURT |
| 1496 | 47.6 | 3.2 | 814 | 5 | BU526317 | BU526317 | AGENCOURT |
| 1497 | 47.6 | 3.2 | 820 | 5 | BU604400 | BU604400 | AGENCOURT |
| 1498 | 47.6 | 3.2 | 821 | 5 | BU525907 | BU525907 | AGENCOURT |
| 1499 | 47.6 | 3.2 | 824 | 5 | BU07958 | BU07958 | AGENCOURT |
| 1500 | 47.6 | 3.2 | 824 | 5 | BU938947 | BU938947 | AGENCOURT |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----------|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| RESULT 1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----------|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|

JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequefgenoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
Location/Qualifiers
1..1158
/organism="Homo sapiens"
/mol_type="mRNA"
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ORIGIN

Query Match 77.5%; Score 1151.6; DB 3; Length 1158;
Best Local Similarity 99.7%; Pred. No. 4.5e-293;
Matches 1154; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Oy 307 GACCTGATGCTTTTAAAGAGATGATGAGAAAGCTTGGTGTCCCAAGACCCTGGAG 366
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Oy 367 ATGAAGAGATGATCTCAGAGGTGACAGAGGGGTGACGTATATCTTACCGAAGC 426
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Db 121 TTTGGACATGATGCTGGGGGAAAGGTGGGTGCTGCTCAAGTTAGTATGATGTTTGA 180
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Oy 1027 CCATGCTTCCAGTGTCTGTGTCAACCCAGAGACAGCCACTGGGGCCCGCTGCCCA 1086
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Db 721 CCATGCTTCCAGTGTCTGTGTCAACCCAGAGACAGCCACTCGGGGCCCGCTGCCCA 780

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Db 841 AGAGCTTGGCATTTGGAGAGCCCTTCAAGAGATACCAAGAGAACCTTCCATCTGTCTC 900

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Db 1141 TGTCTGACCCCAATCTGC 1158

RESULT 4

AL556428 944 bp mRNA linear EST 02-APR-2004

LOCUS AL556428

DEFINITION AL556428 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens

ACCESSION CDNA clone CS0DK004Y121 5-PRIME, mRNA sequence.

VERSION AL556428

KEYWORDS AL556428.3 GI:46181850

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS 1 (bases 1 to 944)

TITLE Li, W.B., Graber, C., Jesse, J. and Polayes, D.

JOURNAL Full-length cDNA libraries and normalization

COMMENT Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31278230.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE

Email: sequefgenoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5100.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?b=CS0DK004CF11QPI&c=5100.f.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK004Y121"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."


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Db      599  GCCAGGGCAGGGA--GCTTCCAGCTGTGTGCCCTCACTTGGAGGAAACCAAGMACTCTCCA 541
Oy      896  TCCCTTCAAGAAAGTCTCAAGCAAGTTCAAGCTCACTGACCTGGCTCTGACGAGAACCC 955
Db      540  TCTCTTCAAGAAAGTCTCAAGCAAGTTCAAGCTCACTGACCTGGCTCTGAGAGAACCC 481
Oy      956  CAGGCACTCTGAGAAAGCTTGGAGTAAAGGCAAGGCTGACGAGGCTCTTTCGGGTTTC 1015
Db      480  CAGGCACTCTGAGAAAGCTTGGAGTAAAGGCAAGGCTGACGAGGCTCTTTCGGGTTTC 421
Oy      1016  CTTGACAGTGCATGTGTTCAGTGTCTGTGTGTCACCAAGACACACGACCACTCGGGGCC 1075
Db      420  CTTGACAGTGCATGTGTTCAGTGTCTGTGTGTCACCAAGACACACGACCACTCGGGGCC 361
Oy      1076  CCGCTGCCCCAGCTGATCCCACTCATATCCACCTCTTCATCTCAATGATGATGAG 1135
Db      360  CCGCTGCCCCAGCTGATCCCACTCATATCCACCTCTTCATCTCAATGATGATGAG 301
Oy      1136  GTGGAGAGAAAGAGAGCTTGGATTTGGAGGACCTTCAAGAAAGTACCAAGAAAGAACCTTC 1195
Db      300  GTGGAGAGAAAGAGAGCTTGGATTTGGAGGACCTTCAAGAAAGTACCAAGAAAGAACCTTC 241
Oy      1196  CAGTCTGCTCTCTGAGCCACACCTGTGACAGGACGCTGAGAGGACGCTGACGCTACTG 1255
Db      240  CAGTCTGCTCTCTGAGCCACACCTGTGACAGGACGCTGAGAGGACGCTGACGCTACTG 181
Oy      1256  TCCCTTACTGGGGGACAGAGGGCTTGGAGGACCAAGTGAAGGCTTGGGGG 1314
Db      180  TCCCTTACTGGGGGACAGAGGGCTTGGAGGACCAAGTGAAGTGAAGGCTTGGGGGG 121
Oy      1315  AAAGCTCAGCTCAGTGTCTTCCACCTTTTAAAGAGATCTGAGAGGACCAAGATGGGA 1374
Db      120  AAAGCTCAGCTCAGTGTCTTCCACCTTTTAAAGAGATCTGAGAGGACCAAGATGGGA 61
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Oy      1435  TA 1436
Db      2  TA 1

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RESULT 6
BX400361      894 bp      mRNA      linear      EST 29-APR-2004
LOCUS      BX400361 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
DEFINITION      Homo sapiens cDNA clone CS0DJ009YG24 5-PRIME, mRNA sequence.
ACCESSION      BX400361
VERSION      BX400361.2 GI:46875754
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 894)
L1.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30622186.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5100.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CS0DJ009BD120P1&c=5100.f.
Location/Qualifiers
FEATURES

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source
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/clone="CS0DJ009YG24"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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Query Match      55.8%; Score 828.4; DB 5; Length 894;
Best local Similarity 96.2%; Pred. No. 1.4e-207;
Matches 85; Conservative 8; Mismatches 24; Indels 2; Gaps 2;

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Oy      307  GACCTGATGCTTTAAAGAGATGATGAGAAAGCTGGTGTCCCAAGACCACTTGAG 366
Db      1  GACCTGATGCTTTAAAGAGATGATGAGAAAGCTGGTGTCCCAAGACCACTTGAG 60
Oy      367  ATGAAGAAAGATGATCTCAGAGGTGACAGAGGGGTCAAGTACATATATCTTACGAGAC 426
Db      61  ATGAAGAAAGATGATCTCAGAGGTGACAGAGGGGTCAAGTACATATATCTTACGAGAC 120
Oy      427  TTTGTGAACATGATGCTGGGAAACGGTGGCTGTCTCTCAAGTTAGTATGATGTTTAA 486
Db      121  TTTGTGAACATGATGCTGGGAAACGGTGGCTGTCTCTCAAGTTAGTATGATGTTTAA 180
Oy      487  GAAAGAGCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546
Db      181  GAAAGAGCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Oy      547  AGCTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 606
Db      241  AGCTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Oy      607  ATCTTGTGCTGCTCTCTTGAACACATGATGATCTCTCTCTCTCTCTCTCTCTCTCT 666
Db      301  ATCTTGTGCTGCTCTCTTGAACACATGATGATCTCTCTCTCTCTCTCTCTCTCTCT 360
Oy      667  GGGTTGTTGTGTTTTCATCATATGCTCTTGTAAAGCAAAATATCTGCTTAAAGGG 726
Db      361  GGGTTGTTGTGTTTTCATCATATGCTCTTGTAAAGCAAAATATCTGCTTAAAGGG 420
Oy      727  CTCTGGGTGGGGAATCTGAGCTTGGGTCCCTCTCTCTCTCTCTCTCTCTCTCTCT 786
Db      421  CTCTGGGTGGGGAATCTGAGCTTGGGTCCCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Oy      787  CTCCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846
Db      481  CTCCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Oy      847  GAGGCTTCCAGGC-TGTGTTCCCTCACTTGAAGAA-CCAGCACTCTCATCTTTTCA 904
Db      541  GAGGCTTCCAGGCCTGTGTTCCCTCACTTGAAGAA-CCAGCACTCTCATCTTTTCA 600
Oy      905  AAAGTCTCAAGCCAAAGTTCAAGGCTCACTGACCTGGCTCTGACAGAGAACCCAGGCCA 964
Db      601  AAAGTCTCAAGCCAAAGTTCAAGGCTCACTGACCTGGCTCTGACAGAGAACCCAGGCCA 660
Oy      965  CTGAGAAAGACTTGAATGAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1024
Db      661  CTGAGAAAGACTTGAATGAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Oy      1025  TGCCATGGTTCAGTGTCTGTGTGTCAACCAAGACAGACCACTCGGGGTCCCGTGGCC 1084
Db      721  TGCCATGGTTCAGTGTCTGTGTGTCAACCAAGACAGACCACTCGGGGTCCCGTGGCC 780
Oy      1085  CAGCTGATCCCACTCATTCACACCTCTTCTCATCTCAAGTATGTAAGTGGAGAG 1144

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| DEFINITION | AGENSCOURT 14373241 NIH MGC 181 Homo sapiens cDNA clone IMAGE:30398267 5', mRNA sequence. |
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| ACCESSION | CD514425 |
| VERSION | CD514425.1 GI:31446143 |
| KEYWORDS | EST. |
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. |
| REFERENCE | 1 (bases 1 to 842) NIH-MGC http://mgs.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) |
| AUTHORS | Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgabs-remail.nih.gov |
| TITLE | Tissue Procurement: Dr. Michael Brownstein cDNA Library Preparation: Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDAM482 row: 0 column: 12 High quality sequence stop: 721. |
| FEATURES | Location/Qualifiers 1..842 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:30398267" /tissue_type="White Matter" /dev_stage="unknown" /lab_host="DH10B-Ton A (T1 and T5 phage resistances) " /clone_11b="NIH_MGC 181" /note="Vector: PCMV-SpORF6.1; Site 1: NotI; Site 2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library." |
| ORIGIN | Query Match 50.6%; Score 751.4; DB 6; Length 842; Best Local Similarity 98.3%; Pred. No.3..1e-187; Matches 822; Conservative 0; Mismatches 7; Indels 7; Gaps 6 |
| Db | 3 GGGCACAGCAGGTAGCCGGAGCCCGGACCAAGGCGCTGAGCTCTCTCGTCCGCG 62 1 GGGCACAGCAGGTAGCCGGAGCCCGGACCAAGGCGCTGAGCTCTCTCGTCCGCG 60 |
| QY | 63 CGCGTCCGGAAGCCGTGAGCCCGGAGGCCCGCGCTCGCCATGTCGAGCGACTCAG 122 |
| Db | 61 CGCGTCCGGAAGCCGTGAGCCCGGAGGCCCGCGCTCGCCATGTCGAGCGACTCAG 120 |
| QY | 123 CAACAGTTCCAAAGAGGAGGAGGCGCTTGGCTTCAAGCCCGGACAGAGAGGAGCT 182 |
| Db | 121 CAACAGTTCCAAAGAGGAGGAGGCGCTTGGCTTCAAGCCCGGACAGAGAGGAGCT 180 |
| QY | 183 GGCCTGATCAACCGGAGATTCTGTGTGACCAAGAGTACAGTATGAAGAACTTCC 242 |
| Db | 181 GGCCTGATCAACCGGAGATTCTGTGTGACCAAGAGTACAGTATGAAGAACTTCC 240 |
| QY | 243 AGAAAGCTCACAGCTTCAAGAGAAATACATGAGATTGACCTGAACATTAAGCGCA 302 |
| Db | 241 AGAAAGCTCACAGCTTCAAGAGAAATACATGAGATTGACCTGAACATTAAGCGCA 300 |
| QY | 303 GATTGACCTGATCTTTTAAAGAGATGATGAGAGAGCTTGAGTCCCAAGACCACT 362 |
| Db | 301 GATTGACCTGATCTTTTAAAGAGATGATGAGAGAGCTTGAGTCCCAAGACCACT 360 |
| QY | 363 GGAGATGAAGAGATGATCTCAAGGTGACAGAGGGGCTCAGTATATCTTACCG 422 |

Db 361 GGACATTAAGAGATGATCTCAGAGGTGACAGAGGGGTCAGTAGACCTATATCTACCG 420
 Oy 423 AGACTTTGTGAACATGATGCTGGGGAACGCTCGGCTGTCTCAAGTTAGTCATGATGTT 482
 Db 421 AGACTTTGTGAACATGATGCTGGGGAACGCTCGGCTGTCTCAAGTTAGTCATGATGTT 480
 Oy 483 TGAAGAAAAAGCCACAGAGACAGCCCCAGACCAGTTGGGCCCTCTCAAGAGAGACAT 542
 Db 481 TGAAGAAAAAGCCACAGAGACAGCCCCAGACCAGTTGGGCCCTCTCAAGAGAGACAT 540
 Oy 543 TGTACGCTGCTCTGAGAGACCCCGGCTGAGCTCCCGACGCTTCCACCCATACCTCCCT 602
 Db 541 TGTACGCTGCTCTGAGAGACCCCGGCTGAGCTCCCGACGCTTCCACCCATACCTCCCT 600
 Oy 603 CCGGATCTGTGTCGCTCTTGAACACACTGATATCTCTCTCTCATTTGTTTGGTCA 662
 Db 601 CCGGATCTGTGTCGCTCTTGAACACACTGATATCTCTCTCTCATTTGTTTGGTCA 660
 Oy 663 TTGAGGGTTTGTGTGTTTCATCAATGTCTTTGTAAAGACAAATTAATTCGCTTAA 722
 Db 661 TTGAGGGTTTGTGTGTTTCATCAATGTCTTTGTAAAGACAAATTAATTCGCTTAA 720
 Oy 723 -GGGGCTCTGGGTC-GGGGAATCTGAGCTTT-GGGTCCCTCCCTCTCTTCCCT-C 778
 Db 721 GGGGGCTCTGGGTCGGGGGAATCTGAGCTCTGGGGTCCCTCTCTCTTCCCTCC 780
 Oy 779 CTTCGCCGCTCCCTGT-GCAGAGGGGCTGA--TATCAACCAAAAATTAGAGGGG 831
 Db 781 CTTCGCCGCTCCCTGTGCAAGAGGGCTGAAATATCAAAACCAAAAATTAGAGGGG 836

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RESULT 12
BX421987
LOCUS
DEFINITION
BX421987 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA
clone CSODH006YD09.5-PRIME, mRNA sequence.
ACCESSION
BX421987
VERSION
BX421987.2 GI:46934324
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 L.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
On May 13, 2003 this sequence version replaced gi:30659228.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5100.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdnats-CS0DH006CB05QPI&c=5100.f.
Location/Qualifiers
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FEATURES
SOURCE

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/organism="Homo sapiens"
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/clone="CS0DH006YD09"
/tissue_type="T CELLS (JURKAT CELL LINE)"
/clone_1ib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into

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QY 437 TGATGCTGGGAAACGGTGGCTGTCTCAAGTTAGTCATGTTGAAGAAAACCA 496
 DB 424 TGAATGCTGGGAAACGGTGGCTGTCTCAAGTTAGTCATGTTGAAGAAAACCA 483
 QY 497 ACGAGAGAGAGCCCAAGCCAGTTGGCCCTCCAGAGAGAGACATTGCTAGCCCT 556
 DB 484 ACGAGAGAGAGCCCAAGCCAGTTGGCCCTCCAGAGAGAGACATTGCTAGCCCT 543
 QY 557 GAGAGACCCGCTGAGCTCCCAAGCTCCCAAGCCCAAGCTCCCAAGCTCCCAAGCT 616
 DB 544 GAGAGACCCGCTGAGCTCCCAAGCTCCCAAGCTCCCAAGCTCCCAAGCTCCCAAGCT 603
 QY 617 CCTTCTTGAACAACATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 675
 DB 604 CCTTCTTGAACAACATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 663
 QY 676 TGTGTTTTCATCATGTCTTTGTAAGACAAATTAATCTGCTTAAAGGGGCTTGGG 733
 DB 664 TGTGTTTTCATCATGTCTTTGTAAGACAAATTAATCTGCTTAAAGGGGCTTGGG 723
 QY 734 --TGGGGAATCTGAGCTTGGGCTCCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT 789
 DB 724 TCGGGGAATCTGAGCTTGGGCTCCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 781

RESULT 14
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 LOCUS UI-CF-FNO-aex-g-19-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
 DEFINITION UI-CF-FNO-aex-g-19-0-UI 3', mRNA sequence.
 ACCESSION CA312962
 VERSION CA312962.1 GI:24531060
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 701)
 AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 9704477
 PUBMED 8889548

COMMENT Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171

Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 SOURCE Location/Qualifiers

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 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-FNO"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site: Ecor I; Site 2: Not I;
 UI-CF-FNO is a subtracted cDNA library derived from two

normalized Human lung epithelial cell libraries (EN1 and
 D01). The library was subtracted according to
 Ronaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. For additional information, contact:
 paul-mccray@uiowa.edu
 paul-mccray@uiowa.edu
 TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
 6hr to LPS 24h
 TAG LIB=UI-CF-FNO
 TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 47.2%; Score 701; DB 6; Length 701;
 Best local Similarity 100.0%; Pred. No. 6.4e-174;
 Matches 701; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 785 CGCTCCCTGTCAGAGAGGCTGATTCAAACCAAACTAGAGGGGCGAGGCGCA 844
 DB 701 CGCTCCCTGTCAGAGAGGCTGATTCAAACCAAACTAGAGGGGCGAGGCGCA 642
 QY 845 GGGAGGCTTCAGAGCTGTGTCCCTCACTTGAAGAACAGCACTTTCATCTTTGAG 904
 DB 641 GGGAGGCTTCAGAGCTGTGTCCCTCACTTGAAGAACAGCACTTTCATCTTTGAG 582
 QY 905 AAAGTCCAGAGCAAGTTGAGCTGACCTGACCTGCTGAGAGAGACCCAGGCACT 964
 DB 581 AAAGTCCAGAGCAAGTTGAGCTGACCTGACCTGCTGAGAGAGACCCAGGCACT 522
 QY 965 CTGAGAAACCTTGGAGTGGGAGCAAGGCTGAGGCTCTTTCGGTTTCTTGGAGAG 1024
 DB 521 CTGAGAAACCTTGGAGTGGGAGCAAGGCTGAGGCTCTTTCGGTTTCTTGGAGAG 462
 QY 1025 TGCATAGTTTCAAGTGTCTGTGTGTCACCGAGAGCAAGCACTCGGGGCTCCGCTGCC 1084
 DB 461 TGCATAGTTTCAAGTGTCTGTGTGTCACCGAGAGCAAGCACTCGGGGCTCCGCTGCC 402
 QY 1085 CAGCTGATCCCACTGATTCACACCTCTTCTCATCTCAGTATGTAAGTGGAGAG 1144
 DB 401 CAGCTGATCCCACTGATTCACACCTCTTCTCATCTCAGTATGTAAGTGGAGAG 342
 QY 1145 AAAGAGCTTGGAGCTTGGAGAGGCTTTCAGAGAGTACAGAGAGAACTCTCAGTCTGC 1204
 DB 341 AAAGAGCTTGGAGCTTGGAGAGGCTTTCAGAGAGTACAGAGAGAACTCTCAGTCTGC 282
 QY 1205 TCTCTGAGCAACCTGTGTGAGGAGCTGAGAGGAGCAAGCTCAGTCTCTACT 1264
 DB 281 TCTCTGAGCAACCTGTGTGAGGAGCTGAGAGGAGCAAGCTCAGTCTCTACT 222
 QY 1265 GGGGAGAGAGAGGCTTCGAGAGGAGAGGAGCTGAGGCTTGGGGGAGAAAGTCAAGC 1324
 DB 221 GGGGAGAGAGAGGCTTCGAGAGGAGAGGAGCTGAGGCTTGGGGGAGAAAGTCAAGC 162
 QY 1325 TCAGTGTGTTCACCTTTTGAAGAGATCTGAGGAGGAGCAAGATGGAGATGAGAGAG 1384
 DB 161 TCAGTGTGTTCACCTTTTGAAGAGATCTGAGGAGGAGCAAGATGGAGATGAGAGAG 102
 QY 1385 TAAATGTCTCAGGCAAGATGAGAGAGCTGTAGGCAAGACTGAGAAATACAGGTTG 1444
 DB 101 TAAATGTCTCAGGCAAGATGAGAGAGCTGTAGGCAAGACTGAGAAATACAGGTTG 42
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RESULT 15
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 DEFINITION AUI33192 NT2RP4 Homo sapiens cDNA clone NT2RP4001514 5', mRNA
 ACCESSION AUI33192
 VERSION AUI33192.1 GI:10993731
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 701)

REFERENCE
 Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y., Saio, K., Yamamoto, J.,
 Nishikawa, T., Nakamura, Y., Nagai, T., Sugano, S., Masuno, Y., and
 Isogai, T.
 HRI human cDNA project (Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y.,
 Saio, K., Yamamoto, J., Nishikawa, T., Nakamura, Y., Nagai, T.,
 Sugano, S., Masuno, Y., Isogai, T.)
 Unpublished (2000)

JOURNAL
 COMMENT
 Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kigarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genom@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.
 Location/Qualifiers
 1..701
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 /cell_type="teratocarcinoma"
 /cell_line="NT2"
 /clone_1ib="NT2RP4"
 /note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
 cells after 2-weeks retinoic acid (RA) induction"

ORIGIN

Query Match 46.5%; Score 690; DB 1; Length 701;
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 Matches 693; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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 Db 1 GAACCTCCCGACGCTTCCACCCCATCTCCCTCCGATCTTGGCTTCTTGACACA 60
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Dy 630 CTGATGATCTCTCTCTCTCAATTGTTGGTCATTGAGGGTTGTTGTTTCATCAA 689
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 Db 61 CTGATGATCTCTCTCTCTCAATTGTTGGTCATTGAGGGTTGTTGTTTCATCAA 120
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Dy 690 TGCTTTGTAAAGCAAAATTATCTGCTTAAAGGGCTCTGGGTCGGGAATCTGAGC 749
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Dy 750 CTGGGTCCT 809
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 Db 181 CTGGGTCCT 240
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Dy 810 TCAAAACCAAAACTAGAGGGGGCAGGGGCAGGGGCAGGGGCAGGGGCAGGGGCAG 869
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 Db 241 TCAAAACCAAAACTAGAGGGGGCAGGGGCAGGGGCAGGGGCAGGGGCAGGGGCAG 300
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Dy 870 TCACTGGAGGAGCAGCACTCTCCATCTCTTCAAGAAAGTCTCCAAGCCAAGTTCAGGCT 929
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 Db 301 TCACTGGAGGAGCAGCACTCTCTCAATCTCTTCAAGAAAGTCTCCAAGCCAAGTTCAGGCT 360
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Dy 930 CACTGACCTGGCTCTGACGAGGAGCCCAAGGCCACTCTGAGAAAGCTTGAAGTAAAGGACA 989
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 Db 361 CACTGACCTGGCTCTGACGAGGAGCCCAAGGCCACTCTGAGAAAGCTTGAAGTAAAGGACA 420
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Dy 990 AGGCTGCAAGGGCTCTTCTGGGTTCTTGGACAGTGCATGTTCCAGTCTCTGGGT 1049
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 Db 421 AGGCTGCAAGGGCTCTTCTGGGTTCTTGGACAGTGCATGTTCCAGTCTCTGGGT 480
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Dy 1050 CACCAGGACACAGCACTCGGGGCCCGCTGCCCAAGTATCCCACTCATTCACAC 1109
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Db 481 CACCAGGACACAGCACTCGGGGCCCGCTGCCCAAGTATCCCACTCATTCACAC 540
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Dy 1110 CTCTTTCATCTCAGTATGATGTGAAGGTGGAGAAAGAGCTTGGCATTTGGAGCCCT 1169
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Db 541 CTCTTTCATCTCAGTATGATGTGAAGGTGGAGAAAGAGCTTGGCATTTGGAGCCCT 600
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Dy 1170 TCAAGAAAGTACCAAGAAAGAACCTCCAGTCTCTCTGAGCCACACTGTGACAGGAG 1229
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Db 601 TCAAGAAAGTACCAAGAAAGAACCTTTCAGTCTCTCTGAGCCACACTGTGACAGGAG 660
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Dy 1230 CTGAGAGGACGCTGACAGCCCTTACTGTCTTACTGAGGACA 1270
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Db 661 CTGAAAGCAGCGTGCAGCCCTTACTGATCCCTTACTGAGGACA 701
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Search completed: March 29, 2005, 01:31:36
 Job time : 5461 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using BW model

Run on: March 29, 2005, 03:23:39 ; Search time 2717 Seconds
(without alignments)
3257.125 Million cell updates/sec

Perfect score: 1485
Sequence: 1 gcggccacacgcagctagcc.....tgaaaaaaaaaaaaaa 1485

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications_NA:*

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19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------------|-------------------|
| 51 | 1485 | 100.0 | 1485 | US-10-219-085-109 | Sequence 209, App |
| 52 | 1485 | 100.0 | 1485 | US-10-219-085-109 | Sequence 109, App |
| 53 | 1485 | 100.0 | 1485 | US-10-223-084-209 | Sequence 209, App |
| 54 | 1485 | 100.0 | 1485 | US-10-223-088-209 | Sequence 209, App |
| 55 | 1485 | 100.0 | 1485 | US-10-223-090-209 | Sequence 209, App |
| 56 | 1485 | 100.0 | 1485 | US-10-223-087-209 | Sequence 209, App |
| 57 | 1485 | 100.0 | 1485 | US-10-223-083-209 | Sequence 209, App |
| 58 | 1485 | 100.0 | 1485 | US-10-223-089-209 | Sequence 209, App |
| 59 | 1485 | 100.0 | 1485 | US-10-013-909A-195 | Sequence 195, App |
| 60 | 1485 | 100.0 | 1485 | US-10-223-081-209 | Sequence 209, App |
| 61 | 1485 | 100.0 | 1485 | US-10-223-082-209 | Sequence 209, App |
| 62 | 1485 | 100.0 | 1485 | US-10-305-654-209 | Sequence 209, App |

| | | | | | |
|-----|--------|-------|-------|----------------------|---------------------|
| 15 | 1485 | 100.0 | 1485 | US-10-081-056-209 | Sequence 209, App |
| 182 | 1430.8 | 95.4 | 1731 | US-10-098-841-256 | Sequence 256, App |
| 183 | 1423.2 | 95.8 | 3470 | US-10-001-887-29 | Sequence 29, App |
| 184 | 1423.2 | 95.8 | 3470 | US-10-958-863-29 | Sequence 29, App |
| 185 | 1236 | 83.2 | 1343 | US-10-172-118-2540 | Sequence 2540, App |
| 186 | 1236 | 83.2 | 1343 | US-10-342-887-2540 | Sequence 2540, App |
| 187 | 476.2 | 32.1 | 593 | US-09-918-995-27025 | Sequence 27025, App |
| 188 | 472.4 | 31.8 | 528 | US-10-240-425-80 | Sequence 80, App |
| 189 | 451.4 | 30.4 | 453 | US-10-343-662-33 | Sequence 33, App |
| 190 | 278.4 | 18.7 | 393 | US-10-001-887-28 | Sequence 28, App |
| 191 | 278.4 | 18.7 | 393 | US-10-958-863-28 | Sequence 28, App |
| 192 | 192.2 | 12.9 | 444 | US-10-343-662-32 | Sequence 32, App |
| 193 | 192.2 | 12.9 | 658 | US-09-782-142-5 | Sequence 5, App |
| 194 | 192.2 | 12.9 | 658 | US-10-300-257-5 | Sequence 5, App |
| 195 | 192.2 | 12.9 | 760 | US-10-723-860-5430 | Sequence 5430, App |
| 196 | 191 | 12.9 | 639 | US-10-172-118-639 | Sequence 639, App |
| 197 | 191 | 12.9 | 639 | US-10-342-887-639 | Sequence 639, App |
| 198 | 191 | 12.9 | 639 | US-10-775-169-181 | Sequence 181, App |
| 199 | 178.4 | 12.0 | 467 | US-10-242-535A-29340 | Sequence 29340, App |
| 200 | 178.4 | 12.0 | 467 | US-10-085-783A-29340 | Sequence 29340, App |
| 201 | 159 | 10.7 | 480 | US-10-242-535A-34848 | Sequence 34848, App |
| 202 | 159 | 10.7 | 480 | US-10-085-783A-34848 | Sequence 34848, App |
| 203 | 154 | 10.4 | 460 | US-10-242-535A-52580 | Sequence 52580, App |
| 204 | 154 | 10.4 | 460 | US-10-085-783A-52580 | Sequence 52580, App |
| 205 | 146 | 9.8 | 451 | US-10-242-535A-28647 | Sequence 28647, App |
| 206 | 146 | 9.8 | 451 | US-10-085-783A-28647 | Sequence 28647, App |
| 207 | 144 | 9.7 | 372 | US-10-242-535A-32608 | Sequence 32608, App |
| 208 | 144 | 9.7 | 372 | US-10-085-783A-32608 | Sequence 32608, App |
| 209 | 142.4 | 9.6 | 353 | US-10-242-535A-37737 | Sequence 37737, App |
| 210 | 142.4 | 9.6 | 353 | US-10-085-783A-37737 | Sequence 37737, App |
| 211 | 137.4 | 9.3 | 358 | US-10-242-535A-56491 | Sequence 56491, App |
| 212 | 137.4 | 9.3 | 358 | US-10-085-783A-56491 | Sequence 56491, App |
| 213 | 128.2 | 8.6 | 340 | US-10-242-535A-53116 | Sequence 53116, App |
| 214 | 128.2 | 8.6 | 340 | US-10-085-783A-53116 | Sequence 53116, App |
| 215 | 117.8 | 7.9 | 379 | US-10-085-783A-53116 | Sequence 29594, App |
| 216 | 117 | 7.9 | 117 | US-10-343-662-14 | Sequence 14, App |
| 217 | 104.2 | 7.0 | 117 | US-10-343-662-15 | Sequence 15, App |
| 218 | 98.8 | 6.0 | 117 | US-10-343-662-16 | Sequence 16, App |
| 219 | 79.4 | 5.3 | 1363 | US-10-172-118-1093 | Sequence 1093, App |
| 220 | 79.4 | 5.3 | 1363 | US-10-159-563-150 | Sequence 150, App |
| 221 | 79.4 | 5.3 | 1363 | US-10-342-887-1093 | Sequence 1093, App |
| 222 | 79.4 | 5.3 | 13818 | US-10-741-600-18010 | Sequence 18010, App |
| 223 | 79.4 | 5.3 | 38449 | US-10-741-600-17793 | Sequence 17793, App |
| 224 | 73.4 | 4.9 | 325 | US-10-723-860-829 | Sequence 829, App |
| 225 | 68.8 | 4.6 | 1897 | US-10-302-172-444 | Sequence 444, App |
| 226 | 68.8 | 4.6 | 1924 | US-09-971-992-217 | Sequence 217, App |
| 227 | 64.2 | 4.3 | 717 | US-09-764-875-27 | Sequence 27, App |
| 228 | 64.2 | 4.3 | 2369 | US-10-252-157-401 | Sequence 401, App |
| 229 | 63.2 | 4.3 | 1358 | US-10-641-643-84 | Sequence 84, App |
| 230 | 63 | 4.2 | 505 | US-09-764-881-49 | Sequence 49, App |
| 231 | 63 | 4.2 | 505 | US-09-764-881-49 | Sequence 49, App |
| 232 | 63 | 4.2 | 505 | US-09-764-875-350 | Sequence 350, App |
| 233 | 63 | 4.2 | 505 | US-10-242-747-49 | Sequence 49, App |
| 234 | 63 | 4.2 | 505 | US-10-158-057-109 | Sequence 109, App |
| 235 | 62.6 | 4.2 | 117 | US-10-343-662-11 | Sequence 11, App |
| 236 | 59.4 | 4.0 | 117 | US-10-343-662-12 | Sequence 12, App |
| 237 | 59.4 | 4.0 | 117 | US-10-343-662-13 | Sequence 13, App |
| 238 | 55 | 3.7 | 233 | US-10-242-535A-10451 | Sequence 10451, App |
| 239 | 55 | 3.7 | 233 | US-10-085-783A-10451 | Sequence 10451, App |
| 240 | 54.4 | 3.7 | 186 | US-09-864-761-19243 | Sequence 19243, App |
| 241 | 54.4 | 3.7 | 346 | US-10-242-535A-9291 | Sequence 9291, App |
| 242 | 54.4 | 3.7 | 346 | US-10-085-783A-9291 | Sequence 9291, App |
| 243 | 54.4 | 3.7 | 500 | US-09-864-761-5515 | Sequence 2515, App |
| 244 | 54.2 | 3.6 | 6907 | US-10-312-84-1 | Sequence 1, App |
| 245 | 54.2 | 3.6 | 11339 | US-10-312-84-1 | Sequence 1, App |
| 246 | 49.6 | 3.3 | 996 | US-10-437-963-43762 | Sequence 43762, App |
| 247 | 46.6 | 3.1 | 996 | US-10-425-114-27884 | Sequence 27884, App |
| 248 | 46.6 | 3.1 | 996 | US-10-425-115-68928 | Sequence 68928, App |
| 249 | 46.6 | 3.1 | 2451 | US-10-282-122A-14697 | Sequence 14697, App |
| 250 | 46 | 3.1 | 768 | US-10-260-338-3829 | Sequence 3629, App |
| 251 | 46 | 3.1 | 933 | US-10-767-701-15528 | Sequence 15528, App |
| 252 | 46 | 3.1 | 1241 | US-10-767-701-14604 | Sequence 14604, App |
| 253 | 45.8 | 3.1 | 1911 | US-10-411-910A-225 | Sequence 225, App |

| | | | | | | | | | | | | | |
|-----|------|-----|-------|----|----------------------|---------------------|-----|------|-----|---------|----|----------------------|---------------------|
| 254 | 45.6 | 3.1 | 1001 | 18 | US-10-723-860-6582 | Sequence 6582, Ap | 327 | 41.2 | 2.8 | 941 | 18 | US-10-425-115-89653 | Sequence 89653, A |
| 255 | 45.2 | 3.0 | 303 | 10 | US-09-237-183A-559 | Sequence 559, App | 328 | 41.2 | 2.8 | 942 | 18 | US-10-739-930-2800 | Sequence 2800, Ap |
| 256 | 45.2 | 3.0 | 433 | 18 | US-10-674-124A-12589 | Sequence 12589, A | 329 | 41.2 | 2.8 | 1228 | 18 | US-10-425-115-40697 | Sequence 40697, A |
| 257 | 45 | 3.0 | 1112 | 17 | US-10-152-119A-1701 | Sequence 1701, Ap | 330 | 41.2 | 2.8 | 1296 | 18 | US-10-425-115-40696 | Sequence 40696, A |
| 258 | 44.6 | 3.0 | 516 | 19 | US-10-696-639-982 | Sequence 982, App | 331 | 41.2 | 2.8 | 1769 | 18 | US-10-425-115-40698 | Sequence 40698, A |
| 259 | 44.6 | 3.0 | 863 | 17 | US-10-424-599-39046 | Sequence 39046, A | 332 | 41.2 | 2.8 | 3450 | 18 | US-10-425-115-139580 | Sequence 123580, A |
| 260 | 44.6 | 3.0 | 3372 | 14 | US-10-067-457-2 | Sequence 2, Appl1 | 333 | 41 | 2.8 | 975 | 9 | US-09-938-842A-2193 | Sequence 2193, Ap |
| 261 | 44.6 | 3.0 | 3459 | 17 | US-10-311-795-3 | Sequence 3, Appl1 | 334 | 41 | 2.8 | 975 | 11 | US-09-938-842A-2193 | Sequence 2193, Ap |
| 262 | 44.4 | 3.0 | 787 | 15 | US-10-425-114-18116 | Sequence 18116, A | 335 | 40.6 | 2.7 | 1129 | 18 | US-10-653-047-7032 | Sequence 7032, Ap |
| 263 | 44.4 | 3.0 | 787 | 15 | US-10-259-165-594 | Sequence 594, App | 336 | 40.6 | 2.7 | 426 | 18 | US-10-637-963-99465 | Sequence 99465, A |
| 264 | 44.4 | 3.0 | 801 | 17 | US-10-260-238-3631 | Sequence 3631, Ap | 337 | 40.6 | 2.7 | 560 | 18 | US-10-767-795-4912 | Sequence 4912, Ap |
| 265 | 44.4 | 3.0 | 842 | 17 | US-10-260-238-3636 | Sequence 3636, Ap | 338 | 40.6 | 2.7 | 724 | 17 | US-10-767-795-4912 | Sequence 2936, Ap |
| 266 | 44.4 | 3.0 | 909 | 17 | US-10-260-238-3639 | Sequence 3639, Ap | 339 | 40.6 | 2.7 | 1794 | 18 | US-10-260-238-2936 | Sequence 66912, A |
| 267 | 44.4 | 3.0 | 909 | 17 | US-10-435-114-5085 | Sequence 5085, Ap | 340 | 40.6 | 2.7 | 164407 | 18 | US-10-437-963-66912 | Sequence 305, App |
| 268 | 44.4 | 3.0 | 910 | 17 | US-10-435-114-5085 | Sequence 28387, Ap | 341 | 40.4 | 2.7 | 974 | 11 | US-09-876-143-1398 | Sequence 1398, Ap |
| 269 | 44.4 | 3.0 | 958 | 17 | US-10-425-115-129635 | Sequence 129635, A | 342 | 40.4 | 2.7 | 974 | 11 | US-09-876-143-1398 | Sequence 1399, Ap |
| 270 | 44.4 | 3.0 | 975 | 18 | US-10-425-115-129635 | Sequence 129635, A | 343 | 40.4 | 2.7 | 2240 | 17 | US-10-108-260A-1195 | Sequence 1195, Ap |
| 271 | 44.4 | 3.0 | 1196 | 18 | US-10-425-115-129635 | Sequence 129635, A | 344 | 40.2 | 2.7 | 654 | 9 | US-09-917-800A-1352 | Sequence 30537, A |
| 272 | 44 | 3.0 | 1251 | 10 | US-09-989-025A-7 | Sequence 129659, A | 345 | 40.2 | 2.7 | 679 | 18 | US-10-425-115-30537 | Sequence 30538, A |
| 273 | 44 | 3.0 | 2175 | 14 | US-10-175-523-17 | Sequence 17, Appl1 | 346 | 40.2 | 2.7 | 1070 | 17 | US-10-425-114-35458 | Sequence 68330, A |
| 274 | 44 | 3.0 | 2247 | 16 | US-10-119-428-34 | Sequence 34, Appl1 | 347 | 40.2 | 2.7 | 1762 | 18 | US-10-425-115-68330 | Sequence 61316, A |
| 275 | 44 | 3.0 | 2247 | 17 | US-10-129-172-31 | Sequence 31, Appl1 | 348 | 40.2 | 2.7 | 2394 | 17 | US-10-282-122A-31744 | Sequence 5472, Ap |
| 276 | 44 | 3.0 | 2247 | 17 | US-10-221-278-31 | Sequence 31, Appl1 | 349 | 40.2 | 2.7 | 3446 | 18 | US-10-723-860-5472 | Sequence 5, Appl1 |
| 277 | 43.8 | 2.9 | 255 | 10 | US-09-237-183A-828 | Sequence 828, App | 350 | 40.2 | 2.7 | 3513 | 14 | US-10-175-523-102 | Sequence 102, Appl1 |
| 278 | 43.6 | 2.9 | 1161 | 9 | US-09-954-531-575 | Sequence 575, App | 351 | 40.2 | 2.7 | 3513 | 14 | US-10-175-523-102 | Sequence 102, Appl1 |
| 279 | 43.6 | 2.9 | 1170 | 18 | US-10-411-910A-227 | Sequence 227, App | 352 | 40.2 | 2.7 | 3513 | 17 | US-10-152-319A-1362 | Sequence 1362, Ap |
| 280 | 43.4 | 2.9 | 2465 | 10 | US-09-953-348-83 | Sequence 83, Appl1 | 353 | 40.2 | 2.7 | 3513 | 18 | US-10-437-963-67100 | Sequence 67100, A |
| 281 | 43.4 | 2.9 | 2465 | 15 | US-10-267-255-83 | Sequence 83, Appl1 | 354 | 40 | 2.7 | 1278 | 18 | US-10-086-738A-1 | Sequence 1 |
| 282 | 43.4 | 2.9 | 18034 | 15 | US-09-953-348-75 | Sequence 75, Appl1 | 355 | 40 | 2.7 | 1397 | 18 | US-10-437-963-76274 | Sequence 76274, A |
| 283 | 43.4 | 2.9 | 18034 | 15 | US-10-267-255-75 | Sequence 75, Appl1 | 356 | 40 | 2.7 | 406 | 18 | US-10-425-115-90606 | Sequence 90606, A |
| 284 | 43.2 | 2.9 | 294 | 10 | US-09-237-183A-618 | Sequence 618, Appl1 | 357 | 39.8 | 2.7 | 289 | 10 | US-10-674-124A-754 | Sequence 754, App |
| 285 | 43.2 | 2.9 | 447 | 10 | US-09-989-025A-3 | Sequence 3, Appl1 | 358 | 39.8 | 2.7 | 290 | 18 | US-10-674-124A-754 | Sequence 754, App |
| 286 | 43.2 | 2.9 | 878 | 17 | US-10-425-114-4443 | Sequence 4443, App | 359 | 39.8 | 2.7 | 329 | 10 | US-09-237-183A-709 | Sequence 709, App |
| 287 | 43.2 | 2.9 | 1227 | 17 | US-10-425-114-725 | Sequence 725, App | 360 | 39.8 | 2.7 | 406 | 18 | US-10-425-115-90606 | Sequence 90606, A |
| 288 | 43.2 | 2.9 | 1227 | 17 | US-10-425-114-725 | Sequence 725, App | 361 | 39.8 | 2.7 | 1339 | 14 | US-10-062-727-404 | Sequence 404, App |
| 289 | 43.2 | 2.9 | 1936 | 17 | US-10-425-114-37755 | Sequence 37755, A | 362 | 39.8 | 2.7 | 1139 | 17 | US-10-191-803-111 | Sequence 111, App |
| 290 | 43.2 | 2.9 | 1936 | 17 | US-10-425-114-37755 | Sequence 37755, A | 363 | 39.8 | 2.7 | 1139 | 17 | US-10-191-803-111 | Sequence 111, App |
| 291 | 43.2 | 2.9 | 1936 | 17 | US-10-425-114-37755 | Sequence 37755, A | 364 | 39.8 | 2.7 | 1139 | 17 | US-10-191-803-111 | Sequence 111, App |
| 292 | 43 | 2.9 | 289 | 10 | US-09-237-183A-676 | Sequence 676, App | 365 | 39.8 | 2.7 | 156 | 18 | US-10-437-963-30745 | Sequence 30745, A |
| 293 | 43 | 2.9 | 378 | 14 | US-10-062-727-395 | Sequence 676, App | 366 | 39.8 | 2.7 | 1890 | 17 | US-10-369-493-30745 | Sequence 30745, A |
| 294 | 43 | 2.9 | 450 | 14 | US-10-062-727-395 | Sequence 6609, App | 367 | 39.6 | 2.7 | 1929 | 17 | US-10-369-493-30745 | Sequence 30745, A |
| 295 | 43 | 2.9 | 450 | 14 | US-10-062-727-395 | Sequence 542, App | 368 | 39.6 | 2.7 | 541 | 17 | US-10-260-228-3634 | Sequence 3634, App |
| 296 | 42.8 | 2.9 | 803 | 17 | US-10-425-114-22255 | Sequence 862, App | 369 | 39.6 | 2.7 | 545 | 18 | US-10-260-228-3634 | Sequence 3634, App |
| 297 | 42.8 | 2.9 | 803 | 17 | US-10-425-114-22255 | Sequence 22255, A | 370 | 39.6 | 2.7 | 695 | 17 | US-10-425-114-745 | Sequence 745, App |
| 298 | 42.8 | 2.9 | 820 | 17 | US-10-260-238-3635 | Sequence 22255, A | 371 | 39.6 | 2.7 | 709 | 17 | US-10-260-238-3635 | Sequence 709, App |
| 299 | 42.8 | 2.9 | 820 | 17 | US-10-260-238-3635 | Sequence 3635, App | 372 | 39.6 | 2.7 | 727 | 17 | US-10-425-114-3541 | Sequence 3541, App |
| 300 | 42.6 | 2.9 | 1668 | 18 | US-10-411-910A-326 | Sequence 2210, App | 373 | 39.6 | 2.7 | 727 | 17 | US-10-425-114-3541 | Sequence 3541, App |
| 301 | 42.6 | 2.9 | 306 | 10 | US-09-237-183A-609 | Sequence 622, App | 374 | 39.6 | 2.7 | 915 | 18 | US-10-739-930-3113 | Sequence 25942, A |
| 302 | 42.6 | 2.9 | 313 | 10 | US-09-237-183A-609 | Sequence 622, App | 375 | 39.6 | 2.7 | 915 | 18 | US-10-739-930-3113 | Sequence 25942, A |
| 303 | 42.4 | 2.9 | 282 | 18 | US-10-674-124A-3952 | Sequence 3952, App | 376 | 39.6 | 2.7 | 1039 | 17 | US-10-425-114-25780 | Sequence 40636, A |
| 304 | 42.2 | 2.8 | 756 | 18 | US-10-437-963-101008 | Sequence 3952, App | 377 | 39.6 | 2.7 | 1039 | 17 | US-10-425-114-25780 | Sequence 40636, A |
| 305 | 42.2 | 2.8 | 756 | 18 | US-10-437-963-101008 | Sequence 101008, A | 378 | 39.6 | 2.7 | 1088 | 17 | US-10-424-599-94036 | Sequence 94036, A |
| 306 | 42.2 | 2.8 | 756 | 18 | US-10-437-963-101008 | Sequence 101008, A | 379 | 39.6 | 2.7 | 1140 | 18 | US-10-424-599-94036 | Sequence 94036, A |
| 307 | 41.6 | 2.8 | 1948 | 18 | US-10-425-115-92916 | Sequence 92916, A | 380 | 39.6 | 2.7 | 1140 | 18 | US-10-424-599-94036 | Sequence 94036, A |
| 308 | 41.6 | 2.8 | 1948 | 18 | US-10-425-115-92916 | Sequence 92916, A | 381 | 39.6 | 2.7 | 1140 | 18 | US-10-424-599-94036 | Sequence 94036, A |
| 309 | 41.4 | 2.8 | 905 | 9 | US-09-748-033- | Sequence 35084, A | 382 | 39.4 | 2.7 | 6120 | 15 | US-10-240-445-314 | Sequence 314, App |
| 310 | 41.4 | 2.8 | 1647 | 15 | US-10-425-115-31253 | Sequence 7, Appl1 | 383 | 39.4 | 2.7 | 3673778 | 16 | US-10-425-115-114139 | Sequence 114139, A |
| 311 | 41.2 | 2.8 | 447 | 18 | US-10-259-165-688 | Sequence 31253, A | 384 | 39.4 | 2.7 | 421 | 18 | US-10-674-124A-33425 | Sequence 33425, A |
| 312 | 41.2 | 2.8 | 727 | 17 | US-10-260-238-3640 | Sequence 688, App | 385 | 39.4 | 2.7 | 442 | 18 | US-10-674-124A-33425 | Sequence 33425, A |
| 313 | 41.2 | 2.8 | 727 | 17 | US-10-260-238-3640 | Sequence 688, App | 386 | 39.4 | 2.7 | 471 | 18 | US-10-437-963-71075 | Sequence 71075, A |
| 314 | 41.2 | 2.8 | 738 | 17 | US-10-425-114-28012 | Sequence 3640, App | 387 | 39.4 | 2.7 | 996 | 17 | US-10-085-117-267 | Sequence 267, App |
| 315 | 41.2 | 2.8 | 744 | 18 | US-10-425-114-17862 | Sequence 28012, A | 388 | 39.4 | 2.7 | 996 | 17 | US-10-085-117-267 | Sequence 267, App |
| 316 | 41.2 | 2.8 | 744 | 18 | US-10-425-114-17862 | Sequence 17862, A | 389 | 39.4 | 2.7 | 1830 | 13 | US-10-027-633-99068 | Sequence 99068, A |
| 317 | 41.2 | 2.8 | 744 | 18 | US-10-425-114-17862 | Sequence 17862, A | 390 | 39.2 | 2.6 | 1830 | 13 | US-10-027-633-99068 | Sequence 99068, A |
| 318 | 41.2 | 2.8 | 744 | 18 | US-10-425-114-17862 | Sequence 89651, A | 391 | 39.2 | 2.6 | 1830 | 13 | US-10-027-633-99068 | Sequence 99068, A |
| 319 | 41.2 | 2.8 | 744 | 18 | US-10-425-114-17862 | Sequence 89651, A | 392 | 39.2 | 2.6 | 1830 | 13 | US-10-027-633-99068 | Sequence 99068, A |
| 320 | 41.2 | 2.8 | 744 | 18 | US-10-425-114-17862 | Sequence 89651, A | 393 | 39.2 | 2.6 | 1830 | 13 | US-10-027-633-99068 | Sequence 99068, A |
| 321 | 41.2 | 2.8 | 744 | 18 | US-10-425-114-17862 | Sequence 89651, A | 394 | 39.2 | 2.6 | 1830 | 13 | US-10-027-633-99068 | Sequence 99068, A |
| 322 | 41.2 | 2.8 | 744 | 18 | US-10-425-114-17862 | Sequence 89651, A | 395 | 39.2 | 2.6 | 1830 | 13 | US-10-027-633-99068 | Sequence 99068, A |
| 323 | 41.2 | 2.8 | 744 | 18 | US-10-425-114-17862 | Sequence 89651, A | 396 | 39.2 | 2.6 | 1830 | 13 | US-10-027-633-99068 | Sequence 99068, A |
| 324 | 41.2 | 2.8 | 744 | 18 | US-10-425-114-17862 | Sequence 89651, A | 397 | 39.2 | 2.6 | 1830 | 13 | US-10-027-633-99068 | Sequence 99068, A |
| 325 | 41.2 | 2.8 | 744 | 18 | US-10-425-114-17862 | Sequence 89651, A | 398 | 39.2 | 2.6 | 1830 | 13 | US-10-027-633-99068 | Sequence 99068, A |
| 326 | 41.2 | 2.8 | 744 | 18 | US-10-425-114-17862 | Sequence 89651, A | 399 | 39 | 2.6 | 402 | 10 | US-09-918-995-3927 | Sequence 3927, App |

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| 400 | 39 | 2.6 | 451 | 10 | US-09-918-995-5666 | Sequence 5666, Ap |
| 401 | 39 | 2.6 | 663 | 18 | US-10-739-930-4372 | Sequence 4372, Ap |
| C 402 | 39 | 2.6 | 681 | 13 | US-10-027-632-141458 | Sequence 141458, A |
| C 403 | 39 | 2.6 | 681 | 13 | US-10-027-632-141460 | Sequence 141460, A |
| C 404 | 39 | 2.6 | 681 | 17 | US-10-027-632-141458 | Sequence 141458, A |
| C 405 | 39 | 2.6 | 681 | 17 | US-10-027-632-141460 | Sequence 141460, A |
| 406 | 39 | 2.6 | 844 | 14 | US-10-116-802-53 | Sequence 53, Appl |
| 407 | 39 | 2.6 | 846 | 10 | US-09-919-039-319 | Sequence 319, Appl |
| 408 | 39 | 2.6 | 1116 | 16 | US-10-353-826-8 | Sequence 8, Appl |
| 409 | 39 | 2.6 | 1158 | 10 | US-09-919-039-320 | Sequence 320, Appl |
| 410 | 39 | 2.6 | 1173 | 16 | US-10-353-826-3 | Sequence 3, Appl |
| 411 | 39 | 2.6 | 1225 | 18 | US-10-723-860-6099 | Sequence 6099, Ap |
| 412 | 39 | 2.6 | 1248 | 13 | US-10-002-600-112 | Sequence 112, Ap |
| 413 | 39 | 2.6 | 1284 | 14 | US-10-086-738A-2 | Sequence 2, Appl |
| 414 | 39 | 2.6 | 1284 | 14 | US-10-086-738A-3 | Sequence 3, Appl |
| 415 | 39 | 2.6 | 1929 | 9 | US-09-554-000-1 | Sequence 1, Appl |
| 416 | 39 | 2.6 | 1929 | 9 | US-09-554-000-5 | Sequence 5, Appl |
| 417 | 39 | 2.6 | 1959 | 9 | US-09-554-000-3 | Sequence 3, Appl |
| 418 | 39 | 2.6 | 1971 | 9 | US-09-554-000-7 | Sequence 7, Appl |
| C 419 | 39 | 2.6 | 6171 | 15 | US-10-311-455-762 | Sequence 762, Ap |
| 420 | 39 | 2.6 | 137560 | 18 | US-10-481-112-1 | Sequence 1, Appl |
| 421 | 38.8 | 2.6 | 278 | 14 | US-10-062-727-818 | Sequence 818, Ap |
| 422 | 38.8 | 2.6 | 396 | 18 | US-10-437-963-3172 | Sequence 3172, Ap |
| 423 | 38.8 | 2.6 | 773 | 18 | US-10-767-701-15509 | Sequence 15509, A |
| 424 | 38.8 | 2.6 | 777 | 17 | US-10-424-599-5665 | Sequence 5665, A |
| 425 | 38.8 | 2.6 | 1008 | 17 | US-10-191-803-732 | Sequence 732, Ap |
| 426 | 38.8 | 2.6 | 1008 | 17 | US-10-152-319A-2103 | Sequence 2103, Ap |
| 427 | 38.8 | 2.6 | 2474 | 18 | US-10-425-115-43967 | Sequence 43967, A |
| 428 | 38.6 | 2.6 | 455 | 16 | US-10-039-86-42746 | Sequence 22746, A |
| C 429 | 38.6 | 2.6 | 516 | 18 | US-10-437-963-32307 | Sequence 32307, A |
| 430 | 38.6 | 2.6 | 550 | 18 | US-10-767-701-5385 | Sequence 5385, Ap |
| 431 | 38.6 | 2.6 | 773 | 14 | US-10-052-283-398 | Sequence 398, Ap |
| 432 | 38.6 | 2.6 | 2107 | 9 | US-09-981-353-49 | Sequence 49, Appl |
| 433 | 38.6 | 2.6 | 2110 | 17 | US-10-172-118-1846 | Sequence 1846, Ap |
| 434 | 38.6 | 2.6 | 2110 | 17 | US-10-342-887-1846 | Sequence 1846, Ap |
| 435 | 38.6 | 2.6 | 2110 | 18 | US-10-717-597-35 | Sequence 35, Appl |
| 436 | 38.6 | 2.6 | 2432 | 18 | US-10-437-963-47424 | Sequence 47424, A |
| 445 | 38.6 | 2.6 | 2945 | 14 | US-10-237-535-87 | Sequence 87, Appl |
| 454 | 38.6 | 2.6 | 2945 | 14 | US-10-239-196-87 | Sequence 87, Appl |
| 545 | 38.6 | 2.6 | 95982 | 13 | US-10-087-192-2029 | Sequence 2029, Ap |
| 546 | 38.4 | 2.6 | 233 | 10 | US-09-237-183A-783 | Sequence 837, Ap |
| 547 | 38.4 | 2.6 | 257 | 10 | US-09-237-183A-783 | Sequence 783, Ap |
| 548 | 38.4 | 2.6 | 268 | 10 | US-09-237-183A-773 | Sequence 773, Ap |
| 549 | 38.4 | 2.6 | 274 | 10 | US-09-237-183A-689 | Sequence 689, Ap |
| 550 | 38.4 | 2.6 | 286 | 10 | US-09-237-183A-646 | Sequence 646, Ap |
| 551 | 38.4 | 2.6 | 306 | 10 | US-09-237-183A-576 | Sequence 576, Ap |
| 552 | 38.4 | 2.6 | 316 | 10 | US-09-237-183A-564 | Sequence 564, Ap |
| 553 | 38.4 | 2.6 | 360 | 10 | US-09-237-183A-1058 | Sequence 1058, Ap |
| 554 | 38.4 | 2.6 | 383 | 10 | US-09-237-183A-1049 | Sequence 1049, Ap |
| 555 | 38.4 | 2.6 | 392 | 17 | US-10-260-338-2964 | Sequence 2964, Ap |
| 556 | 38.4 | 2.6 | 413 | 10 | US-09-237-183A-1063 | Sequence 1063, Ap |
| 557 | 38.4 | 2.6 | 425 | 10 | US-09-237-183A-1059 | Sequence 1029, Ap |
| 558 | 38.4 | 2.6 | 433 | 10 | US-09-237-183A-1047 | Sequence 1047, Ap |
| C 559 | 38.4 | 2.6 | 442 | 9 | US-09-880-107-1917 | Sequence 1917, Ap |
| 560 | 38.4 | 2.6 | 450 | 11 | US-09-997-722-273 | Sequence 273, Ap |
| 561 | 38.4 | 2.6 | 469 | 10 | US-09-237-183A-1020 | Sequence 1020, Ap |
| 562 | 38.4 | 2.6 | 512 | 10 | US-09-237-183A-1021 | Sequence 1021, Ap |
| 563 | 38.4 | 2.6 | 591 | 17 | US-10-264-049-1660 | Sequence 1660, Ap |
| 564 | 38.4 | 2.6 | 870 | 17 | US-10-425-114-6017 | Sequence 6017, Ap |
| 565 | 38.4 | 2.6 | 1227 | 17 | US-10-425-114-19280 | Sequence 19280, A |
| 566 | 38.4 | 2.6 | 1262 | 17 | US-10-425-114-2619 | Sequence 19280, A |
| 567 | 38.4 | 2.6 | 1431 | 17 | US-10-425-114-16306 | Sequence 16306, A |
| 568 | 38.4 | 2.6 | 1436 | 17 | US-10-425-114-1505 | Sequence 1605, Ap |
| 569 | 38.4 | 2.6 | 1455 | 17 | US-10-425-114-1067 | Sequence 1067, Ap |
| 570 | 38.4 | 2.6 | 2307 | 17 | US-10-425-114-35558 | Sequence 35509, A |
| 571 | 38.4 | 2.6 | 2505 | 17 | US-10-425-114-35609 | Sequence 35609, A |
| 572 | 38.4 | 2.6 | 2638 | 17 | US-10-425-114-2574 | Sequence 2574, Ap |
| 573 | 38.4 | 2.6 | 2986 | 17 | US-10-425-114-2283 | Sequence 2283, Ap |
| 574 | 38.4 | 2.6 | 2996 | 17 | US-10-425-114-26440 | Sequence 26430, A |
| 575 | 38.4 | 2.6 | 3419 | 17 | US-10-425-114-5310 | Sequence 5310, Ap |
| 576 | 38.4 | 2.6 | 4106 | 18 | US-10-425-114-17556 | Sequence 17556, A |
| 577 | 38.4 | 2.6 | 4106 | 18 | US-10-425-115-90606 | Sequence 96060, A |
| 578 | 38.4 | 2.6 | 99232 | 18 | US-10-331-053-16 | Sequence 16, Appl |
| 579 | 38.4 | 2.6 | 99588 | 13 | US-10-087-192-1780 | Sequence 1780, Ap |
| 580 | 38.4 | 2.6 | 101241 | 13 | US-10-087-192-1339 | Sequence 1339, Ap |
| 581 | 38.2 | 2.6 | 281 | 10 | US-09-237-183A-677 | Sequence 677, Ap |
| 582 | 38.2 | 2.6 | 288 | 10 | US-09-237-183A-650 | Sequence 650, Ap |
| 583 | 38.2 | 2.6 | 307 | 10 | US-09-237-183A-612 | Sequence 612, Ap |
| 584 | 38.2 | 2.6 | 504 | 18 | US-10-767-701-28690 | Sequence 28690, A |
| C 585 | 38.2 | 2.6 | 594 | 14 | US-10-123-155-10 | Sequence 10, Appl |
| C 586 | 38.2 | 2.6 | 603 | 16 | US-10-029-386-20492 | Sequence 20492, A |
| C 587 | 38.2 | 2.6 | 735 | 18 | US-10-425-115-86499 | Sequence 86499, A |
| 601 | 38.2 | 2.6 | 800 | 17 | US-10-260-338-3633 | Sequence 3633, Ap |
| 602 | 38.2 | 2.6 | 800 | 17 | US-10-156-761-5323 | Sequence 5323, Ap |
| C 603 | 38.2 | 2.6 | 1032 | 15 | US-10-425-115-129591 | Sequence 129591, A |
| C 604 | 38.2 | 2.6 | 1814 | 18 | US-10-369-493-28024 | Sequence 28024, A |
| C 605 | 38.2 | 2.6 | 2313 | 17 | US-10-369-493-30779 | Sequence 30779, A |
| 606 | 38.2 | 2.6 | 2421 | 17 | US-10-282-122A-11634 | Sequence 11634, A |
| 607 | 38.2 | 2.6 | 2421 | 17 | US-10-282-122A-12945 | Sequence 12945, A |
| 608 | 38.2 | 2.6 | 3250 | 17 | US-10-170-385-122 | Sequence 122, Ap |
| 609 | 38.2 | 2.6 | 4139 | 17 | US-10-439-388-122 | Sequence 24, Appl |
| 610 | 38.2 | 2.6 | 50460 | 13 | US-10-087-192-1633 | Sequence 1633, Ap |
| C 611 | 38.2 | 2.6 | 9025608 | 15 | US-10-156-761-1 | Sequence 1, Appl |
| C 612 | 38.2 | 2.6 | 345 | 14 | US-10-062-727-930 | Sequence 930, Ap |
| 613 | 38 | 2.6 | 359 | 14 | US-10-062-727-641 | Sequence 641, Ap |
| 614 | 38 | 2.6 | 375 | 18 | US-10-674-124A-1390 | Sequence 1390, Ap |
| 615 | 38 | 2.6 | 404 | 14 | US-10-062-727-415 | Sequence 415, Ap |
| 616 | 38 | 2.6 | 414 | 14 | US-10-062-727-669 | Sequence 669, Ap |
| 617 | 38 | 2.6 | 450 | 9 | US-09-938-842A-2653 | Sequence 2653, Ap |
| 618 | 38 | 2.6 | 450 | 11 | US-09-938-842A-2653 | Sequence 2653, Ap |
| C 619 | 38 | 2.6 | 486 | 18 | US-10-767-701-23897 | Sequence 23897, A |
| C 620 | 38 | 2.6 | 501 | 18 | US-10-027-632-195334 | Sequence 195334, A |
| C 621 | 38 | 2.6 | 501 | 17 | US-10-027-632-195334 | Sequence 195334, A |
| C 622 | 38 | 2.6 | 695 | 9 | US-09-770-149-285 | Sequence 285, Ap |
| C 623 | 38 | 2.6 | 868 | 17 | US-10-425-114-6936 | Sequence 6936, Ap |
| C 624 | 38 | 2.6 | 894 | 18 | US-10-425-115-89655 | Sequence 89655, A |
| 625 | 38 | 2.6 | 903 | 18 | US-10-437-963-26878 | Sequence 26878, A |
| 626 | 38 | 2.6 | 907 | 17 | US-10-425-114-26933 | Sequence 26943, A |
| 627 | 38 | 2.6 | 1061 | 18 | US-10-437-963-51439 | Sequence 51439, A |
| C 628 | 38 | 2.6 | 1713 | 18 | US-10-425-115-112862 | Sequence 112862, A |
| C 629 | 38 | 2.6 | 1808 | 18 | US-10-739-930-2978 | Sequence 2978, Ap |
| 630 | 38 | 2.6 | 1953 | 18 | US-10-425-115-17586 | Sequence 17586, Ap |
| C 631 | 38 | 2.6 | 3893 | 18 | US-10-437-963-51441 | Sequence 51441, A |
| C 632 | 38 | 2.6 | 6907 | 15 | US-10-311-455-550 | Sequence 540, Ap |
| C 633 | 38 | 2.6 | 62944 | 9 | US-09-954-456-2257 | Sequence 2257, Ap |
| 634 | 38 | 2.6 | 62944 | 11 | US-09-968-007A-129 | Sequence 129, Ap |
| C 635 | 38 | 2.6 | 109559 | 18 | US-10-322-281-137 | Sequence 137, Ap |
| C 636 | 38 | 2.6 | 3673778 | 16 | US-10-312-841-2 | Sequence 2, Appl |
| C 637 | 38 | 2.6 | 242 | 10 | US-09-237-183A-812 | Sequence 812, Ap |
| 638 | 37.8 | 2.5 | 391 | 10 | US-09-918-995-5449 | Sequence 5449, Ap |
| 639 | 37.8 | 2.5 | 449 | 10 | US-09-918-995-11791 | Sequence 11791, A |
| 640 | 37.8 | 2.5 | 455 | 10 | US-09-918-995-15644 | Sequence 15644, A |
| 641 | 37.8 | 2.5 | 459 | 10 | US-09-918-995-4655 | Sequence 4655, Ap |
| 642 | 37.8 | 2.5 | 465 | 10 | US-09-918-995-3264 | Sequence 3284, Ap |
| 643 | 37.8 | 2.5 | 478 | 10 | US-09-918-995-14016 | Sequence 14016, A |
| 644 | 37.8 | 2.5 | 557 | 10 | US-09-930-213-168 | Sequence 168, Ap |
| 645 | 37.8 | 2.5 | 681 | 13 | US-10-027-632-141457 | Sequence 141457, A |
| C 646 | 37.8 | 2.5 | 724 | 18 | US-10-425-115-50608 | Sequence 50608, A |
| C 647 | 37.8 | 2.5 | 788 | 18 | US-10-425-115-135851 | Sequence 135851, A |
| 648 | 37.8 | 2.5 | 906 | 17 | US-10-425-114-1174 | Sequence 1174, Ap |
| 649 | 37.8 | 2.5 | 906 | 17 | US-10-425-114-1174 | Sequence 20983, A |
| 650 | 37.8 | 2.5 | 1312 | 15 | US-10-084-817-13 | Sequence 14163, A |
| 651 | 37.8 | 2.5 | 1404 | 17 | US-10-337-963-7533 | Sequence 7533, Ap |
| 652 | 37.8 | 2.5 | 1578 | 18 | US-10-437-963-37206 | Sequence 37206, A |
| 653 | 37.8 | 2.5 | 1839 | 18 | US-10-198-846-11555 | Sequence 11555, A |
| 654 | 37.8 | 2.5 | 3397 | 14 | US-09-997-722-199 | Sequence 199, Ap |
| 655 | 37.8 | 2.5 | 9025608 | 15 | US-10-156-761-1 | Sequence 1, Appl |
| 656 | 37.6 | 2.5 | 450 | 18 | US-10-674-124A-13880 | Sequence 13880, A |
| C 665 | 37.6 | 2.5 | 451 | 18 | US-10-767-701-22400 | Sequence 22400, A |

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|-------|------|-----|--------|----|----------------------|----------------------|-------|------|-----|--------|----|----------------------|----------------------|
| 666 | 37.6 | 2.5 | 799 | 17 | US-10-369-493-29947 | Sequence 29947, A | 741 | 36.8 | 2.5 | 534 | 18 | US-10-437-963-53472 | Sequence 53472, A |
| C 667 | 37.6 | 2.5 | 804 | 18 | US-10-437-963-18891 | Sequence 18891, A | 742 | 36.8 | 2.5 | 636 | 9 | US-09-770-149-646 | Sequence 646, App |
| 668 | 37.6 | 2.5 | 1107 | 18 | US-10-425-115-78308 | Sequence 78308, A | 743 | 36.8 | 2.5 | 711 | 15 | US-10-156-761-3275 | Sequence 3275, App |
| 669 | 37.6 | 2.5 | 1208 | 17 | US-10-425-114-23365 | Sequence 23365, A | C 744 | 36.8 | 2.5 | 1734 | 18 | US-10-437-963-1188 | Sequence 1188, App |
| 670 | 37.6 | 2.5 | 1230 | 18 | US-10-437-963-2927 | Sequence 2927, App | 745 | 36.8 | 2.5 | 3430 | 18 | US-10-767-701-14869 | Sequence 14869, A |
| 671 | 37.6 | 2.5 | 1531 | 17 | US-10-425-114-17427 | Sequence 17427, A | C 746 | 36.8 | 2.5 | 9980 | 9 | US-09-880-107-1352 | Sequence 3352, App |
| 672 | 37.6 | 2.5 | 1507 | 18 | US-10-425-115-9354 | Sequence 9354, App | C 747 | 36.8 | 2.5 | 9980 | 11 | US-09-968-007-476 | Sequence 476, App |
| 673 | 37.6 | 2.5 | 1867 | 17 | US-10-425-114-10952 | Sequence 10952, A | C 748 | 36.8 | 2.5 | 38828 | 16 | US-10-384-893-17 | Sequence 17, App |
| C 674 | 37.6 | 2.5 | 1798 | 13 | US-10-027-632-98757 | Sequence 98757, A | C 749 | 36.8 | 2.5 | 38828 | 17 | US-10-463-190-17 | Sequence 17, App |
| C 675 | 37.6 | 2.5 | 1798 | 17 | US-10-027-632-98757 | Sequence 98757, A | C 750 | 36.8 | 2.5 | 38828 | 17 | US-10-095-248-17 | Sequence 17, App |
| 676 | 37.6 | 2.5 | 2255 | 18 | US-10-739-930-1681 | Sequence 1681, App | C 751 | 36.8 | 2.5 | 38828 | 18 | US-10-788-606-17 | Sequence 17, App |
| C 677 | 37.6 | 2.5 | 3955 | 9 | US-09-855-722-4 | Sequence 4, App | 752 | 36.8 | 2.5 | 48878 | 19 | US-10-741-600-17664 | Sequence 17664, A |
| C 678 | 37.6 | 2.5 | 3955 | 14 | US-10-219-248-4 | Sequence 4, App | 753 | 36.8 | 2.5 | 64467 | 14 | US-10-274-409-3 | Sequence 3, App |
| C 679 | 37.6 | 2.5 | 3955 | 14 | US-10-219-247-4 | Sequence 4, App | 754 | 36.8 | 2.5 | 64467 | 19 | US-10-932-135-3 | Sequence 3, App |
| C 680 | 37.6 | 2.5 | 4749 | 16 | US-10-091-625-3 | Sequence 3, App | 755 | 36.8 | 2.5 | 118067 | 15 | US-10-081-327-32 | Sequence 32, App |
| C 681 | 37.6 | 2.5 | 4749 | 16 | US-10-091-625-3 | Sequence 3, App | 756 | 36.8 | 2.5 | 201239 | 19 | US-10-278-698-246 | Sequence 246, App |
| C 682 | 37.6 | 2.5 | 4749 | 17 | US-10-461-668-3 | Sequence 3, App | 757 | 36.8 | 2.5 | 201239 | 19 | US-10-278-698-246 | Sequence 246, App |
| C 683 | 37.6 | 2.5 | 4749 | 17 | US-10-388-263-376 | Sequence 376, App | 758 | 36.8 | 2.5 | 295 | 10 | US-10-578-698-760 | Sequence 760, App |
| C 684 | 37.6 | 2.5 | 4974 | 16 | US-10-091-625-10 | Sequence 10, App | 759 | 36.6 | 2.5 | 3430 | 10 | US-09-237-183-615 | Sequence 615, App |
| C 685 | 37.6 | 2.5 | 4974 | 16 | US-10-091-625-10 | Sequence 10, App | 760 | 36.6 | 2.5 | 438 | 9 | US-09-237-183-615 | Sequence 615, App |
| C 686 | 37.6 | 2.5 | 4974 | 17 | US-10-461-668-10 | Sequence 10, App | C 761 | 36.6 | 2.5 | 490 | 13 | US-10-027-632-270955 | Sequence 270955, App |
| C 687 | 37.6 | 2.5 | 4974 | 17 | US-10-388-263-380 | Sequence 380, App | C 762 | 36.6 | 2.5 | 490 | 17 | US-10-027-632-270955 | Sequence 270955, App |
| C 688 | 37.6 | 2.5 | 5077 | 18 | US-10-789-378-37 | Sequence 37, App | C 763 | 36.6 | 2.5 | 689 | 17 | US-10-260-238-2713 | Sequence 2713, App |
| C 689 | 37.6 | 2.5 | 115780 | 18 | US-10-367-094-96 | Sequence 96, App | C 764 | 36.6 | 2.5 | 700 | 18 | US-10-767-701-5750 | Sequence 5750, App |
| C 690 | 37.6 | 2.5 | 175590 | 10 | US-09-911-077-13 | Sequence 13, App | C 765 | 36.6 | 2.5 | 700 | 18 | US-10-027-632-168583 | Sequence 168583, App |
| C 691 | 37.6 | 2.5 | 175590 | 18 | US-10-724-806-13 | Sequence 13, App | 770 | 36.6 | 2.5 | 792 | 13 | US-10-027-632-168584 | Sequence 168584, App |
| C 692 | 37.6 | 2.5 | 256493 | 13 | US-10-087-192-1000 | Sequence 1000, App | 771 | 36.6 | 2.5 | 792 | 13 | US-10-027-632-168585 | Sequence 168585, App |
| C 693 | 37.4 | 2.5 | 536 | 17 | US-10-338-110-119 | Sequence 119, App | 772 | 36.6 | 2.5 | 792 | 13 | US-10-027-632-168586 | Sequence 168586, App |
| C 694 | 37.4 | 2.5 | 681 | 13 | US-10-027-632-141459 | Sequence 141459, App | 773 | 36.6 | 2.5 | 792 | 13 | US-10-027-632-168587 | Sequence 168587, App |
| C 695 | 37.4 | 2.5 | 681 | 17 | US-10-027-632-141459 | Sequence 141459, App | 774 | 36.6 | 2.5 | 792 | 17 | US-10-027-632-168588 | Sequence 168588, App |
| C 696 | 37.4 | 2.5 | 806 | 18 | US-10-437-963-414 | Sequence 414, App | 775 | 36.6 | 2.5 | 792 | 17 | US-10-027-632-168589 | Sequence 168589, App |
| 697 | 37.4 | 2.5 | 823 | 18 | US-10-425-115-60966 | Sequence 60966, A | 776 | 36.6 | 2.5 | 792 | 17 | US-10-027-632-168586 | Sequence 168586, App |
| 700 | 37.4 | 2.5 | 1930 | 17 | US-10-260-238-564 | Sequence 564, App | 777 | 36.6 | 2.5 | 905 | 9 | US-09-748-033-5 | Sequence 5, App |
| 701 | 37.4 | 2.5 | 2052 | 17 | US-10-437-963-58102 | Sequence 58102, A | C 778 | 36.6 | 2.5 | 1086 | 18 | US-10-425-115-47026 | Sequence 47026, A |
| 702 | 37.4 | 2.5 | 2209 | 17 | US-10-114-270-189 | Sequence 189, App | C 779 | 36.6 | 2.5 | 1182 | 17 | US-10-260-238-882 | Sequence 882, App |
| 703 | 37.4 | 2.5 | 2485 | 9 | US-09-923-444-1 | Sequence 1, App | C 780 | 36.6 | 2.5 | 1294 | 9 | US-09-748-033-2 | Sequence 2, App |
| C 704 | 37.2 | 2.5 | 358 | 18 | US-10-674-124-9730 | Sequence 9730, App | C 781 | 36.6 | 2.5 | 1367 | 18 | US-10-437-963-16510 | Sequence 16510, A |
| C 705 | 37.2 | 2.5 | 471 | 18 | US-10-674-124-9730 | Sequence 9730, App | C 782 | 36.6 | 2.5 | 1434 | 15 | US-10-156-761-4335 | Sequence 4335, App |
| C 706 | 37.2 | 2.5 | 471 | 18 | US-10-437-963-38537 | Sequence 38537, A | C 783 | 36.6 | 2.5 | 2460 | 18 | US-10-437-963-7546 | Sequence 7546, App |
| 707 | 37.2 | 2.5 | 476 | 18 | US-10-856-499-1441 | Sequence 1441, App | 784 | 36.6 | 2.5 | 2470 | 18 | US-10-425-115-28592 | Sequence 28592, A |
| 708 | 37.2 | 2.5 | 524 | 18 | US-10-767-701-18076 | Sequence 18076, App | 785 | 36.6 | 2.5 | 2470 | 18 | US-10-156-761-2866 | Sequence 2866, App |
| C 709 | 37.2 | 2.5 | 1122 | 18 | US-10-437-963-12816 | Sequence 12816, A | C 786 | 36.6 | 2.5 | 49806 | 13 | US-10-087-192-1021 | Sequence 1021, App |
| 710 | 37.2 | 2.5 | 1485 | 15 | US-10-156-761-2495 | Sequence 2495, App | C 787 | 36.4 | 2.5 | 215 | 9 | US-10-674-124-20437 | Sequence 20437, A |
| C 711 | 37.2 | 2.5 | 1782 | 11 | US-09-972-211-57 | Sequence 57, App | 788 | 36.4 | 2.5 | 272 | 18 | US-09-923-876-5713 | Sequence 5713, App |
| C 712 | 37.2 | 2.5 | 1782 | 17 | US-10-096-625-57 | Sequence 57, App | 789 | 36.4 | 2.5 | 272 | 10 | US-09-923-876-5713 | Sequence 5713, App |
| C 713 | 37.2 | 2.5 | 1881 | 17 | US-10-210-130-147 | Sequence 147, App | 790 | 36.4 | 2.5 | 313 | 17 | US-10-424-599-46165 | Sequence 46165, A |
| C 714 | 37.2 | 2.5 | 1936 | 17 | US-10-425-114-201 | Sequence 201, App | 791 | 36.4 | 2.5 | 381 | 18 | US-10-674-124-877 | Sequence 877, App |
| C 715 | 37.2 | 2.5 | 1936 | 18 | US-10-425-115-9792 | Sequence 9792, A | 792 | 36.4 | 2.5 | 450 | 17 | US-10-260-238-5943 | Sequence 5943, App |
| C 716 | 37.2 | 2.5 | 7791 | 9 | US-09-764-877-3700 | Sequence 3700, App | C 793 | 36.4 | 2.5 | 456 | 18 | US-10-357-930-59467 | Sequence 59467, A |
| C 717 | 37.2 | 2.5 | 7791 | 17 | US-10-242-515-3700 | Sequence 3700, App | 794 | 36.4 | 2.5 | 486 | 10 | US-09-918-995-9799 | Sequence 9799, App |
| C 718 | 37.2 | 2.5 | 21457 | 18 | US-10-322-281-15 | Sequence 15, App | C 795 | 36.4 | 2.5 | 488 | 18 | US-10-437-963-23623 | Sequence 23623, A |
| C 719 | 37.2 | 2.5 | 80959 | 9 | US-09-858-546-3 | Sequence 3, App | 796 | 36.4 | 2.5 | 516 | 18 | US-10-425-115-83463 | Sequence 83463, A |
| 720 | 37.2 | 2.5 | 261817 | 13 | US-10-087-192-2002 | Sequence 2002, App | 797 | 36.4 | 2.5 | 516 | 18 | US-10-437-963-82862 | Sequence 82862, A |
| 721 | 37 | 2.5 | 289 | 10 | US-09-237-183-632 | Sequence 632, App | C 798 | 36.4 | 2.5 | 541 | 13 | US-10-027-632-141919 | Sequence 141919, App |
| 722 | 37 | 2.5 | 572 | 13 | US-10-027-632-215791 | Sequence 215791, App | C 799 | 36.4 | 2.5 | 541 | 17 | US-10-027-632-141919 | Sequence 141919, App |
| 723 | 37 | 2.5 | 572 | 17 | US-10-027-632-215791 | Sequence 215791, App | C 800 | 36.4 | 2.5 | 588 | 18 | US-10-437-963-96529 | Sequence 96529, App |
| C 724 | 37 | 2.5 | 623 | 17 | US-10-425-114-21114 | Sequence 21114, A | 801 | 36.4 | 2.5 | 606 | 17 | US-10-260-238-3638 | Sequence 3638, App |
| 725 | 37 | 2.5 | 1092 | 17 | US-10-282-122-11190 | Sequence 11790, A | C 802 | 36.4 | 2.5 | 642 | 18 | US-10-425-115-133958 | Sequence 133958, App |
| C 726 | 37 | 2.5 | 1567 | 18 | US-10-739-930-4900 | Sequence 4900, App | C 803 | 36.4 | 2.5 | 649 | 17 | US-10-425-115-18748 | Sequence 18748, A |
| C 727 | 37 | 2.5 | 1934 | 10 | US-09-882-227-201 | Sequence 201, App | C 804 | 36.4 | 2.5 | 662 | 17 | US-10-260-238-3638 | Sequence 3638, App |
| C 728 | 37 | 2.5 | 2256 | 15 | US-10-156-761-4122 | Sequence 4122, App | C 805 | 36.4 | 2.5 | 683 | 18 | US-10-437-963-67076 | Sequence 67076, A |
| C 729 | 37 | 2.5 | 2496 | 18 | US-10-467-963-51365 | Sequence 51365, A | C 806 | 36.4 | 2.5 | 811 | 18 | US-10-437-963-1368 | Sequence 1368, App |
| C 730 | 37 | 2.5 | 3644 | 18 | US-10-468-335-3 | Sequence 3, App | C 807 | 36.4 | 2.5 | 842 | 18 | US-10-425-115-3016 | Sequence 3016, App |
| C 731 | 37 | 2.5 | 11910 | 15 | US-10-156-761-2879 | Sequence 2879, App | C 808 | 36.4 | 2.5 | 868 | 17 | US-10-260-238-3638 | Sequence 3638, App |
| 732 | 37 | 2.5 | 44442 | 17 | US-10-395-740-15 | Sequence 15, App | C 809 | 36.4 | 2.5 | 936 | 18 | US-10-437-963-82873 | Sequence 82873, App |
| 733 | 37 | 2.5 | 90541 | 9 | US-09-753-359A-3 | Sequence 3, App | 810 | 36.4 | 2.5 | 987 | 15 | US-10-156-761-3333 | Sequence 3333, App |
| 734 | 37 | 2.5 | 90541 | 16 | US-10-207-973-3 | Sequence 3, App | 811 | 36.4 | 2.5 | 1306 | 9 | US-09-954-456-732 | Sequence 732, App |
| 735 | 37 | 2.5 | 90541 | 18 | US-10-799-676-3 | Sequence 3, App | 812 | 36.4 | 2.5 | 1306 | 9 | US-09-954-456-732 | Sequence 732, App |
| 736 | 37 | 2.5 | 125746 | 15 | US-10-156-761-15102 | Sequence 15102, A | C 813 | 36.4 | 2.5 | 1306 | 9 | US-09-954-456-732 | Sequence 732, App |
| 737 | 36.8 | 2.5 | 262 | 10 | US-09-237-183-8136 | Sequence 836, App | C 814 | 36.4 | 2.5 | 1383 | 18 | US-10-425-115-137853 | Sequence 137853, A |
| 738 | 36.8 | 2.5 | 309 | 18 | US-10-425-115-8163 | Sequence 8163, App | C 815 | 36.4 | 2.5 | 1405 | 18 | US-10-425-115-133967 | Sequence 133967, App |
| 739 | 36.8 | 2.5 | 518 | 16 | US-10-029-386-11351 | Sequence 11351, A | 816 | 36.4 | 2.5 | 1541 | 18 | US-10-739-930-2845 | Sequence 2845, App |
| C 740 | 36.8 | 2.5 | 518 | 16 | US-10-029-386-11770 | Sequence 11770, A | C 817 | 36.4 | 2.5 | 1710 | 17 | US-10-210-130-143 | Sequence 143, App |

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| 818 | 36.4 | 2.5 | 1809 | 15 | US-10-156-761-6413 | Sequence 6413, Ap |
| 819 | 36.4 | 2.5 | 2202 | 15 | US-10-156-761-6617 | Sequence 6617, Ap |
| 820 | 36.4 | 2.5 | 2425 | 18 | US-10-602-494-22 | Sequence 22, Appl |
| 821 | 36.4 | 2.5 | 2746 | 9 | US-09-963-832-254 | Sequence 254, Appl |
| 822 | 36.4 | 2.5 | 5877 | 14 | US-10-152-886-34 | Sequence 54, Appl |
| 823 | 36.4 | 2.5 | 32121 | 14 | US-10-103-313-604 | Sequence 604, Appl |
| 824 | 36.4 | 2.5 | 35236 | 13 | US-10-087-192-370 | Sequence 370, Appl |
| 825 | 36.4 | 2.5 | 90043 | 13 | US-10-087-192-1141 | Sequence 1141, Ap |
| 826 | 36.4 | 2.5 | 97415 | 18 | US-10-332-281-387 | Sequence 287, Appl |
| 827 | 36.4 | 2.5 | 107820 | 10 | US-09-792-616-1 | Sequence 1, Appl1 |
| 828 | 36.4 | 2.5 | 107820 | 18 | US-10-764-328-1 | Sequence 1, Appl1 |
| 829 | 36.4 | 2.5 | 151858 | 18 | US-10-322-281-653 | Sequence 653, Appl |
| 830 | 36.4 | 2.5 | 172984 | 19 | US-10-484-577-661 | Sequence 661, Appl |
| 831 | 36.4 | 2.5 | 186591 | 19 | US-10-484-577-682 | Sequence 682, Appl |
| 832 | 36.4 | 2.5 | 208648 | 19 | US-10-484-577-663 | Sequence 663, Appl |
| 833 | 36.4 | 2.5 | 208648 | 19 | US-10-484-577-668 | Sequence 668, Appl |
| 834 | 36.2 | 2.4 | 294 | 18 | US-09-237-183A-640 | Sequence 640, Appl |
| 835 | 36.2 | 2.4 | 399 | 17 | US-10-674-124A-3003 | Sequence 3003, Appl |
| 836 | 36.2 | 2.4 | 399 | 17 | US-10-242-535A-10965 | Sequence 10965, A |
| 837 | 36.2 | 2.4 | 399 | 17 | US-10-085-783A-10965 | Sequence 10965, A |
| 838 | 36.2 | 2.4 | 403 | 18 | US-10-674-124A-14245 | Sequence 14245, A |
| 839 | 36.2 | 2.4 | 433 | 18 | US-10-674-124A-21413 | Sequence 21413, A |
| 840 | 36.2 | 2.4 | 738 | 17 | US-10-424-599-11781 | Sequence 11781, A |
| 841 | 36.2 | 2.4 | 756 | 18 | US-10-425-115-1153 | Sequence 119220, A |
| 842 | 36.2 | 2.4 | 805 | 18 | US-10-425-115-1153 | Sequence 4153, Ap |
| 843 | 36.2 | 2.4 | 870 | 15 | US-10-156-761-4573 | Sequence 4573, Ap |
| 844 | 36.2 | 2.4 | 901 | 18 | US-10-437-963-47879 | Sequence 47879, A |
| 845 | 36.2 | 2.4 | 1011 | 18 | US-10-437-963-88631 | Sequence 88631, A |
| 846 | 36.2 | 2.4 | 1086 | 14 | US-10-083-168-78 | Sequence 78, Appl |
| 847 | 36.2 | 2.4 | 1120 | 9 | US-09-969-708-340 | Sequence 340, Appl |
| 848 | 36.2 | 2.4 | 1120 | 10 | US-09-873-367C-686 | Sequence 686, Appl |
| 849 | 36.2 | 2.4 | 1120 | 18 | US-10-717-597-134 | Sequence 134, Appl |
| 850 | 36.2 | 2.4 | 1303 | 18 | US-10-723-860-5468 | Sequence 5468, Appl |
| 851 | 36.2 | 2.4 | 1629 | 17 | US-10-425-114-33600 | Sequence 33600, A |
| 852 | 36.2 | 2.4 | 1907 | 18 | US-10-425-115-156020 | Sequence 156020, A |
| 853 | 36.2 | 2.4 | 2041 | 17 | US-09-814-353-20998 | Sequence 20998, A |
| 854 | 36.2 | 2.4 | 2044 | 17 | US-10-094-749-90 | Sequence 90, Appl1 |
| 855 | 36.2 | 2.4 | 2355 | 17 | US-10-282-122A-39279 | Sequence 39279, A |
| 856 | 36.2 | 2.4 | 2429 | 17 | US-10-425-114-3569 | Sequence 3569, Ap |
| 857 | 36.2 | 2.4 | 2642 | 18 | US-10-425-115-156016 | Sequence 156016, A |
| 858 | 36.2 | 2.4 | 2658 | 17 | US-10-425-114-33369 | Sequence 23369, A |
| 859 | 36.2 | 2.4 | 2801 | 18 | US-10-425-115-32466 | Sequence 32466, A |
| 860 | 36.2 | 2.4 | 5230 | 18 | US-10-475-476-20 | Sequence 20, Appl1 |
| 861 | 36.2 | 2.4 | 11771 | 17 | US-10-415-620-1 | Sequence 1, Appl1 |
| 862 | 36.2 | 2.4 | 11117 | 18 | US-10-482-936-1 | Sequence 1, Appl1 |
| 863 | 36.2 | 2.4 | 11117 | 18 | US-10-482-936-3 | Sequence 1, Appl1 |
| 864 | 36.2 | 2.4 | 15872 | 9 | US-09-861-289-1 | Sequence 1, Appl1 |
| 865 | 36.2 | 2.4 | 15872 | 9 | US-09-860-846-1 | Sequence 1, Appl1 |
| 866 | 36.2 | 2.4 | 15872 | 10 | US-09-988-384B-1 | Sequence 1, Appl1 |
| 867 | 36.2 | 2.4 | 15872 | 10 | US-09-836-821-1 | Sequence 1, Appl1 |
| 868 | 36.2 | 2.4 | 15872 | 16 | US-10-271-889-44 | Sequence 44, Appl1 |
| 869 | 36.2 | 2.4 | 2262 | 13 | US-10-087-192-1063 | Sequence 1063, Appl |
| 870 | 36.2 | 2.4 | 27485 | 18 | US-10-332-281-196 | Sequence 196, Appl |
| 871 | 36.2 | 2.4 | 89829 | 18 | US-10-332-281-359 | Sequence 359, Appl |
| 872 | 36.2 | 2.4 | 183334 | 19 | US-10-741-600-17646 | Sequence 17646, A |
| 873 | 36.2 | 2.4 | 317 | 18 | US-10-674-124A-12042 | Sequence 12042, A |
| 874 | 36.2 | 2.4 | 327 | 18 | US-10-425-115-75246 | Sequence 75246, A |
| 875 | 36.2 | 2.4 | 433 | 18 | US-10-674-124A-8934 | Sequence 8934, Ap |
| 876 | 36.2 | 2.4 | 452 | 18 | US-10-723-860-1904 | Sequence 1904, Ap |
| 877 | 36.2 | 2.4 | 602 | 18 | US-10-425-115-40635 | Sequence 40635, A |
| 878 | 36.2 | 2.4 | 738 | 18 | US-10-437-963-88086 | Sequence 88086, A |
| 879 | 36.2 | 2.4 | 813 | 18 | US-10-437-963-9395 | Sequence 9395, Ap |
| 880 | 36.2 | 2.4 | 1032 | 15 | US-10-156-761-1110 | Sequence 1110, Ap |
| 881 | 36.2 | 2.4 | 1063 | 18 | US-10-767-701-13615 | Sequence 13615, A |
| 882 | 36.2 | 2.4 | 1431 | 18 | US-10-437-963-26802 | Sequence 26802, A |
| 883 | 36.2 | 2.4 | 1649 | 17 | US-10-425-114-26399 | Sequence 26399, A |
| 884 | 36.2 | 2.4 | 1766 | 18 | US-10-437-963-66848 | Sequence 66848, A |
| 885 | 36.2 | 2.4 | 1914 | 18 | US-10-437-963-88485 | Sequence 88485, A |
| 886 | 36.2 | 2.4 | 2235 | 17 | US-10-359-493-42996 | Sequence 42996, A |
| 887 | 36.2 | 2.4 | 2280 | 18 | US-10-437-963-96359 | Sequence 96359, A |
| 888 | 36.2 | 2.4 | 2892 | 18 | US-10-437-963-40093 | Sequence 40093, A |
| 889 | 36.2 | 2.4 | 3099 | 17 | US-10-282-122A-29968 | Sequence 29968, A |
| 890 | 36.2 | 2.4 | 3779 | 9 | US-09-925-300-712 | Sequence 712, Appl |
| 891 | 36.2 | 2.4 | 15362 | 9 | US-09-764-877-2856 | Sequence 2856, Ap |
| 892 | 36.2 | 2.4 | 15362 | 17 | US-10-242-515-2856 | Sequence 2856, Ap |
| 893 | 36.2 | 2.4 | 19303 | 18 | US-10-433-887-81 | Sequence 81, Appl |
| 894 | 36.2 | 2.4 | 28000 | 16 | US-10-091-625-11 | Sequence 11, Appl |
| 895 | 36.2 | 2.4 | 28000 | 16 | US-10-096-399A-11 | Sequence 11, Appl |
| 896 | 36.2 | 2.4 | 28000 | 17 | US-10-461-668-11 | Sequence 11, Appl |
| 897 | 36.2 | 2.4 | 28000 | 17 | US-10-388-263-381 | Sequence 381, Appl |
| 898 | 36.2 | 2.4 | 60900 | 13 | US-10-087-192-1123 | Sequence 1123, Appl |
| 899 | 36.2 | 2.4 | 189158 | 13 | US-10-087-192-415 | Sequence 415, Appl |
| 900 | 36.2 | 2.4 | 192673 | 18 | US-10-331-053-1 | Sequence 1, Appl1 |
| 901 | 36.2 | 2.4 | 217409 | 13 | US-10-087-192-1954 | Sequence 1954, Ap |
| 902 | 35.8 | 2.4 | 469 | 10 | US-09-918-995-31647 | Sequence 31647, A |
| 903 | 35.8 | 2.4 | 561 | 15 | US-10-259-165-357 | Sequence 357, Appl |
| 904 | 35.8 | 2.4 | 564 | 15 | US-10-259-165-3 | Sequence 3, Appl1 |
| 905 | 35.8 | 2.4 | 602 | 13 | US-10-027-632-21353 | Sequence 21353, A |
| 906 | 35.8 | 2.4 | 602 | 13 | US-10-027-632-21339 | Sequence 21339, A |
| 907 | 35.8 | 2.4 | 602 | 13 | US-10-027-632-213540 | Sequence 213540, A |
| 908 | 35.8 | 2.4 | 602 | 17 | US-10-027-632-213538 | Sequence 213538, A |
| 909 | 35.8 | 2.4 | 602 | 17 | US-10-027-632-213539 | Sequence 213539, A |
| 910 | 35.8 | 2.4 | 602 | 17 | US-10-027-632-213540 | Sequence 213540, A |
| 911 | 35.8 | 2.4 | 646 | 18 | US-10-767-701-24140 | Sequence 24140, A |
| 912 | 35.8 | 2.4 | 648 | 17 | US-10-152-819A-21406 | Sequence 21406, Ap |
| 913 | 35.8 | 2.4 | 747 | 17 | US-10-424-599-136586 | Sequence 136586, A |
| 915 | 35.8 | 2.4 | 751 | 18 | US-10-425-115-88093 | Sequence 88093, A |
| 917 | 35.8 | 2.4 | 774 | 13 | US-10-042-417-39 | Sequence 39, Appl1 |
| 919 | 35.8 | 2.4 | 1457 | 15 | US-10-037-270-408 | Sequence 408, Appl |
| 920 | 35.8 | 2.4 | 1457 | 17 | US-10-117-722-408 | Sequence 408, Appl |
| 921 | 35.8 | 2.4 | 2247 | 18 | US-10-437-963-83558 | Sequence 83558, A |
| 922 | 35.8 | 2.4 | 2281 | 17 | US-10-108-260A-57 | Sequence 57, Appl1 |
| 923 | 35.8 | 2.4 | 2394 | 17 | US-10-112-944-54 | Sequence 54, Appl1 |
| 924 | 35.8 | 2.4 | 2490 | 17 | US-10-112-944-53 | Sequence 53, Appl1 |
| 925 | 35.8 | 2.4 | 2546 | 17 | US-10-425-114-32586 | Sequence 32586, A |
| 926 | 35.8 | 2.4 | 2572 | 17 | US-10-319-315-2 | Sequence 2, Appl1 |
| 927 | 35.8 | 2.4 | 2785 | 18 | US-10-425-115-48930 | Sequence 48930, A |
| 928 | 35.8 | 2.4 | 2874 | 15 | US-10-259-165-251 | Sequence 251, Appl |
| 929 | 35.8 | 2.4 | 3168 | 17 | US-10-120-988-409 | Sequence 409, Appl |
| 930 | 35.8 | 2.4 | 4080 | 17 | US-10-172-118-1520 | Sequence 1520, Ap |
| 931 | 35.8 | 2.4 | 4080 | 17 | US-10-342-887-1850 | Sequence 1850, Ap |
| 932 | 35.8 | 2.4 | 4263 | 18 | US-10-437-963-26800 | Sequence 26800, A |
| 933 | 35.8 | 2.4 | 14427 | 15 | US-10-156-761-1540 | Sequence 1540, Ap |
| 934 | 35.8 | 2.4 | 43950 | 9 | US-09-735-934A-3 | Sequence 3, Appl1 |
| 935 | 35.8 | 2.4 | 43950 | 13 | US-10-060-332-3 | Sequence 3, Appl1 |
| 936 | 35.8 | 2.4 | 43950 | 15 | US-10-339-657-3 | Sequence 3, Appl1 |
| 937 | 35.8 | 2.4 | 43950 | 18 | US-10-885-879-3 | Sequence 3, Appl1 |
| 938 | 35.8 | 2.4 | 62658 | 18 | US-10-322-281-420 | Sequence 420, Appl |
| 939 | 35.8 | 2.4 | 160556 | 18 | US-10-719-993-6827 | Sequence 6827, Ap |
| 940 | 35.6 | 2.4 | 174 | 9 | US-09-922-217-325 | Sequence 325, Appl |
| 941 | 35.6 | 2.4 | 174 | 9 | US-09-922-217-168 | Sequence 325, Appl |
| 942 | 35.6 | 2.4 | 174 | 9 | US-09-833-263-325 | Sequence 325, Appl |
| 943 | 35.6 | 2.4 | 174 | 9 | US-09-833-263-168 | Sequence 368, Appl |
| 944 | 35.6 | 2.4 | 174 | 13 | US-10-025-380-325 | Sequence 388, Appl |
| 945 | 35.6 | 2.4 | 242 | 9 | US-09-923-876-2699 | Sequence 2699, Ap |
| 946 | 35.6 | 2.4 | 242 | 10 | US-09-923-876-2699 | Sequence 2699, Ap |
| 947 | 35.6 | 2.4 | 309 | 10 | US-09-237-183A-570 | Sequence 570, Appl |
| 948 | 35.6 | 2.4 | 326 | 18 | US-10-674-124A-21108 | Sequence 21108, A |
| 949 | 35.6 | 2.4 | 369 | 18 | US-10-674-124A-6702 | Sequence 6702, Ap |
| 950 | 35.6 | 2.4 | 458 | 18 | US-10-021-223-6653 | Sequence 6653, Ap |
| 951 | 35.6 | 2.4 | 478 | 18 | US-10-425-115-134316 | Sequence 134316, A |
| 952 | 35.6 | 2.4 | 486 | 13 | US-10-027-632-135836 | Sequence 135836, A |
| 953 | 35.6 | 2.4 | 486 | 17 | US-10-027-632-135836 | Sequence 135836, A |
| 954 | 35.6 | 2.4 | 504 | 10 | US-09-918-995-32397 | Sequence 32397, A |
| 955 | 35.6 | 2.4 | 546 | 18 | US-10-425-115-5031 | Sequence 5031, Ap |
| 956 | 35.6 | 2.4 | 575 | 9 | US-09-864-761-10733 | Sequence 20733, A |
| 957 | 35.6 | 2.4 | 575 | 13 | US-10-027-632-50030 | Sequence 50030, A |
| 958 | 35.6 | 2.4 | 575 | 13 | US-10-027-632-81841 | Sequence 81841, A |
| 959 | 35.6 | 2.4 | 575 | 13 | US-10-027-632-302015 | Sequence 302015, A |
| 960 | 35.6 | 2.4 | 575 | 17 | US-10-027-632-81841 | Sequence 81841, A |
| 961 | 35.6 | 2.4 | 575 | 17 | US-10-027-632-302015 | Sequence 302015, A |
| 962 | 35.6 | 2.4 | 575 | 17 | US-10-425-115-6919 | Sequence 6919, Ap |
| 963 | 35.6 | 2.4 | 607 | 18 | US-10-424-599-44383 | Sequence 44383, A |
| 964 | 35.6 | 2.4 | 626 | 17 | US-10-424-599-44383 | Sequence 44383, A |
| 965 | 35.6 | 2.4 | 663 | 18 | US-10-425-115-117063 | Sequence 117063, A |

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|-------|------|-----|--------|----|----------------------|--------------------|-------|------|-----|--------|----|----------------------|--------------------|
| C 966 | 35.6 | 2.4 | 687 | 18 | US-10-363-345A-5817 | Sequence 5817, Ap | 1039 | 35.4 | 2.4 | 1501 | 17 | US-10-425-114-18635 | Sequence 18635, A |
| C 967 | 35.6 | 2.4 | 687 | 18 | US-10-363-345A-5818 | Sequence 5818, Ap | 1040 | 35.4 | 2.4 | 1526 | 15 | US-10-177-293-34 | Sequence 34, Appl |
| C 968 | 35.6 | 2.4 | 692 | 18 | US-10-425-115-117059 | Sequence 117059, A | C1041 | 35.4 | 2.4 | 1701 | 18 | US-10-437-963-101326 | Sequence 101326, A |
| C 969 | 35.6 | 2.4 | 700 | 13 | US-10-027-632-148457 | Sequence 148457, A | 1042 | 35.4 | 2.4 | 1770 | 17 | US-10-282-122A-27524 | Sequence 27524, A |
| C 970 | 35.6 | 2.4 | 700 | 13 | US-10-027-632-148458 | Sequence 148458, A | 1043 | 35.4 | 2.4 | 2573 | 18 | US-10-437-963-33523 | Sequence 33523, Ap |
| C 971 | 35.6 | 2.4 | 700 | 17 | US-10-027-632-148457 | Sequence 148457, A | 1044 | 35.4 | 2.4 | 2809 | 18 | US-10-425-115-115447 | Sequence 115447, A |
| C 972 | 35.6 | 2.4 | 700 | 17 | US-10-027-632-148458 | Sequence 148458, A | 1045 | 35.4 | 2.4 | 3535 | 14 | US-10-198-846-13957 | Sequence 13957, A |
| C 973 | 35.6 | 2.4 | 744 | 18 | US-10-437-963-37931 | Sequence 37931, A | 1046 | 35.4 | 2.4 | 3734 | 18 | US-10-425-115-113388 | Sequence 113388, A |
| C 974 | 35.6 | 2.4 | 745 | 13 | US-10-027-632-144387 | Sequence 144387, A | C1047 | 35.4 | 2.4 | 5012 | 18 | US-10-719-993-252 | Sequence 252, App |
| C 975 | 35.6 | 2.4 | 747 | 17 | US-10-363-493-41119 | Sequence 41119, A | C1048 | 35.4 | 2.4 | 5099 | 18 | US-10-719-993-255 | Sequence 255, App |
| C 976 | 35.6 | 2.4 | 747 | 17 | US-10-363-493-41119 | Sequence 41119, A | C1049 | 35.4 | 2.4 | 5186 | 18 | US-10-719-993-257 | Sequence 257, App |
| C 977 | 35.6 | 2.4 | 851 | 17 | US-10-425-114-14245 | Sequence 14245, A | 1050 | 35.4 | 2.4 | 23318 | 18 | US-10-322-281-504 | Sequence 504, App |
| C 978 | 35.6 | 2.4 | 851 | 18 | US-10-425-115-141528 | Sequence 141528, A | C1051 | 35.4 | 2.4 | 26000 | 18 | US-10-476-022-10 | Sequence 10, Appl |
| C 979 | 35.6 | 2.4 | 977 | 18 | US-10-437-963-90300 | Sequence 90300, A | C1052 | 35.4 | 2.4 | 42027 | 18 | US-10-417-375-58 | Sequence 58, Appl |
| C 980 | 35.6 | 2.4 | 977 | 18 | US-10-425-115-117057 | Sequence 117057, A | C1053 | 35.4 | 2.4 | 84410 | 18 | US-10-322-281-747 | Sequence 747, App |
| C 981 | 35.6 | 2.4 | 1175 | 18 | US-10-425-115-117058 | Sequence 117058, A | C1054 | 35.4 | 2.4 | 90026 | 13 | US-10-087-192-229 | Sequence 229, App |
| C 982 | 35.6 | 2.4 | 1215 | 18 | US-10-425-115-117066 | Sequence 117066, A | 1055 | 35.4 | 2.4 | 96597 | 11 | US-09-997-722-73 | Sequence 73, Appl |
| C 983 | 35.6 | 2.4 | 1248 | 18 | US-10-425-115-117064 | Sequence 117064, A | C1056 | 35.4 | 2.4 | 659158 | 9 | US-09-771-208-70 | Sequence 20, Appl |
| C 984 | 35.6 | 2.4 | 1265 | 18 | US-10-425-115-117069 | Sequence 117069, A | C1057 | 35.4 | 2.4 | 775062 | 18 | US-10-674-124A-1933 | Sequence 6844, Ap |
| C 985 | 35.6 | 2.4 | 1271 | 18 | US-10-437-963-38282 | Sequence 38282, A | C1058 | 35.2 | 2.4 | 325 | 18 | US-10-674-124A-1933 | Sequence 14933, A |
| C 986 | 35.6 | 2.4 | 1428 | 15 | US-10-156-761-5428 | Sequence 5428, Ap | 1059 | 35.2 | 2.4 | 406 | 9 | US-09-960-352-5045 | Sequence 5045, Ap |
| C 987 | 35.6 | 2.4 | 1469 | 18 | US-10-739-930-1975 | Sequence 1975, Ap | 1060 | 35.2 | 2.4 | 557 | 17 | US-10-369-493-2762 | Sequence 2762, A |
| C 988 | 35.6 | 2.4 | 1488 | 18 | US-10-437-963-22612 | Sequence 22612, A | 1061 | 35.2 | 2.4 | 606 | 18 | US-10-437-963-70077 | Sequence 70077, A |
| C 989 | 35.6 | 2.4 | 1369 | 9 | US-09-864-761-3972 | Sequence 3972, Ap | C1062 | 35.2 | 2.4 | 655 | 17 | US-10-424-599-10435 | Sequence 10435, A |
| C 990 | 35.6 | 2.4 | 2035 | 19 | US-10-959-539-65 | Sequence 65, Appl | 1063 | 35.2 | 2.4 | 879 | 15 | US-10-156-761-3503 | Sequence 3503, Ap |
| C 991 | 35.6 | 2.4 | 2066 | 17 | US-10-210-130-151 | Sequence 151, Appl | 1064 | 35.2 | 2.4 | 927 | 15 | US-10-156-761-6692 | Sequence 6692, Ap |
| C 992 | 35.6 | 2.4 | 2205 | 17 | US-10-369-493-44269 | Sequence 44269, A | C1065 | 35.2 | 2.4 | 967 | 13 | US-10-027-632-25326 | Sequence 25326, A |
| C 993 | 35.6 | 2.4 | 2216 | 14 | US-10-123-036-1 | Sequence 1, Appl | C1066 | 35.2 | 2.4 | 967 | 17 | US-10-027-632-25326 | Sequence 25326, A |
| C 994 | 35.6 | 2.4 | 2219 | 15 | US-10-007-926A-333 | Sequence 333, Appl | C1067 | 35.2 | 2.4 | 967 | 15 | US-10-156-761-7246 | Sequence 7246, Ap |
| C 995 | 35.6 | 2.4 | 2244 | 18 | US-10-437-963-68841 | Sequence 68841, A | 1068 | 35.2 | 2.4 | 999 | 15 | US-10-156-761-3794 | Sequence 3794, Ap |
| C 996 | 35.6 | 2.4 | 2487 | 13 | US-10-027-632-103365 | Sequence 103365, A | C1069 | 35.2 | 2.4 | 1010 | 17 | US-10-343-348-17 | Sequence 17, Appl |
| C 997 | 35.6 | 2.4 | 2487 | 17 | US-10-027-632-103365 | Sequence 103365, A | C1070 | 35.2 | 2.4 | 1325 | 18 | US-10-425-115-52338 | Sequence 5238, A |
| C 998 | 35.6 | 2.4 | 2586 | 17 | US-10-369-493-31958 | Sequence 31958, A | 1071 | 35.2 | 2.4 | 2289 | 17 | US-10-437-963-44541 | Sequence 44541, A |
| C 999 | 35.6 | 2.4 | 6997 | 18 | US-10-335-053-242 | Sequence 242, App | 1072 | 35.2 | 2.4 | 2403 | 11 | US-09-997-722-111 | Sequence 111, App |
| 1000 | 35.6 | 2.4 | 27980 | 18 | US-10-719-993-6935 | Sequence 6935, Ap | 1073 | 35.2 | 2.4 | 2887 | 11 | US-09-997-722-110 | Sequence 110, App |
| 1001 | 35.6 | 2.4 | 49087 | 18 | US-10-322-636-1 | Sequence 1, Appl | C1074 | 35.2 | 2.4 | 17934 | 15 | US-10-311-455-1631 | Sequence 1631, Ap |
| 1002 | 35.6 | 2.4 | 49175 | 18 | US-10-367-094-4 | Sequence 4, Appl | C1075 | 35.2 | 2.4 | 58038 | 19 | US-10-741-600-17942 | Sequence 17942, A |
| 1003 | 35.6 | 2.4 | 92219 | 18 | US-10-322-281-805 | Sequence 805, Appl | C1076 | 35.2 | 2.4 | 66972 | 13 | US-10-087-192-574 | Sequence 574, App |
| 1004 | 35.6 | 2.4 | 110079 | 14 | US-10-175-523-96 | Sequence 96, Appl | C1077 | 35.2 | 2.4 | 76846 | 13 | US-10-087-192-799 | Sequence 799, App |
| 1005 | 35.6 | 2.4 | 118931 | 13 | US-10-087-192-1108 | Sequence 1108, Ap | 1078 | 35.2 | 2.4 | 142947 | 18 | US-10-719-993-6967 | Sequence 6967, Ap |
| 1006 | 35.6 | 2.4 | 201143 | 17 | US-10-240-425-1099 | Sequence 1099, Ap | C1079 | 35.2 | 2.4 | 333811 | 19 | US-10-741-600-17681 | Sequence 17681, A |
| 1007 | 35.6 | 2.4 | 203127 | 18 | US-10-741-601-5654 | Sequence 5654, Ap | 1080 | 35.2 | 2.4 | 744882 | 17 | US-10-292-749-1369 | Sequence 1369, Ap |
| 1008 | 35.6 | 2.4 | 203127 | 19 | US-10-741-600-17666 | Sequence 17666, A | 1081 | 35.2 | 2.4 | 224 | 10 | US-09-237-182A-840 | Sequence 840, App |
| C1009 | 35.6 | 2.4 | 493999 | 18 | US-10-719-993-6787 | Sequence 6787, A | 1082 | 35.2 | 2.4 | 235 | 10 | US-09-237-182A-840 | Sequence 840, App |
| 1010 | 35.4 | 2.4 | 293 | 18 | US-10-674-124A-10333 | Sequence 10333, A | 1083 | 35.2 | 2.4 | 270 | 10 | US-09-237-182A-840 | Sequence 840, App |
| C1011 | 35.4 | 2.4 | 310 | 18 | US-10-674-124A-15991 | Sequence 15991, A | C1084 | 35.2 | 2.4 | 281 | 18 | US-10-674-124A-24544 | Sequence 24544, A |
| 1012 | 35.4 | 2.4 | 325 | 17 | US-10-242-535A-519 | Sequence 519, App | 1085 | 35.2 | 2.4 | 305 | 18 | US-10-674-124A-12289 | Sequence 12289, A |
| 1013 | 35.4 | 2.4 | 325 | 17 | US-10-085-783A-519 | Sequence 519, App | 1086 | 35.2 | 2.4 | 344 | 9 | US-09-960-352-5692 | Sequence 5692, Ap |
| 1014 | 35.4 | 2.4 | 365 | 18 | US-10-674-124A-1930 | Sequence 1930, Ap | 1087 | 35.2 | 2.4 | 393 | 18 | US-10-723-860-2396 | Sequence 2396, Ap |
| 1015 | 35.4 | 2.4 | 385 | 9 | US-09-960-352-7745 | Sequence 4013, Ap | 1088 | 35.2 | 2.4 | 418 | 13 | US-10-674-124A-25651 | Sequence 25651, A |
| 1016 | 35.4 | 2.4 | 413 | 9 | US-09-960-352-7745 | Sequence 7745, Ap | C1089 | 35.2 | 2.4 | 453 | 18 | US-10-027-632-135018 | Sequence 135018, A |
| 1017 | 35.4 | 2.4 | 416 | 9 | US-09-960-352-2019 | Sequence 2019, Ap | C1090 | 35.2 | 2.4 | 453 | 17 | US-10-027-632-135018 | Sequence 135018, A |
| 1018 | 35.4 | 2.4 | 428 | 9 | US-09-960-352-2677 | Sequence 2677, Ap | C1091 | 35.2 | 2.4 | 460 | 18 | US-10-027-632-135018 | Sequence 135018, A |
| 1019 | 35.4 | 2.4 | 450 | 9 | US-09-960-352-335 | Sequence 335, App | C1092 | 35.2 | 2.4 | 487 | 10 | US-10-674-124A-18980 | Sequence 18980, A |
| 1020 | 35.4 | 2.4 | 492 | 10 | US-09-918-995-1737 | Sequence 1737, Ap | 1093 | 35.2 | 2.4 | 520 | 18 | US-09-918-995-32151 | Sequence 32151, A |
| C1021 | 35.4 | 2.4 | 565 | 18 | US-10-767-701-7758 | Sequence 7758, Ap | C1094 | 35.2 | 2.4 | 538 | 16 | US-10-767-701-25899 | Sequence 25899, A |
| 1022 | 35.4 | 2.4 | 606 | 18 | US-10-767-701-25686 | Sequence 25686, A | 1095 | 35.2 | 2.4 | 598 | 16 | US-10-029-386-5741 | Sequence 5741, Ap |
| C1023 | 35.4 | 2.4 | 675 | 15 | US-10-156-761-3903 | Sequence 3903, Ap | 1096 | 35.2 | 2.4 | 648 | 17 | US-10-027-632-18469 | Sequence 18469, A |
| 1024 | 35.4 | 2.4 | 701 | 19 | US-10-278-698-426 | Sequence 426, App | 1097 | 35.2 | 2.4 | 663 | 17 | US-10-027-632-18469 | Sequence 18469, A |
| 1025 | 35.4 | 2.4 | 701 | 19 | US-10-278-698-940 | Sequence 940, App | C1098 | 35.2 | 2.4 | 714 | 18 | US-10-425-114-3517 | Sequence 3517, Ap |
| 1026 | 35.4 | 2.4 | 735 | 18 | US-10-437-963-101335 | Sequence 101335, A | 1099 | 35.2 | 2.4 | 744 | 17 | US-10-437-963-65621 | Sequence 65621, A |
| C1027 | 35.4 | 2.4 | 807 | 18 | US-10-437-963-101330 | Sequence 101330, A | 1100 | 35.2 | 2.4 | 744 | 17 | US-10-425-114-1318 | Sequence 1318, Ap |
| 1028 | 35.4 | 2.4 | 866 | 18 | US-10-437-963-12852 | Sequence 12852, A | 1101 | 35.2 | 2.4 | 759 | 17 | US-10-425-114-23009 | Sequence 23009, A |
| 1029 | 35.4 | 2.4 | 889 | 17 | US-10-425-115-11763 | Sequence 11763, A | 1102 | 35.2 | 2.4 | 794 | 17 | US-10-425-114-24501 | Sequence 24501, A |
| C1030 | 35.4 | 2.4 | 955 | 18 | US-10-425-115-30638 | Sequence 30638, A | 1103 | 35.2 | 2.4 | 797 | 17 | US-10-425-114-18888 | Sequence 18888, A |
| C1031 | 35.4 | 2.4 | 973 | 18 | US-10-437-963-40387 | Sequence 40387, A | 1104 | 35.2 | 2.4 | 797 | 17 | US-10-425-114-17945 | Sequence 17945, A |
| 1032 | 35.4 | 2.4 | 995 | 18 | US-10-437-963-22608 | Sequence 22608, A | 1105 | 35.2 | 2.4 | 812 | 17 | US-10-425-114-21468 | Sequence 21468, A |
| 1033 | 35.4 | 2.4 | 1087 | 18 | US-10-767-701-5388 | Sequence 5388, Ap | 1106 | 35.2 | 2.4 | 814 | 17 | US-10-291-177-55 | Sequence 55, Appl |
| 1034 | 35.4 | 2.4 | 1135 | 18 | US-10-437-963-73222 | Sequence 73222, A | 1107 | 35.2 | 2.4 | 814 | 17 | US-10-221-278-55 | Sequence 5533, Ap |
| 1035 | 35.4 | 2.4 | 1146 | 18 | US-10-437-963-80370 | Sequence 80370, A | 1108 | 35.2 | 2.4 | 816 | 18 | US-10-767-701-5533 | Sequence 5533, Ap |
| C1036 | 35.4 | 2.4 | 1190 | 18 | US-10-437-963-36882 | Sequence 36882, A | 1109 | 35.2 | 2.4 | 888 | 15 | US-10-119-926-6 | Sequence 6, Appl |
| 1037 | 35.4 | 2.4 | 1301 | 17 | US-10-424-599-85423 | Sequence 85423, A | 1110 | 35.2 | 2.4 | 870 | 17 | US-10-369-493-43223 | Sequence 42323, A |
| 1038 | 35.4 | 2.4 | 1320 | 18 | US-10-437-963-13534 | Sequence 13534, A | 1111 | 35.2 | 2.4 | 1020 | 18 | US-10-425-115-149778 | Sequence 149778, A |

| | | | | | | | | | | | | | |
|------|------|-----|--------|----|----------------------|--------------------|------|------|-----|--------|----|----------------------|--------------------|
| 1112 | 35 | 2.4 | 1216 | 17 | US-10-310-154-210 | Sequence 310, App | 1185 | 34.8 | 2.3 | 3237 | 17 | US-10-369-493-25803 | Sequence 25803, A |
| 1113 | 35 | 2.4 | 1481 | 17 | US-10-425-114-31221 | Sequence 31221, A | 1186 | 34.8 | 2.3 | 4172 | 9 | US-09-764-860-1024 | Sequence 1024, Ap |
| 1115 | 35 | 2.4 | 1498 | 17 | US-09-919-039-09 | Sequence 99, Appl | 1187 | 34.8 | 2.3 | 4172 | 14 | US-10-074-095-1024 | Sequence 1024, Ap |
| 1116 | 35 | 2.4 | 1517 | 17 | US-10-425-114-8896 | Sequence 8896, Ap | 1188 | 34.8 | 2.3 | 4172 | 17 | US-10-212-872-1024 | Sequence 1024, Ap |
| 1117 | 35 | 2.4 | 1579 | 18 | US-10-437-963-43328 | Sequence 43328, A | 1189 | 34.8 | 2.3 | 5100 | 10 | US-09-954-483A-14 | Sequence 14, Appl |
| 1118 | 35 | 2.4 | 1607 | 18 | US-10-425-115-89472 | Sequence 89472, A | 1190 | 34.8 | 2.3 | 3152 | 9 | US-09-764-855-328 | Sequence 328, Ap |
| 1119 | 35 | 2.4 | 1698 | 17 | US-10-210-130-149 | Sequence 149, Appl | 1191 | 34.8 | 2.3 | 33152 | 14 | US-09-764-872-518 | Sequence 518, App |
| 1120 | 35 | 2.4 | 1890 | 17 | US-10-276-774-68 | Sequence 68, Appl | 1192 | 34.8 | 2.3 | 33152 | 14 | US-10-072-349-328 | Sequence 328, App |
| 1121 | 35 | 2.4 | 2011 | 10 | US-09-981-151A-15 | Sequence 15, Appl | 1193 | 34.8 | 2.3 | 94672 | 13 | US-10-087-192-655 | Sequence 655, App |
| 1122 | 35 | 2.4 | 2139 | 17 | US-10-369-493-11751 | Sequence 41751, A | 1194 | 34.8 | 2.3 | 94672 | 13 | US-10-087-192-1069 | Sequence 1069, App |
| 1123 | 35 | 2.4 | 2182 | 18 | US-10-425-115-79752 | Sequence 79752, A | 1195 | 34.8 | 2.3 | 116561 | 18 | US-10-723-860-409 | Sequence 409, App |
| 1124 | 35 | 2.4 | 2200 | 10 | US-09-849-138-25 | Sequence 25, Appl | 1196 | 34.8 | 2.3 | 138115 | 18 | US-10-322-281-377 | Sequence 377, App |
| 1125 | 35 | 2.4 | 2200 | 11 | US-09-972-211-59 | Sequence 59, Appl | 1197 | 34.8 | 2.3 | 228139 | 13 | US-10-087-192-232 | Sequence 232, App |
| 1126 | 35 | 2.4 | 2200 | 11 | US-09-972-211-61 | Sequence 61, Appl | 1198 | 34.8 | 2.3 | 493631 | 13 | US-10-087-192-205 | Sequence 205, App |
| 1127 | 35 | 2.4 | 2200 | 17 | US-10-210-130-141 | Sequence 141, App | 1199 | 34.8 | 2.3 | 684187 | 18 | US-10-367-094-71 | Sequence 71, Appl |
| 1128 | 35 | 2.4 | 2200 | 17 | US-10-036-625-59 | Sequence 59, Appl | 1200 | 34.6 | 2.3 | 267 | 9 | US-09-823-101-9 | Sequence 9, Appl |
| 1129 | 35 | 2.4 | 2200 | 17 | US-10-036-625-61 | Sequence 61, Appl | 1201 | 34.6 | 2.3 | 336 | 18 | US-10-674-124A-1488 | Sequence 1488, A |
| 1130 | 35 | 2.4 | 2535 | 18 | US-10-425-115-18723 | Sequence 18723, A | 1202 | 34.6 | 2.3 | 372 | 18 | US-10-425-115-177235 | Sequence 177235, A |
| 1131 | 35 | 2.4 | 2645 | 18 | US-10-437-963-11058 | Sequence 31058, A | 1203 | 34.6 | 2.3 | 422 | 9 | US-09-864-761-1041 | Sequence 1041, Ap |
| 1132 | 35 | 2.4 | 2768 | 18 | US-10-723-860-8321 | Sequence 8321, Ap | 1204 | 34.6 | 2.3 | 422 | 18 | US-10-425-115-22626 | Sequence 22626, A |
| 1133 | 35 | 2.4 | 3570 | 17 | US-10-336-472-15 | Sequence 15, Appl | 1205 | 34.6 | 2.3 | 447 | 18 | US-10-425-115-24275 | Sequence 24275, A |
| 1134 | 35 | 2.4 | 4318 | 18 | US-10-437-963-21360 | Sequence 21360, A | 1206 | 34.6 | 2.3 | 549 | 18 | US-10-425-115-74784 | Sequence 74784, A |
| 1135 | 35 | 2.4 | 4595 | 18 | US-10-437-963-53344 | Sequence 53344, A | 1207 | 34.6 | 2.3 | 636 | 13 | US-10-027-632-308921 | Sequence 308921, A |
| 1136 | 35 | 2.4 | 4775 | 17 | US-10-336-472-17 | Sequence 17, Appl | 1208 | 34.6 | 2.3 | 636 | 13 | US-10-027-632-308922 | Sequence 308922, A |
| 1137 | 35 | 2.4 | 5780 | 17 | US-10-336-472-19 | Sequence 19, Appl | 1209 | 34.6 | 2.3 | 636 | 17 | US-10-027-632-308921 | Sequence 308921, A |
| 1138 | 35 | 2.4 | 6008 | 17 | US-10-336-472-21 | Sequence 21, Appl | 1210 | 34.6 | 2.3 | 665 | 18 | US-10-425-115-63700 | Sequence 63700, A |
| 1139 | 35 | 2.4 | 6008 | 18 | US-10-717-597-197 | Sequence 197, App | 1211 | 34.6 | 2.3 | 693 | 14 | US-10-123-155-406 | Sequence 406, App |
| 1140 | 35 | 2.4 | 6269 | 17 | US-10-292-798-1421 | Sequence 1421, Ap | 1212 | 34.6 | 2.3 | 698 | 13 | US-10-027-632-25570 | Sequence 25570, A |
| 1141 | 35 | 2.4 | 6647 | 10 | US-09-764-891-8442 | Sequence 8442, Ap | 1213 | 34.6 | 2.3 | 698 | 13 | US-10-027-632-25571 | Sequence 25571, A |
| 1142 | 35 | 2.4 | 8360 | 15 | US-10-017-161-1633 | Sequence 1633, Ap | 1214 | 34.6 | 2.3 | 698 | 17 | US-10-027-632-25570 | Sequence 25570, A |
| 1143 | 35 | 2.4 | 8360 | 17 | US-10-292-798-1303 | Sequence 1303, Ap | 1215 | 34.6 | 2.3 | 698 | 17 | US-10-027-632-25571 | Sequence 25571, A |
| 1144 | 35 | 2.4 | 11211 | 15 | US-10-017-161-1765 | Sequence 1765, Ap | 1216 | 34.6 | 2.3 | 730 | 13 | US-10-027-632-151953 | Sequence 151953, A |
| 1145 | 35 | 2.4 | 15579 | 10 | US-09-764-891-8443 | Sequence 8443, Ap | 1217 | 34.6 | 2.3 | 730 | 13 | US-10-027-632-151953 | Sequence 151953, A |
| 1146 | 35 | 2.4 | 30535 | 18 | US-10-451-503A-7 | Sequence 7, Appl | 1218 | 34.6 | 2.3 | 740 | 17 | US-10-260-338-3630 | Sequence 3630, Ap |
| 1147 | 35 | 2.4 | 33454 | 13 | US-10-087-192-1111 | Sequence 1111, Ap | 1219 | 34.6 | 2.3 | 807 | 17 | US-10-425-114-30318 | Sequence 30318, A |
| 1148 | 35 | 2.4 | 44748 | 13 | US-10-087-192-325 | Sequence 325, App | 1220 | 34.6 | 2.3 | 861 | 18 | US-10-437-963-56550 | Sequence 56550, A |
| 1149 | 35 | 2.4 | 56258 | 13 | US-10-087-192-913 | Sequence 913, App | 1221 | 34.6 | 2.3 | 870 | 17 | US-10-425-114-18555 | Sequence 18555, A |
| 1150 | 35 | 2.4 | 57181 | 19 | US-10-741-600-17781 | Sequence 17781, A | 1222 | 34.6 | 2.3 | 899 | 18 | US-10-437-963-182750 | Sequence 182750, A |
| 1151 | 35 | 2.4 | 96599 | 11 | US-09-997-722-13 | Sequence 13, Appl | 1223 | 34.6 | 2.3 | 929 | 18 | US-10-425-115-180964 | Sequence 180964, A |
| 1152 | 35 | 2.4 | 121434 | 18 | US-10-303-165-11 | Sequence 11, Appl | 1224 | 34.6 | 2.3 | 978 | 18 | US-10-437-963-64115 | Sequence 64115, A |
| 1153 | 35 | 2.4 | 154504 | 18 | US-10-322-696-67 | Sequence 67, Appl | 1225 | 34.6 | 2.3 | 1086 | 9 | US-09-995-225-7 | Sequence 7, Appl |
| 1154 | 34.8 | 2.3 | 166 | 18 | US-10-674-124A-21458 | Sequence 21258, A | 1226 | 34.6 | 2.3 | 1086 | 10 | US-09-992-331-1 | Sequence 1, Appl |
| 1155 | 34.8 | 2.3 | 389 | 18 | US-10-674-124A-20448 | Sequence 20448, A | 1227 | 34.6 | 2.3 | 1086 | 10 | US-09-995-225-7 | Sequence 7, Appl |
| 1156 | 34.8 | 2.3 | 437 | 18 | US-10-674-124A-4968 | Sequence 4968, Ap | 1228 | 34.6 | 2.3 | 1086 | 13 | US-10-086-181-3 | Sequence 3, Appl |
| 1157 | 34.8 | 2.3 | 471 | 18 | US-10-437-963-17773 | Sequence 77773, A | 1229 | 34.6 | 2.3 | 1086 | 14 | US-10-083-168-11 | Sequence 11, Appl |
| 1158 | 34.8 | 2.3 | 498 | 18 | US-10-674-124A-14540 | Sequence 14540, A | 1230 | 34.6 | 2.3 | 1086 | 14 | US-10-083-168-80 | Sequence 80, Appl |
| 1159 | 34.8 | 2.3 | 568 | 9 | US-09-770-152-319 | Sequence 89207, A | 1231 | 34.6 | 2.3 | 1086 | 15 | US-10-262-313-1 | Sequence 1, Appl |
| 1160 | 34.8 | 2.3 | 673 | 18 | US-10-437-963-89217 | Sequence 89217, A | 1232 | 34.6 | 2.3 | 1160 | 13 | US-10-015-498-1 | Sequence 1, Appl |
| 1161 | 34.8 | 2.3 | 733 | 18 | US-10-767-701-12439 | Sequence 12439, A | 1233 | 34.6 | 2.3 | 1203 | 18 | US-10-437-963-36937 | Sequence 36937, A |
| 1162 | 34.8 | 2.3 | 747 | 17 | US-10-260-238-1637 | Sequence 1637, Ap | 1234 | 34.6 | 2.3 | 1252 | 18 | US-10-425-115-31573 | Sequence 31573, A |
| 1163 | 34.8 | 2.3 | 781 | 13 | US-10-027-632-155529 | Sequence 155529, A | 1235 | 34.6 | 2.3 | 1278 | 17 | US-10-369-493-45417 | Sequence 45417, A |
| 1164 | 34.8 | 2.3 | 821 | 18 | US-10-767-701-15527 | Sequence 15527, A | 1236 | 34.6 | 2.3 | 1321 | 18 | US-10-149-826-59 | Sequence 59, Appl |
| 1165 | 34.8 | 2.3 | 860 | 18 | US-10-425-115-131510 | Sequence 131510, A | 1237 | 34.6 | 2.3 | 1349 | 10 | US-09-988-462-20 | Sequence 20, Appl |
| 1166 | 34.8 | 2.3 | 1057 | 18 | US-10-437-963-1511 | Sequence 1511, Ap | 1238 | 34.6 | 2.3 | 1368 | 17 | US-10-369-493-43288 | Sequence 43288, A |
| 1167 | 34.8 | 2.3 | 1149 | 15 | US-10-156-761-1907 | Sequence 1907, Ap | 1239 | 34.6 | 2.3 | 1372 | 15 | US-10-017-161-2187 | Sequence 2187, Ap |
| 1168 | 34.8 | 2.3 | 1176 | 18 | US-10-626-445-6 | Sequence 6, Appl | 1240 | 34.6 | 2.3 | 1521 | 18 | US-10-292-798-1833 | Sequence 1833, Ap |
| 1169 | 34.8 | 2.3 | 1375 | 15 | US-09-770-621-1 | Sequence 1, Appl | 1241 | 34.6 | 2.3 | 1558 | 17 | US-10-424-599-82488 | Sequence 82488, A |
| 1170 | 34.8 | 2.3 | 1375 | 15 | US-10-286-993-1 | Sequence 1, Appl | 1242 | 34.6 | 2.3 | 1599 | 19 | US-10-762-027-66 | Sequence 66, Appl |
| 1171 | 34.8 | 2.3 | 1542 | 18 | US-10-739-930-4426 | Sequence 4426, Ap | 1243 | 34.6 | 2.3 | 1743 | 13 | US-10-086-181-1 | Sequence 1, Appl |
| 1172 | 34.8 | 2.3 | 1566 | 18 | US-10-437-963-15117 | Sequence 15117, A | 1244 | 34.6 | 2.3 | 1743 | 14 | US-10-077-598-2 | Sequence 2, Appl |
| 1173 | 34.8 | 2.3 | 1599 | 18 | US-10-437-963-74114 | Sequence 74134, A | 1245 | 34.6 | 2.3 | 1743 | 14 | US-10-171-027-2 | Sequence 2, Appl |
| 1174 | 34.8 | 2.3 | 1756 | 18 | US-10-425-115-64321 | Sequence 64321, A | 1246 | 34.6 | 2.3 | 1743 | 14 | US-10-075-987-2 | Sequence 2, Appl |
| 1175 | 34.8 | 2.3 | 1837 | 17 | US-10-282-122A-15375 | Sequence 15375, A | 1247 | 34.6 | 2.3 | 2070 | 15 | US-10-156-761-8 | Sequence 8, Appl |
| 1176 | 34.8 | 2.3 | 2013 | 18 | US-10-437-963-12377 | Sequence 12377, A | 1248 | 34.6 | 2.3 | 2277 | 17 | US-10-437-963-37533 | Sequence 37533, A |
| 1177 | 34.8 | 2.3 | 2077 | 17 | US-10-282-122A-15312 | Sequence 15312, A | 1249 | 34.6 | 2.3 | 2355 | 17 | US-10-382-122A-38920 | Sequence 38920, A |
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| C1270 | 34.6 | 2.3 | 3537 | 9 | US-09-858-546-1 | Sequence 1, Appl1 | 1346 | 34.4 | 2.3 | 142201 | 18 | US-10-719-993-6869 | Sequence 6869, Ap |
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| C1272 | 34.6 | 2.3 | 5960 | 19 | US-10-762-107-64 | Sequence 64, Appl | C1348 | 34.2 | 2.3 | 238 | 9 | US-09-923-876-2694 | Sequence 2694, Ap |
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| 1281 | 34.6 | 2.3 | 223555 | 13 | US-09-735-933-3 | Sequence 3, Appl1 | C1353 | 34.2 | 2.3 | 372 | 18 | US-10-674-124A-14216 | Sequence 14216, A |
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| C1281 | 34.4 | 2.3 | 256 | 18 | US-10-087-192-331 | Sequence 331, App | C1355 | 34.2 | 2.3 | 420 | 14 | US-10-074-475-127 | Sequence 127, App |
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| C1287 | 34.4 | 2.3 | 463 | 18 | US-10-674-124A-26428 | Sequence 26428, A | C1361 | 34.2 | 2.3 | 527 | 17 | US-10-057-475B-9347 | Sequence 9347, Ap |
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| C1289 | 34.4 | 2.3 | 479 | 18 | US-10-674-124A-18991 | Sequence 18991, A | C1363 | 34.2 | 2.3 | 527 | 18 | US-10-764-324-9347 | Sequence 9347, Ap |
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 1445.6 | 97.3 | 3449 | 3 | US-09-049-672A-16 |
| 2 | 602.8 | 40.6 | 632 | 4 | US-09-010-147B-11 |
| 3 | 192.2 | 12.9 | 491 | 3 | US-08-361-441B-43 |
| 4 | 192.2 | 12.9 | 658 | 3 | US-08-792-013-5 |
| 5 | 186 | 12.5 | 658 | 4 | US-09-513-999C-3905 |
| 6 | 183.2 | 12.3 | 597 | 4 | US-09-513-999C-14979 |
| 7 | 180.4 | 12.1 | 627 | 3 | US-08-361-441B-4 |
| 8 | 180.4 | 12.1 | 651 | 1 | US-08-171-385-4 |
| 9 | 131.4 | 8.8 | 507 | 4 | US-09-513-999C-10617 |
| 10 | 94.8 | 6.4 | 331 | 1 | US-08-171-385-1 |
| 11 | 94.8 | 6.4 | 331 | 3 | US-08-361-441B-1 |
| 12 | 79.4 | 5.3 | 1363 | 4 | US-09-949-016-5139 |
| 13 | 79.4 | 5.3 | 1363 | 4 | US-09-949-016-5140 |
| 14 | 79.4 | 5.3 | 5502 | 4 | US-09-949-016-16881 |
| 15 | 79.4 | 5.3 | 5502 | 4 | US-09-949-016-16882 |
| 16 | 76.2 | 5.1 | 1235 | 3 | US-09-004-171-1 |
| 17 | 68.8 | 4.6 | 1897 | 4 | US-09-799-451-444 |
| 18 | 64.2 | 4.3 | 582 | 4 | US-09-010-147B-13 |
| 19 | 63.2 | 4.3 | 1358 | 4 | US-09-023-655-84 |
| 20 | 61 | 4.1 | 7218 | 1 | US-08-232-463-14 |
| 21 | 54.6 | 3.7 | 55 | 4 | US-09-513-999C-30846 |
| 22 | 54.6 | 3.7 | 7218 | 1 | US-08-232-463-14 |
| 23 | 45.6 | 3.1 | 452 | 4 | US-09-513-999C-1145 |
| 24 | 45.6 | 3.1 | 547 | 4 | US-09-513-999C-3905 |
| 25 | 45.6 | 3.1 | 677 | 4 | US-09-949-016-465 |
| 26 | 45.6 | 3.1 | 677 | 4 | US-09-949-016-4472 |
| 27 | 44.6 | 3.0 | 3235 | 4 | US-09-949-016-1392 |

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| C | 28 | 44.6 | 3.0 | 3372 | 4 | US-09-949-016-165 | Sequence 165, App |
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| C | 30 | 44.6 | 3.0 | 31868 | 4 | US-09-949-016-11907 | Sequence 11907, A |
| C | 31 | 44.4 | 3.0 | 1251 | 4 | US-09-989-025A-7 | Sequence 7, Appl1 |
| C | 32 | 43.6 | 2.9 | 1161 | 4 | US-09-949-016-579 | Sequence 579, App |
| C | 33 | 43.6 | 2.9 | 1173 | 3 | US-09-285-601-1 | Sequence 1, Appl1 |
| C | 34 | 43.6 | 2.9 | 1620 | 4 | US-09-949-016-4404 | Sequence 4404, Ap |
| C | 35 | 43.6 | 2.9 | 5159 | 4 | US-09-949-016-12321 | Sequence 12321, A |
| C | 36 | 43.6 | 2.9 | 5621 | 4 | US-09-949-016-16146 | Sequence 16146, A |
| C | 37 | 43.6 | 2.9 | 6709 | 3 | US-09-285-601-3 | Sequence 3, Appl1 |
| C | 38 | 43.4 | 2.9 | 2466 | 4 | US-09-266-965-33 | Sequence 83, Appl |
| C | 39 | 43.4 | 2.9 | 18034 | 4 | US-09-266-965-75 | Sequence 75, Appl |
| C | 40 | 43.2 | 2.9 | 447 | 4 | US-09-989-025A-3 | Sequence 3, Appl1 |
| C | 41 | 43.2 | 2.9 | 564 | 4 | US-09-513-999C-3836 | Sequence 3836, Ap |
| C | 42 | 40.8 | 2.7 | 37385 | 4 | US-09-949-016-12466 | Sequence 12466, A |
| C | 43 | 40.8 | 2.7 | 37388 | 4 | US-09-949-016-16846 | Sequence 16846, A |
| C | 44 | 40.6 | 2.7 | 304533 | 4 | US-09-949-016-15371 | Sequence 15371, A |
| C | 45 | 40.6 | 2.7 | 304533 | 4 | US-09-949-016-15372 | Sequence 15372, A |
| C | 46 | 40.4 | 2.7 | 41522 | 4 | US-09-949-016-11932 | Sequence 11932, A |
| C | 47 | 40.4 | 2.7 | 41523 | 4 | US-09-949-016-15764 | Sequence 15764, A |
| C | 48 | 39.8 | 2.7 | 681 | 4 | US-09-513-999C-14967 | Sequence 14967, A |
| C | 49 | 39.4 | 2.7 | 28819 | 4 | US-09-949-016-15806 | Sequence 15806, A |
| C | 50 | 39 | 2.6 | 686 | 4 | US-09-949-016-5118 | Sequence 5118, Ap |
| C | 51 | 39 | 2.6 | 744 | 4 | US-09-368-819A-1 | Sequence 1, Appl1 |
| C | 52 | 39 | 2.6 | 795 | 4 | US-09-368-819A-3 | Sequence 3, Appl1 |
| C | 53 | 39 | 2.6 | 846 | 4 | US-09-919-039-119 | Sequence 319, App |
| C | 54 | 39 | 2.6 | 1158 | 4 | US-09-919-039-120 | Sequence 320, App |
| C | 55 | 39 | 2.6 | 1173 | 3 | US-08-993-380-3 | Sequence 3, Appl1 |
| C | 56 | 39 | 2.6 | 1929 | 2 | US-08-818-253-1 | Sequence 1, Appl1 |
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| C | 59 | 39 | 2.6 | 1929 | 3 | US-08-818-252-5 | Sequence 5, Appl1 |
| C | 60 | 39 | 2.6 | 1959 | 2 | US-08-818-253-3 | Sequence 3, Appl1 |
| C | 61 | 39 | 2.6 | 1959 | 2 | US-08-818-252-3 | Sequence 3, Appl1 |
| C | 62 | 39 | 2.6 | 1971 | 2 | US-08-818-253-7 | Sequence 7, Appl1 |
| C | 63 | 39 | 2.6 | 1971 | 3 | US-08-818-252-7 | Sequence 7, Appl1 |
| C | 64 | 38.6 | 2.6 | 2110 | 4 | US-09-949-016-11105 | Sequence 1105, Ap |
| C | 65 | 38.6 | 2.6 | 2111 | 4 | US-09-949-016-12847 | Sequence 12847, A |
| C | 66 | 38.6 | 2.6 | 40546 | 4 | US-09-949-016-12915 | Sequence 12915, A |
| C | 67 | 38.6 | 2.6 | 40546 | 4 | US-09-949-016-12915 | Sequence 12915, A |
| C | 68 | 38.4 | 2.6 | 214 | 4 | US-09-513-999C-27341 | Sequence 27341, A |
| C | 69 | 38.4 | 2.6 | 916 | 3 | US-09-239-909-3 | Sequence 3, Appl1 |
| C | 70 | 38.4 | 2.6 | 152070 | 4 | US-09-949-016-15402 | Sequence 15402, A |
| C | 71 | 38.2 | 2.6 | 2492 | 4 | US-09-949-016-5560 | Sequence 5560, App |
| C | 72 | 38.2 | 2.6 | 3250 | 4 | US-09-949-016-800 | Sequence 800, App |
| C | 73 | 38.2 | 2.6 | 173787 | 4 | US-09-949-016-12542 | Sequence 12542, A |
| C | 74 | 38.2 | 2.6 | 173791 | 4 | US-09-949-016-17302 | Sequence 17302, A |
| C | 75 | 38 | 2.6 | 10505 | 4 | US-09-902-540-1044 | Sequence 1044, Ap |
| C | 76 | 38 | 2.6 | 57837 | 4 | US-09-949-016-14371 | Sequence 14371, A |
| C | 77 | 38 | 2.6 | 57839 | 4 | US-09-949-016-17601 | Sequence 17601, A |
| C | 78 | 37.8 | 2.5 | 4911 | 3 | US-09-718-852-1 | Sequence 1, Appl1 |
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| C | 81 | 37.6 | 2.5 | 1344 | 4 | US-09-252-991A-5239 | Sequence 5239, Ap |
| C | 82 | 37.6 | 2.5 | 1794 | 4 | US-09-252-991A-5181 | Sequence 5181, Ap |
| C | 83 | 37.6 | 2.5 | 2547 | 4 | US-09-252-991A-5234 | Sequence 5234, Ap |
| C | 84 | 37.6 | 2.5 | 3955 | 3 | US-09-214-228-4 | Sequence 4, Appl1 |
| C | 85 | 37.6 | 2.5 | 3955 | 4 | US-09-855-722-4 | Sequence 4, Appl1 |
| C | 86 | 37.4 | 2.5 | 2485 | 4 | US-08-424-444B-1 | Sequence 1, Appl1 |
| C | 87 | 37.4 | 2.5 | 2486 | 5 | PCT-US94-05163A-1 | Sequence 1, Appl1 |
| C | 88 | 37.2 | 2.5 | 387 | 4 | US-09-902-540-8061 | Sequence 8061, Ap |
| C | 89 | 37.2 | 2.5 | 476 | 4 | US-09-640-211A-1441 | Sequence 1441, Ap |
| C | 90 | 37.2 | 2.5 | 864 | 4 | US-09-252-991A-15661 | Sequence 15661, A |
| C | 91 | 37.2 | 2.5 | 1304 | 4 | US-09-902-540-8596 | Sequence 2596, Ap |
| C | 92 | 37.2 | 2.5 | 1428 | 4 | US-09-252-991A-15727 | Sequence 15727, A |
| C | 93 | 37.2 | 2.5 | 2679 | 4 | US-09-252-991A-15523 | Sequence 15523, A |
| C | 94 | 37.2 | 2.5 | 5967 | 4 | US-09-949-016-11662 | Sequence 11662, Ap |
| C | 95 | 37.2 | 2.5 | 11502 | 4 | US-09-902-540-1064 | Sequence 1064, Ap |
| C | 96 | 37.2 | 2.5 | 16584 | 4 | US-09-902-540-11119 | Sequence 11119, Ap |
| C | 97 | 37.2 | 2.5 | 64377 | 4 | US-09-949-016-15212 | Sequence 15212, A |
| C | 98 | 37.2 | 2.5 | 64377 | 4 | US-09-949-016-15213 | Sequence 15213, A |
| C | 99 | 37.2 | 2.5 | 64377 | 4 | US-09-949-016-15214 | Sequence 15214, A |
| C | 100 | 37.2 | 2.5 | 64377 | 4 | US-09-949-016-15215 | Sequence 15215, A |

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| 101 | 37.2 | 2.5 | 64377 | 4 | US-09-949-016-15216 | Sequence 15216, A | 174 | 35.8 | 2.4 | 3168 | 4 | US-09-774-528-409 | Sequence 409, App |
| 102 | 37 | 2.5 | 429 | 4 | US-09-252-991A-7812 | Sequence 7812, Ap | 175 | 35.8 | 2.4 | 11125 | 4 | US-09-902-540-1158 | Sequence 1158, Ap |
| 103 | 37 | 2.5 | 1218 | 4 | US-09-902-540-9113 | Sequence 9113, Ap | 176 | 35.8 | 2.4 | 43950 | 3 | US-09-735-934A-3 | Sequence 3, Appl1 |
| 104 | 37 | 2.5 | 1434 | 4 | US-09-252-991A-7601 | Sequence 7601, Ap | 177 | 35.8 | 2.4 | 43950 | 4 | US-10-060-332-3 | Sequence 3, Appl1 |
| 105 | 37 | 2.5 | 1626 | 4 | US-09-902-540-7950 | Sequence 7950, Ap | 178 | 35.8 | 2.4 | 43950 | 4 | US-10-339-657-3 | Sequence 3, Appl1 |
| 106 | 37 | 2.5 | 1995 | 4 | US-09-902-540-9209 | Sequence 9209, Ap | 179 | 35.8 | 2.4 | 258775 | 4 | US-09-949-016-16435 | Sequence 16435, A |
| 107 | 37 | 2.5 | 2169 | 4 | US-09-252-991A-7531 | Sequence 7531, Ap | 180 | 35.6 | 2.4 | 174 | 4 | US-09-401-064-325 | Sequence 325, App |
| 108 | 37 | 2.5 | 8820 | 4 | US-09-902-540-974 | Sequence 974, App | 181 | 35.6 | 2.4 | 174 | 4 | US-09-401-064-368 | Sequence 368, App |
| 109 | 37 | 2.5 | 10301 | 4 | US-09-902-540-985 | Sequence 985, App | 182 | 35.6 | 2.4 | 2136 | 4 | US-09-600-991-19 | Sequence 19, Appl |
| 110 | 37 | 2.5 | 41927 | 4 | US-09-902-540-1268 | Sequence 1268, Ap | 183 | 35.6 | 2.4 | 2136 | 4 | US-09-601-040A-11 | Sequence 11, Appl |
| 111 | 37 | 2.5 | 90541 | 4 | US-09-759-359A-3 | Sequence 3, Appl1 | 184 | 35.6 | 2.4 | 2216 | 2 | US-08-666-082B-2 | Sequence 2, Appl1 |
| 112 | 37 | 2.5 | 873 | 4 | US-09-252-991A-1766 | Sequence 1766, Ap | 185 | 35.6 | 2.4 | 2219 | 1 | US-07-882-925A-1 | Sequence 1, Appl1 |
| 113 | 36.8 | 2.5 | 2169 | 4 | US-09-252-991A-1910 | Sequence 1910, Ap | 186 | 35.6 | 2.4 | 2219 | 1 | US-07-882-925A-2 | Sequence 2, Appl1 |
| 114 | 36.8 | 2.5 | 2946 | 4 | US-09-252-991A-2045 | Sequence 2045, Ap | 187 | 35.6 | 2.4 | 2219 | 1 | US-08-184-012C-1 | Sequence 1, Appl1 |
| 115 | 36.8 | 2.5 | 2946 | 4 | US-09-252-991A-2045 | Sequence 12852, A | 188 | 35.6 | 2.4 | 2219 | 1 | US-08-184-012C-2 | Sequence 2, Appl1 |
| 116 | 36.8 | 2.5 | 4123 | 4 | US-09-949-016-12852 | Sequence 6, Appl1 | 189 | 35.6 | 2.4 | 2219 | 4 | US-09-949-016-1110 | Sequence 1110, Ap |
| 117 | 36.8 | 2.5 | 6100 | 1 | US-07-882-925A-6 | Sequence 15018, A | 190 | 35.6 | 2.4 | 2232 | 5 | US-08-334-177-1 | Sequence 1, Appl1 |
| 118 | 36.8 | 2.5 | 6100 | 1 | US-08-184-012C-6 | Sequence 17, Appl | 191 | 35.6 | 2.4 | 2262 | 1 | PCT-US95-13830-1 | Sequence 1, Appl1 |
| 119 | 36.8 | 2.5 | 17922 | 3 | US-09-949-016-15018 | Sequence 17, Appl | 192 | 35.6 | 2.4 | 2262 | 1 | US-08-184-012C-7 | Sequence 7, Appl1 |
| 120 | 36.8 | 2.5 | 35828 | 4 | US-09-449-218D-17 | Sequence 17, Appl | 193 | 35.6 | 2.4 | 2262 | 1 | US-08-785-420-1 | Sequence 1, Appl1 |
| 121 | 36.8 | 2.5 | 35828 | 4 | US-09-668-037A-17 | Sequence 17, Appl | 194 | 35.6 | 2.4 | 15378 | 3 | US-08-785-420-1 | Sequence 1, Appl1 |
| 122 | 36.8 | 2.5 | 35828 | 4 | US-09-668-037A-17 | Sequence 17, Appl | 195 | 35.6 | 2.4 | 60990 | 4 | US-09-949-016-14080 | Sequence 14080, A |
| 123 | 36.8 | 2.5 | 35828 | 4 | US-09-668-037A-17 | Sequence 17, Appl | 196 | 35.6 | 2.4 | 113967 | 4 | US-09-949-016-12277 | Sequence 12277, A |
| 124 | 36.8 | 2.5 | 64467 | 4 | US-09-803-671B-3 | Sequence 3, Appl1 | 197 | 35.6 | 2.4 | 113967 | 4 | US-09-949-016-17051 | Sequence 17051, A |
| 125 | 36.8 | 2.5 | 64467 | 4 | US-10-274-409-3 | Sequence 3, Appl1 | 198 | 35.6 | 2.4 | 142783 | 4 | US-09-949-016-15127 | Sequence 15127, A |
| 126 | 36.8 | 2.5 | 118067 | 4 | US-09-497-855A-32 | Sequence 32, Appl | 199 | 35.4 | 2.4 | 423 | 4 | US-09-252-991A-10025 | Sequence 10025, A |
| 127 | 36.8 | 2.5 | 156651 | 4 | US-09-949-016-17349 | Sequence 17349, A | 200 | 35.4 | 2.4 | 423 | 4 | US-09-949-016-196837 | Sequence 196837, A |
| 128 | 36.6 | 2.5 | 601 | 4 | US-09-949-016-161657 | Sequence 161657, A | 201 | 35.4 | 2.4 | 1116 | 4 | US-09-902-540-384 | Sequence 384, Ap |
| 129 | 36.6 | 2.5 | 1294 | 3 | US-09-023-691-2 | Sequence 2, Appl1 | 202 | 35.4 | 2.4 | 1320 | 4 | US-09-902-540-4412 | Sequence 4412, Ap |
| 130 | 36.6 | 2.5 | 20537 | 4 | US-09-949-016-12887 | Sequence 12887, A | 203 | 35.4 | 2.4 | 1526 | 4 | US-09-949-016-899 | Sequence 899, App |
| 131 | 36.6 | 2.5 | 20538 | 4 | US-09-949-016-17052 | Sequence 17052, A | 204 | 35.4 | 2.4 | 1526 | 4 | US-09-949-016-1636 | Sequence 1636, Ap |
| 132 | 36.6 | 2.5 | 54531 | 4 | US-09-949-016-16267 | Sequence 16267, A | 205 | 35.4 | 2.4 | 1559 | 3 | US-09-019-095A-7 | Sequence 7, Appl1 |
| 133 | 36.6 | 2.5 | 421491 | 4 | US-09-949-016-12805 | Sequence 12805, A | 206 | 35.4 | 2.4 | 16427 | 4 | US-09-902-540-1160 | Sequence 1160, Ap |
| 134 | 36.6 | 2.5 | 421491 | 4 | US-09-949-016-14060 | Sequence 14060, A | 207 | 35.4 | 2.4 | 23677 | 4 | US-09-902-540-1218 | Sequence 1218, Ap |
| 135 | 36.4 | 2.5 | 474 | 4 | US-09-621-976-18033 | Sequence 18033, A | 208 | 35.4 | 2.4 | 25992 | 4 | US-09-949-016-17308 | Sequence 17308, A |
| 136 | 36.4 | 2.5 | 601 | 4 | US-09-949-016-82606 | Sequence 82606, A | 209 | 35.4 | 2.4 | 26000 | 4 | US-09-843-376-10 | Sequence 10, Appl |
| 137 | 36.4 | 2.5 | 19237 | 4 | US-09-949-016-13666 | Sequence 13666, A | 210 | 35.4 | 2.4 | 670689 | 4 | US-09-949-016-12505 | Sequence 12505, A |
| 138 | 36.4 | 2.5 | 44208 | 4 | US-09-949-016-12240 | Sequence 12240, A | 211 | 35.4 | 2.4 | 670689 | 4 | US-09-949-016-14207 | Sequence 14207, A |
| 139 | 36.4 | 2.5 | 44208 | 4 | US-09-949-016-15941 | Sequence 15941, A | 212 | 35.2 | 2.4 | 342 | 4 | US-09-902-540-6243 | Sequence 6243, Ap |
| 140 | 36.4 | 2.5 | 107820 | 4 | US-09-792-616-1 | Sequence 1, Appl1 | 213 | 35.2 | 2.4 | 717 | 4 | US-09-902-540-5828 | Sequence 5828, Ap |
| 141 | 36.4 | 2.5 | 121068 | 4 | US-09-949-016-11138 | Sequence 11138, A | 214 | 35.2 | 2.4 | 1854 | 4 | US-09-902-540-5828 | Sequence 5828, Ap |
| 142 | 36.4 | 2.5 | 133559 | 4 | US-09-949-016-15845 | Sequence 15845, A | 215 | 35.2 | 2.4 | 8083 | 3 | US-09-383-630-4 | Sequence 4, Appl1 |
| 143 | 36.2 | 2.4 | 399 | 4 | US-09-621-976-8976 | Sequence 8976, Ap | 216 | 35.2 | 2.4 | 8083 | 3 | US-09-383-630-5 | Sequence 5, Appl1 |
| 144 | 36.2 | 2.4 | 1989 | 4 | US-09-252-991A-15371 | Sequence 15371, A | 217 | 35.2 | 2.4 | 72704 | 4 | US-09-902-540-1273 | Sequence 1273, Ap |
| 145 | 36.2 | 2.4 | 2058 | 4 | US-09-252-991A-15462 | Sequence 15462, A | 218 | 35.2 | 2.4 | 86414 | 4 | US-09-949-016-12345 | Sequence 12345, A |
| 146 | 36.2 | 2.4 | 2637 | 4 | US-09-252-991A-15463 | Sequence 15463, A | 219 | 35.2 | 2.4 | 86414 | 4 | US-09-949-016-17578 | Sequence 17578, A |
| 147 | 36.2 | 2.4 | 5467 | 4 | US-09-976-594-735 | Sequence 735, App | 220 | 35 | 2.4 | 601 | 4 | US-09-949-016-182049 | Sequence 182049, A |
| 148 | 36.2 | 2.4 | 6640 | 4 | US-09-949-016-797 | Sequence 797, App | 221 | 35 | 2.4 | 1488 | 4 | US-09-949-016-7333 | Sequence 7333, Ap |
| 149 | 36.2 | 2.4 | 9515 | 1 | US-08-920-812-13 | Sequence 13, Appl | 222 | 35 | 2.4 | 1488 | 4 | US-09-919-039-99 | Sequence 99, Appl |
| 150 | 36.2 | 2.4 | 9515 | 1 | US-08-920-827-13 | Sequence 13, Appl | 223 | 35 | 2.4 | 1488 | 4 | US-09-252-991A-17412 | Sequence 17412, A |
| 151 | 36.2 | 2.4 | 9515 | 1 | US-08-921-177-13 | Sequence 13, Appl | 224 | 35 | 2.4 | 6008 | 4 | US-09-949-016-5058 | Sequence 5058, Ap |
| 152 | 36.2 | 2.4 | 9515 | 1 | US-08-362-577C-13 | Sequence 13, Appl | 225 | 35 | 2.4 | 15782 | 4 | US-09-902-540-1094 | Sequence 1094, Ap |
| 153 | 36.2 | 2.4 | 9515 | 2 | US-08-920-828-13 | Sequence 13, Appl | 226 | 35 | 2.4 | 31713 | 4 | US-09-949-016-16960 | Sequence 16960, A |
| 154 | 36.2 | 2.4 | 15872 | 3 | US-09-105-537-1 | Sequence 1, Appl1 | 227 | 34.8 | 2.3 | 530 | 4 | US-09-513-999-14129 | Sequence 14129, A |
| 155 | 36.2 | 2.4 | 15872 | 4 | US-09-091-609-3 | Sequence 3, Appl1 | 228 | 34.8 | 2.3 | 601 | 4 | US-09-949-016-17920 | Sequence 17920, A |
| 156 | 36.2 | 2.4 | 15872 | 4 | US-09-091-609-3 | Sequence 1, Appl1 | 229 | 34.8 | 2.3 | 601 | 4 | US-09-949-016-17921 | Sequence 17921, A |
| 157 | 36.2 | 2.4 | 43280 | 2 | US-08-804-227C-1 | Sequence 1, Appl1 | 230 | 34.8 | 2.3 | 601 | 4 | US-09-949-016-41810 | Sequence 41810, A |
| 158 | 36.2 | 2.4 | 253345 | 4 | US-09-949-016-12656 | Sequence 12656, A | 231 | 34.8 | 2.3 | 601 | 4 | US-09-949-016-41811 | Sequence 41811, A |
| 159 | 36.2 | 2.4 | 253364 | 4 | US-09-949-016-13639 | Sequence 13639, A | 232 | 34.8 | 2.3 | 601 | 4 | US-09-949-016-67157 | Sequence 67157, A |
| 160 | 36 | 2.4 | 601 | 4 | US-09-949-016-13639 | Sequence 14809, A | 233 | 34.8 | 2.3 | 601 | 4 | US-09-949-016-67158 | Sequence 67158, A |
| 161 | 36 | 2.4 | 601 | 4 | US-09-949-016-17919 | Sequence 14809, A | 234 | 34.8 | 2.3 | 601 | 4 | US-09-949-016-186276 | Sequence 186276, A |
| 162 | 36 | 2.4 | 894 | 4 | US-09-252-991A-10016 | Sequence 10016, A | 235 | 34.8 | 2.3 | 601 | 4 | US-09-976-594-359 | Sequence 359, App |
| 163 | 36 | 2.4 | 894 | 4 | US-09-252-991A-10016 | Sequence 10016, A | 236 | 34.8 | 2.3 | 1285 | 4 | US-09-902-540-137 | Sequence 137, App |
| 164 | 36 | 2.4 | 1512 | 4 | US-09-252-991A-1551 | Sequence 1551, Ap | 237 | 34.8 | 2.3 | 1285 | 4 | US-09-902-540-5848 | Sequence 5848, Ap |
| 165 | 36 | 2.4 | 1677 | 4 | US-09-252-991A-1551 | Sequence 1551, Ap | 238 | 34.8 | 2.3 | 1375 | 2 | US-08-468-812-1 | Sequence 1, Appl1 |
| 166 | 36 | 2.4 | 2271 | 3 | US-09-902-540-6006 | Sequence 6006, Ap | 239 | 34.8 | 2.3 | 1375 | 2 | US-08-590-563-1 | Sequence 1, Appl1 |
| 167 | 36 | 2.4 | 4315 | 4 | US-08-882-046-3 | Sequence 3, Appl1 | 240 | 34.8 | 2.3 | 1375 | 4 | US-09-770-621-1 | Sequence 1, Appl1 |
| 168 | 36 | 2.4 | 4315 | 4 | US-09-566-047-3 | Sequence 3, Appl1 | 241 | 34.8 | 2.3 | 1375 | 4 | US-09-235-832-1 | Sequence 1, Appl1 |
| 169 | 36 | 2.4 | 23902 | 4 | US-09-949-016-14220 | Sequence 14220, A | 242 | 34.8 | 2.3 | 1512 | 4 | US-09-902-540-3874 | Sequence 3874, Ap |
| 170 | 35.8 | 2.4 | 774 | 4 | US-09-385-219A-39 | Sequence 3367, Ap | 243 | 34.8 | 2.3 | 11666 | 4 | US-09-949-016-1468 | Sequence 1468, A |
| 171 | 35.8 | 2.4 | 777 | 4 | US-09-902-540-367 | Sequence 3367, Ap | 244 | 34.8 | 2.3 | 21143 | 4 | US-09-902-540-1191 | Sequence 1191, Ap |
| 172 | 35.8 | 2.4 | 783 | 4 | US-09-252-991A-6882 | Sequence 6882, Ap | 245 | 34.8 | 2.3 | 30782 | 4 | US-09-949-016-13724 | Sequence 13724, A |
| 173 | 35.8 | 2.4 | 1457 | 4 | US-09-620-312D-408 | Sequence 408, App | 246 | 34.8 | 2.3 | 31391 | 4 | US-09-949-016-14319 | Sequence 14319, A |

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| C 247 | 34.8 | 2.3 | 34539 | 4 | US-09-949-016-12226 | Sequence 12226, A |
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| C 249 | 34.8 | 2.3 | 45545 | 3 | US-09-146-053-6 | Sequence 6, Appl1 |
| 250 | 34.8 | 2.3 | 135058 | 4 | US-09-949-016-12565 | Sequence 12565, A |
| 251 | 34.8 | 2.3 | 136480 | 4 | US-09-949-016-17064 | Sequence 17064, A |
| 252 | 34.8 | 2.3 | 144158 | 4 | US-09-949-016-11755 | Sequence 11755, A |
| 253 | 34.8 | 2.3 | 144158 | 4 | US-09-949-016-12936 | Sequence 12936, A |
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| 256 | 34.8 | 2.3 | 203475 | 4 | US-09-949-016-14518 | Sequence 14518, A |
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| 262 | 34.8 | 2.3 | 212139 | 4 | US-09-949-016-16065 | Sequence 16065, A |
| 263 | 34.6 | 2.3 | 289 | 3 | US-09-007-005-17 | Sequence 17, Appl1 |
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| 266 | 34.6 | 2.3 | 601 | 4 | US-09-949-016-199459 | Sequence 199459, A |
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| 268 | 34.6 | 2.3 | 601 | 4 | US-09-949-016-199461 | Sequence 199461, A |
| C 269 | 34.6 | 2.3 | 984 | 4 | US-09-252-991A-2298 | Sequence 2298, Ap |
| C 270 | 34.6 | 2.3 | 1036 | 4 | US-09-902-540-4309 | Sequence 4309, Ap |
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| 273 | 34.6 | 2.3 | 1349 | 3 | US-08-459-595A-20 | Sequence 20, Appl1 |
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| 275 | 34.6 | 2.3 | 1349 | 3 | US-08-459-444-20 | Sequence 0, Appl1 |
| 276 | 34.6 | 2.3 | 1349 | 3 | US-09-547-422-20 | Sequence 0, Appl1 |
| 277 | 34.6 | 2.3 | 1349 | 4 | US-09-988-462-20 | Sequence 20, Appl1 |
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| C 283 | 34.6 | 2.3 | 2772 | 4 | US-09-252-991A-10577 | Sequence 10577, A |
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| 290 | 34.4 | 2.3 | 601 | 4 | US-09-949-016-65337 | Sequence 65337, A |
| 291 | 34.4 | 2.3 | 601 | 4 | US-09-949-016-121300 | Sequence 121300, A |
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| C 299 | 34.4 | 2.3 | 10644 | 4 | US-09-902-540-1028 | Sequence 1028, App |
| C 300 | 34.4 | 2.3 | 16442 | 4 | US-08-781-891-208 | Sequence 208, App |
| C 301 | 34.4 | 2.3 | 16442 | 4 | US-09-618-166-208 | Sequence 208, App |
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| C 304 | 34.4 | 2.3 | 60785 | 4 | US-09-949-016-12774 | Sequence 12774, A |
| C 305 | 34.4 | 2.3 | 60785 | 4 | US-09-949-016-15665 | Sequence 15665, A |
| C 306 | 34.4 | 2.3 | 74550 | 4 | US-09-949-016-12310 | Sequence 12310, A |
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| C 310 | 34.4 | 2.3 | 74550 | 4 | US-09-949-016-13650 | Sequence 13650, A |
| C 311 | 34.4 | 2.3 | 237510 | 4 | US-09-949-016-14273 | Sequence 14273, A |
| C 312 | 34.4 | 2.3 | 285 | 4 | US-09-949-016-15473 | Sequence 15473, A |
| C 313 | 34.2 | 2.3 | 364 | 4 | US-09-902-540-9636 | Sequence 9636, Ap |
| C 314 | 34.2 | 2.3 | 505 | 4 | US-09-621-976-17202 | Sequence 17202, A |
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| C 316 | 34.2 | 2.3 | 1767 | 4 | US-09-463-712C-9 | Sequence 9, Appl1 |
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| C 318 | 34.2 | 2.3 | 16011 | 4 | US-09-600-319-3 | Sequence 3, Appl1 |
| 319 | 34.2 | 2.3 | 17173 | 4 | US-09-902-540-1122 | Sequence 1122, Ap |
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| 322 | 34.2 | 2.3 | 46816 | 4 | US-09-949-016-13494 | Sequence 13494, A |
| 323 | 34.2 | 2.3 | 53769 | 4 | US-09-949-016-17527 | Sequence 17527, A |
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| C 326 | 34.2 | 2.3 | 289 | 3 | US-09-007-005-17 | Sequence 17, Appl1 |
| C 327 | 34.2 | 2.3 | 289 | 3 | US-09-244-796-17 | Sequence 17, Appl1 |
| C 328 | 34.2 | 2.3 | 429 | 4 | US-09-252-991A-15318 | Sequence 15318, A |
| C 329 | 34.2 | 2.3 | 601 | 4 | US-09-949-016-29118 | Sequence 29118, A |
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| C 332 | 34.2 | 2.3 | 601 | 4 | US-09-949-016-65338 | Sequence 65338, A |
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| C 337 | 34.2 | 2.3 | 601 | 4 | US-09-949-016-123300 | Sequence 123300, A |
| C 338 | 34.2 | 2.3 | 726 | 4 | US-09-252-991A-15364 | Sequence 15364, A |
| C 339 | 34.2 | 2.3 | 1383 | 4 | US-09-252-991A-15469 | Sequence 15469, A |
| C 340 | 34.2 | 2.3 | 1503 | 4 | US-09-252-991A-15409 | Sequence 15409, A |
| C 341 | 34.2 | 2.3 | 1920 | 4 | US-09-902-540-4811 | Sequence 4811, Ap |
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| C 344 | 34.2 | 2.3 | 12690 | 4 | US-09-949-016-13799 | Sequence 13799, A |
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| C 346 | 34.2 | 2.3 | 27160 | 4 | US-09-949-016-17378 | Sequence 17378, A |
| C 347 | 34.2 | 2.3 | 29326 | 4 | US-09-902-540-1236 | Sequence 1236, Ap |
| C 348 | 34.2 | 2.3 | 29326 | 4 | US-09-949-016-15356 | Sequence 15356, A |
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| C 350 | 34.2 | 2.3 | 89863 | 4 | US-09-949-016-13667 | Sequence 13667, A |
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| C 353 | 34.2 | 2.3 | 168104 | 4 | US-09-949-016-12026 | Sequence 12026, A |
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| C 358 | 34.2 | 2.3 | 672 | 4 | US-09-252-991A-15656 | Sequence 15656, A |
| C 359 | 34.2 | 2.3 | 1004 | 4 | US-09-976-594-292 | Sequence 292, App |
| C 360 | 34.2 | 2.3 | 1120 | 3 | US-09-030-613-1 | Sequence 1, Appl1 |
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| C 363 | 34.2 | 2.3 | 2339 | 4 | US-09-799-451-934 | Sequence 934, App |
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| C 371 | 34.2 | 2.3 | 4162 | 3 | US-08-459-444-26 | Sequence 26, Appl1 |
| C 372 | 34.2 | 2.3 | 4162 | 3 | US-09-547-422-26 | Sequence 26, Appl1 |
| C 373 | 34.2 | 2.3 | 4162 | 4 | US-09-988-462-26 | Sequence 26, Appl1 |
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| C 375 | 34.2 | 2.3 | 5187 | 4 | US-09-902-540-678 | Sequence 678, App |
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| C 378 | 34.2 | 2.3 | 15222 | 4 | US-09-949-016-16912 | Sequence 16912, A |
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| C 387 | 34.2 | 2.3 | 76553 | 4 | US-09-443-501A-2 | Sequence 2, Appl1 |
| C 388 | 34.2 | 2.3 | 86272 | 4 | US-09-949-016-13432 | Sequence 13432, A |
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| C 390 | 34.2 | 2.3 | 87205 | 4 | US-09-949-016-13430 | Sequence 13430, A |
| C 391 | 34.2 | 2.3 | 744 | 4 | US-09-949-016-196019 | Sequence 196019, A |
| C 392 | 34.2 | 2.3 | 894 | 4 | US-09-252-991A-8428 | Sequence 8428, Ap |
| | | | | | US-09-252-991A-2512 | Sequence 2512, Ap |

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| 394 | 33.6 | 2.3 | 1575 | 4 | US-09-949-016-4211 | Sequence 4211, Ap |
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| 396 | 33.6 | 2.3 | 1728 | 2 | US-08-878-957-1 | Sequence 1, Appl1 |
| 397 | 33.6 | 2.3 | 1746 | 1 | US-08-427-097-29 | Sequence 29, Appl |
| 398 | 33.6 | 2.3 | 1746 | 2 | US-08-878-957-29 | Sequence 29, Appl |
| 399 | 33.6 | 2.3 | 1752 | 1 | US-08-427-097-13 | Sequence 13, Appl |
| 400 | 33.6 | 2.3 | 1752 | 1 | US-08-427-097-15 | Sequence 15, Appl |
| 401 | 33.6 | 2.3 | 1752 | 1 | US-08-427-097-19 | Sequence 19, Appl |
| 402 | 33.6 | 2.3 | 1752 | 1 | US-08-427-097-27 | Sequence 27, Appl |
| 403 | 33.6 | 2.3 | 1752 | 2 | US-08-878-957-13 | Sequence 13, Appl |
| 404 | 33.6 | 2.3 | 1752 | 2 | US-08-878-957-15 | Sequence 15, Appl |
| 405 | 33.6 | 2.3 | 1752 | 2 | US-08-878-957-19 | Sequence 19, Appl |
| 406 | 33.6 | 2.3 | 1752 | 2 | US-08-878-957-27 | Sequence 27, Appl |
| 407 | 33.6 | 2.3 | 1785 | 4 | US-09-252-991A-2593 | Sequence 2593, Ap |
| 408 | 33.6 | 2.3 | 1851 | 4 | US-09-252-991A-2704 | Sequence 2704, Ap |
| 409 | 33.6 | 2.3 | 2027 | 1 | US-08-150-203A-1 | Sequence 1, Appl1 |
| 410 | 33.6 | 2.3 | 2027 | 1 | US-08-454-730-1 | Sequence 1, Appl1 |
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| 413 | 33.6 | 2.3 | 2040 | 1 | US-08-479-650-36 | Sequence 36, Appl |
| 414 | 33.6 | 2.3 | 2040 | 1 | US-08-191-86CD-57 | Sequence 57, Appl |
| 415 | 33.6 | 2.3 | 2040 | 1 | US-08-674-169-36 | Sequence 36, Appl |
| 416 | 33.6 | 2.3 | 2040 | 1 | US-08-185-949B-57 | Sequence 57, Appl |
| 417 | 33.6 | 2.3 | 2161 | 5 | PCT-US93-08386-4 | Sequence 4, Appl1 |
| 418 | 33.6 | 2.3 | 2172 | 4 | US-09-252-991A-2325 | Sequence 2325, Ap |
| 419 | 33.6 | 2.3 | 4190 | 3 | US-08-924-345-1 | Sequence 1, Appl1 |
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| 422 | 33.6 | 2.3 | 9840 | 4 | US-09-949-016-1298 | Sequence 1, Appl1 |
| 423 | 33.6 | 2.3 | 41594 | 3 | US-09-949-016-1298 | Sequence 1, Appl1 |
| 424 | 33.6 | 2.3 | 41684 | 4 | US-09-536-059-1 | Sequence 1, Appl1 |
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| 428 | 33.6 | 2.3 | 137753 | 4 | US-09-949-016-17404 | Sequence 17404, A |
| 429 | 33.6 | 2.3 | 169334 | 4 | US-09-949-016-15999 | Sequence 15999, A |
| 430 | 33.6 | 2.3 | 300598 | 4 | US-09-949-016-11868 | Sequence 11868, A |
| 431 | 33.6 | 2.3 | 302604 | 4 | US-09-949-016-14588 | Sequence 14588, A |
| 432 | 33.6 | 2.3 | 302604 | 4 | US-09-949-016-14588 | Sequence 14588, A |
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| 436 | 33.6 | 2.2 | 123 | 3 | US-09-007-005-1 | Sequence 1, Appl1 |
| 437 | 33.4 | 2.2 | 123 | 3 | US-09-244-796-1 | Sequence 1, Appl1 |
| 438 | 33.4 | 2.2 | 573 | 4 | US-09-902-540-7511 | Sequence 7511, Ap |
| 439 | 33.4 | 2.2 | 601 | 4 | US-09-949-016-124937 | Sequence 124937, Sequence 144805, |
| 440 | 33.4 | 2.2 | 601 | 4 | US-09-949-016-14805 | Sequence 3914, Ap |
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| 442 | 33.4 | 2.2 | 988 | 4 | US-09-949-016-2888 | Sequence 3539, Ap |
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| 444 | 33.4 | 2.2 | 1011 | 4 | US-09-252-991A-4029 | Sequence 703, Appl |
| 445 | 33.4 | 2.2 | 1030 | 4 | US-09-902-540-73 | Sequence 73, Appl |
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| 447 | 33.4 | 2.2 | 1137 | 4 | US-09-724-797-53 | Sequence 53, Appl |
| 448 | 33.4 | 2.2 | 1436 | 4 | US-09-252-991A-3888 | Sequence 3888, Ap |
| 449 | 33.4 | 2.2 | 1581 | 4 | US-09-252-991A-3962 | Sequence 3962, Ap |
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| 451 | 33.4 | 2.2 | 1788 | 4 | US-09-902-540-8800 | Sequence 8800, Ap |
| 452 | 33.4 | 2.2 | 2076 | 4 | US-09-252-991A-2935 | Sequence 2935, Ap |
| 453 | 33.4 | 2.2 | 2211 | 4 | US-09-902-540-5403 | Sequence 5403, Ap |
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| 458 | 33.4 | 2.2 | 3876 | 4 | US-09-252-991A-2933 | Sequence 8819, Ap |
| 459 | 33.4 | 2.2 | 6645 | 4 | US-09-902-540-8819 | Sequence 16598, A |
| 460 | 33.4 | 2.2 | 10603 | 4 | US-09-949-016-16598 | Sequence 1039, Ap |
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| 462 | 33.4 | 2.2 | 12898 | 4 | US-09-902-540-1000 | Sequence 3, Appl1 |
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| 465 | 33.4 | 2.2 | 23535 | 4 | US-09-949-016-14630 | Sequence 14630, A |
| 466 | 33.4 | 2.2 | 390890 | 4 | US-09-949-016-14720 | Sequence 14720, A |
| 467 | 33.4 | 2.2 | 455726 | 4 | US-09-949-016-14157 | Sequence 14157, A |
| 468 | 33.4 | 2.2 | 481115 | 4 | US-09-949-016-11940 | Sequence 11940, A |
| 469 | 33.2 | 2.2 | 601 | 4 | US-09-949-016-105288 | Sequence 105288, A |
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| 487 | 33.2 | 2.2 | 3957 | 4 | US-10-237-551-193 | Sequence 193, Ap |
| 488 | 33.2 | 2.2 | 4286 | 4 | US-09-899-634C-1 | Sequence 1, Appl |
| 489 | 33.2 | 2.2 | 6424 | 4 | US-09-902-540-584 | Sequence 584, Ap |
| 490 | 33.2 | 2.2 | 6714 | 3 | US-09-299-141-6 | Sequence 6, Appl |
| 491 | 33.2 | 2.2 | 6924 | 3 | US-09-239-141-9 | Sequence 9, Appl |
| 492 | 33.2 | 2.2 | 6924 | 3 | US-09-239-141-10 | Sequence 10, Appl |
| 493 | 33.2 | 2.2 | 6924 | 3 | US-09-239-141-11 | Sequence 11, Appl |
| 494 | 33.2 | 2.2 | 8033 | 4 | US-09-574-779B-134 | Sequence 134, App |
| 495 | 33.2 | 2.2 | 10528 | 4 | US-09-902-540-945 | Sequence 945, App |
| 496 | 33.2 | 2.2 | 12424 | 4 | US-09-949-016-14975 | Sequence 14975, A |
| 497 | 33.2 | 2.2 | 14367 | 4 | US-09-902-540-1113 | Sequence 1113, Ap |
| 498 | 33.2 | 2.2 | 18917 | 4 | US-09-949-016-13119 | Sequence 11129, A |
| 499 | 33.2 | 2.2 | 18917 | 4 | US-09-949-016-13119 | Sequence 11130, A |
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| 501 | 33.2 | 2.2 | 41617 | 4 | US-09-949-016-14356 | Sequence 14356, A |
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| 507 | 33.2 | 2.2 | 78157 | 4 | US-09-949-016-16467 | Sequence 16467, A |
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| 524 | 33.2 | 2.2 | 2066 | 4 | US-09-976-594-413 | Sequence 413, App |
| 525 | 33.2 | 2.2 | 2073 | 4 | US-09-252-991A-15779 | Sequence 15779, A |
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| 529 | 33.2 | 2.2 | 20250 | 4 | US-09-902-540-1082 | Sequence 1213, Ap |
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| 531 | 33.2 | 2.2 | 44477 | 4 | US-09-949-016-16694 | Sequence 16694, A |
| 532 | 33.2 | 2.2 | 47476 | 4 | US-09-949-016-16767 | Sequence 12179, A |
| 533 | 33.2 | 2.2 | 47476 | 4 | US-09-949-016-16767 | Sequence 14472, A |
| 534 | 33.2 | 2.2 | 74177 | 4 | US-09-949-016-14472 | Sequence 11989, A |
| 535 | 33.2 | 2.2 | 74177 | 4 | US-09-949-016-14472 | Sequence 17388, A |
| 536 | 33.2 | 2.2 | 119762 | 4 | US-09-949-016-17313 | Sequence 17313, A |
| 537 | 33.2 | 2.2 | 137226 | 4 | US-09-949-016-13763 | Sequence 13763, A |
| 538 | 33.2 | 2.2 | 171130 | 4 | US-09-949-016-14861 | Sequence 14861, A |

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| 585 | 32.8 | 2.2 | 4008 | 5 | PCT-US95-11808-5 | Sequence 5, App | C 658 | 32.6 | 2.2 | 601 | 4 | US-09-949-016-112034 | Sequence 112034, A |
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| 592 | 32.8 | 2.2 | 15664 | 1 | US-08-402-066-3 | Sequence 3, App | C 665 | 32.6 | 2.2 | 2214 | 3 | US-08-943-731-57 | Sequence 57, App |
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| 608 | 32.8 | 2.2 | 393753 | 4 | US-09-949-016-1573 | Sequence 14573, A | C 681 | 32.6 | 2.2 | 44789 | 4 | US-09-949-016-13909 | Sequence 13909, A |
| 609 | 32.8 | 2.2 | 393753 | 4 | US-09-949-016-1573 | Sequence 14573, A | C 682 | 32.6 | 2.2 | 53562 | 4 | US-09-949-016-16286 | Sequence 16286, A |
| 610 | 32.8 | 2.2 | 818128 | 4 | US-09-949-016-14546 | Sequence 14546, A | C 683 | 32.6 | 2.2 | 84171 | 4 | US-09-949-016-16356 | Sequence 16356, A |
| 611 | 32.8 | 2.2 | 818128 | 4 | US-09-949-016-14547 | Sequence 14547, A | C 684 | 32.6 | 2.2 | 88557 | 4 | US-09-949-016-17028 | Sequence 17028, A |

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|-----|------|-----|--------|---|----------------------|--------------------|-----|------|-----|--------|---|----------------------|--------------------|
| 685 | 32.6 | 2.2 | 113876 | 4 | US-09-949-016-14828 | Sequence 14828, A | 758 | 33.4 | 2.2 | 35935 | 3 | US-09-244-752-1 | Sequence 1, Appl1 |
| 686 | 32.6 | 2.2 | 113876 | 4 | US-09-949-016-14829 | Sequence 14829, A | 759 | 33.4 | 2.2 | 35935 | 3 | US-09-245-497-1 | Sequence 43, Appl1 |
| 687 | 32.6 | 2.2 | 115508 | 4 | US-09-949-016-11800 | Sequence 11800, A | 760 | 33.4 | 2.2 | 35935 | 3 | US-09-400-670-43 | Sequence 1, Appl1 |
| 688 | 32.6 | 2.2 | 115508 | 4 | US-09-949-016-14826 | Sequence 14826, A | 761 | 33.4 | 2.2 | 35935 | 3 | US-09-562-919-1 | Sequence 1, Appl1 |
| 689 | 32.6 | 2.2 | 115508 | 4 | US-09-949-016-14827 | Sequence 14827, A | 762 | 33.4 | 2.2 | 35935 | 3 | US-09-562-919-1 | Sequence 1, Appl1 |
| 690 | 32.6 | 2.2 | 169998 | 3 | US-09-676-610B-24 | Sequence 24, Appl1 | 763 | 33.4 | 2.2 | 33978 | 4 | US-09-956-335-1 | Sequence 30, Appl1 |
| 691 | 32.6 | 2.2 | 197336 | 4 | US-09-949-016-15884 | Sequence 15584, A | 764 | 33.4 | 2.2 | 36620 | 4 | US-09-952-060-30 | Sequence 25, Appl1 |
| 692 | 32.6 | 2.2 | 197336 | 4 | US-09-949-016-15881 | Sequence 12881, A | 765 | 33.4 | 2.2 | 34747 | 4 | US-09-952-060-25 | Sequence 28, Appl1 |
| 693 | 32.6 | 2.2 | 197337 | 4 | US-09-949-016-14376 | Sequence 14376, A | 766 | 33.4 | 2.2 | 38519 | 4 | US-09-952-060-28 | Sequence 28, Appl1 |
| 694 | 32.6 | 2.2 | 197496 | 4 | US-09-877-177A-10 | Sequence 10, Appl1 | 767 | 33.4 | 2.2 | 119930 | 4 | US-09-949-016-12677 | Sequence 1677, A |
| 695 | 32.6 | 2.2 | 199945 | 4 | US-09-949-016-15436 | Sequence 15436, A | 768 | 33.4 | 2.2 | 119931 | 4 | US-09-949-016-16319 | Sequence 16319, A |
| 696 | 32.6 | 2.2 | 234288 | 4 | US-09-949-016-11272 | Sequence 17272, A | 769 | 33.4 | 2.2 | 122772 | 4 | US-09-949-016-14132 | Sequence 14132, A |
| 697 | 32.6 | 2.2 | 250715 | 4 | US-09-949-016-13294 | Sequence 13294, A | 770 | 33.4 | 2.2 | 123536 | 4 | US-09-949-016-14166 | Sequence 14166, A |
| 698 | 32.6 | 2.2 | 276237 | 4 | US-09-949-016-17504 | Sequence 17504, A | 771 | 33.4 | 2.2 | 123613 | 4 | US-09-949-016-15824 | Sequence 15824, A |
| 699 | 32.4 | 2.2 | 546 | 4 | US-09-902-540-8130 | Sequence 8130, Ap | 772 | 32.4 | 2.2 | 141560 | 4 | US-09-949-016-16476 | Sequence 16476, A |
| 700 | 32.4 | 2.2 | 601 | 4 | US-09-949-016-36290 | Sequence 36290, A | 773 | 32.2 | 2.2 | 187136 | 4 | US-09-949-016-17231 | Sequence 17231, A |
| 701 | 32.4 | 2.2 | 601 | 4 | US-09-949-016-36291 | Sequence 36291, A | 774 | 32.2 | 2.2 | 390 | 4 | US-09-583-110-835 | Sequence 835, App |
| 702 | 32.4 | 2.2 | 601 | 4 | US-09-949-016-86553 | Sequence 86553, A | 775 | 32.2 | 2.2 | 405 | 4 | US-09-107-433-2234 | Sequence 2234, Ap |
| 703 | 32.4 | 2.2 | 601 | 4 | US-09-949-016-86554 | Sequence 86554, A | 776 | 32.2 | 2.2 | 601 | 4 | US-09-949-016-59382 | Sequence 59382, A |
| 704 | 32.4 | 2.2 | 601 | 4 | US-09-949-016-163246 | Sequence 163246, A | 777 | 32.2 | 2.2 | 601 | 4 | US-09-949-016-59383 | Sequence 59383, A |
| 705 | 32.4 | 2.2 | 601 | 4 | US-09-949-016-163247 | Sequence 163247, A | 778 | 32.2 | 2.2 | 601 | 4 | US-09-949-016-92991 | Sequence 92991, A |
| 706 | 32.4 | 2.2 | 601 | 4 | US-09-949-016-168683 | Sequence 168683, A | 779 | 32.2 | 2.2 | 601 | 4 | US-09-949-016-92992 | Sequence 92992, A |
| 707 | 32.4 | 2.2 | 601 | 4 | US-09-949-001-405 | Sequence 405, App | 780 | 32.2 | 2.2 | 606 | 4 | US-09-252-991A-19182 | Sequence 11629, A |
| 708 | 32.4 | 2.2 | 880 | 3 | US-09-056-285A-5 | Sequence 5, Appl1 | 781 | 32.2 | 2.2 | 729 | 4 | US-09-252-991A-8930 | Sequence 8930, Ap |
| 709 | 32.4 | 2.2 | 954 | 4 | US-09-252-991A-5722 | Sequence 5722, Ap | 782 | 32.2 | 2.2 | 729 | 4 | US-09-252-991A-8930 | Sequence 6761, Ap |
| 710 | 32.4 | 2.2 | 954 | 4 | US-09-902-540-3679 | Sequence 3679, Ap | 783 | 32.2 | 2.2 | 741 | 4 | US-09-902-540-6761 | Sequence 6761, Ap |
| 711 | 32.4 | 2.2 | 1070 | 3 | US-09-470-443-7 | Sequence 7, Appl1 | 784 | 32.2 | 2.2 | 945 | 4 | US-09-252-991A-8444 | Sequence 8444, Ap |
| 712 | 32.4 | 2.2 | 1278 | 4 | US-09-239-909-1 | Sequence 5750, Ap | 785 | 32.2 | 2.2 | 945 | 4 | US-09-252-991A-11511 | Sequence 11511, A |
| 713 | 32.4 | 2.2 | 1401 | 3 | US-09-902-540-2051 | Sequence 2051, Ap | 786 | 32.2 | 2.2 | 1128 | 4 | US-09-023-655-1464 | Sequence 1464, App |
| 714 | 32.4 | 2.2 | 1623 | 4 | US-09-902-540-4766 | Sequence 4766, Ap | 787 | 32.2 | 2.2 | 1161 | 4 | US-09-919-039-388 | Sequence 388, App |
| 715 | 32.4 | 2.2 | 1974 | 6 | 5320958-1 | Patent No. 5320958 | 788 | 32.2 | 2.2 | 1209 | 4 | US-09-902-540-9932 | Sequence 9932, Ap |
| 716 | 32.4 | 2.2 | 2176 | 6 | 5320958-1 | Patent No. 5320958 | 789 | 32.2 | 2.2 | 1229 | 4 | US-09-976-594-1058 | Sequence 1058, Ap |
| 717 | 32.4 | 2.2 | 2218 | 6 | 5320958-1 | Patent No. 5320958 | 790 | 32.2 | 2.2 | 1239 | 4 | US-09-902-540-5817 | Sequence 5817, Ap |
| 718 | 32.4 | 2.2 | 2218 | 4 | US-09-350-457A-1 | Sequence 1, Appl1 | 791 | 32.2 | 2.2 | 1356 | 4 | US-09-252-991A-9233 | Sequence 9233, Ap |
| 719 | 32.4 | 2.2 | 3186 | 4 | US-09-397-550-1 | Sequence 1, Appl1 | 792 | 32.2 | 2.2 | 1423 | 1 | US-07-829-954-1 | Sequence 1, Appl1 |
| 720 | 32.4 | 2.2 | 3248 | 4 | US-09-397-550-2 | Sequence 2, Appl1 | 793 | 32.2 | 2.2 | 1423 | 1 | US-07-994-423-1 | Sequence 1, Appl1 |
| 721 | 32.4 | 2.2 | 3327 | 4 | US-09-397-550-3 | Sequence 3, Appl1 | 794 | 32.2 | 2.2 | 1423 | 1 | US-08-421-891-1 | Sequence 1, Appl1 |
| 722 | 32.4 | 2.2 | 5483 | 3 | US-09-470-443-1 | Sequence 1, Appl1 | 795 | 32.2 | 2.2 | 1476 | 4 | US-09-949-016-1726 | Sequence 4734, Ap |
| 723 | 32.4 | 2.2 | 5482 | 4 | US-09-470-443-3 | Sequence 3, Appl1 | 796 | 32.2 | 2.2 | 1632 | 4 | US-09-248-796A-599 | Sequence 599, App |
| 724 | 32.4 | 2.2 | 5482 | 4 | US-09-397-550-19 | Sequence 19, Appl1 | 797 | 32.2 | 2.2 | 2260 | 4 | US-09-919-039-10 | Sequence 10, Appl1 |
| 725 | 32.4 | 2.2 | 5674 | 1 | US-07-807-043B-8 | Sequence 8, Appl1 | 798 | 32.2 | 2.2 | 2363 | 4 | US-09-818-780-22 | Sequence 22, Appl1 |
| 726 | 32.4 | 2.2 | 5674 | 1 | US-08-190-411A-1 | Sequence 1, Appl1 | 799 | 32.2 | 2.2 | 2496 | 4 | US-09-252-991A-8330 | Sequence 8330, Ap |
| 727 | 32.4 | 2.2 | 5674 | 4 | US-08-299-849B-8 | Sequence 8, Appl1 | 800 | 32.2 | 2.2 | 2674 | 3 | US-09-513-783A-173 | Sequence 173, App |
| 728 | 32.4 | 2.2 | 5674 | 2 | US-08-560-024-1 | Sequence 1, Appl1 | 801 | 32.2 | 2.2 | 2685 | 4 | US-09-949-016-4734 | Sequence 4734, Ap |
| 729 | 32.4 | 2.2 | 5674 | 3 | US-08-142-368A-8 | Sequence 8, Appl1 | 802 | 32.2 | 2.2 | 3126 | 4 | US-09-252-991A-8715 | Sequence 8715, Ap |
| 730 | 32.4 | 2.2 | 5674 | 3 | US-08-967-727-8 | Sequence 8, Appl1 | 803 | 32.2 | 2.2 | 3126 | 4 | US-09-252-991A-9066 | Sequence 9066, Ap |
| 731 | 32.4 | 2.2 | 5674 | 3 | US-08-037-230D-8 | Sequence 8, Appl1 | 804 | 32.2 | 2.2 | 3960 | 4 | US-09-902-540-8918 | Sequence 8918, Ap |
| 732 | 32.4 | 2.2 | 5674 | 4 | US-09-583-850-8 | Sequence 8, Appl1 | 805 | 32.2 | 2.2 | 4326 | 4 | US-09-252-991A-11572 | Sequence 11572, A |
| 733 | 32.4 | 2.2 | 5674 | 4 | US-09-579-197-8 | Sequence 8, Appl1 | 806 | 32.2 | 2.2 | 4473 | 4 | US-09-252-991A-11871 | Sequence 11871, A |
| 734 | 32.4 | 2.2 | 5674 | 4 | US-09-404-026-8 | Sequence 8, Appl1 | 807 | 32.2 | 2.2 | 6186 | 3 | US-08-961-527-131 | Sequence 131, App |
| 735 | 32.4 | 2.2 | 5674 | 4 | US-09-312-464-8 | Sequence 8, Appl1 | 808 | 32.2 | 2.2 | 9097 | 4 | US-09-902-540-947 | Sequence 947, App |
| 736 | 32.4 | 2.2 | 5699 | 4 | US-09-949-016-12445 | Sequence 12445, A | 809 | 32.2 | 2.2 | 9367 | 4 | US-09-902-540-951 | Sequence 951, App |
| 737 | 32.4 | 2.2 | 8352 | 4 | US-09-902-540-832 | Sequence 14430, A | 810 | 32.2 | 2.2 | 11101 | 4 | US-09-902-540-1005 | Sequence 1005, App |
| 738 | 32.4 | 2.2 | 16924 | 4 | US-09-902-540-1178 | Sequence 832, App | 811 | 32.2 | 2.2 | 15271 | 4 | US-09-902-540-1051 | Sequence 1051, App |
| 739 | 32.4 | 2.2 | 27934 | 4 | US-09-902-540-1235 | Sequence 1178, Ap | 812 | 32.2 | 2.2 | 26396 | 4 | US-09-949-016-13680 | Sequence 13680, A |
| 740 | 32.4 | 2.2 | 32166 | 4 | US-09-562-930-11 | Sequence 1235, Ap | 813 | 32.2 | 2.2 | 28509 | 4 | US-09-902-540-1240 | Sequence 1240, Ap |
| 741 | 32.4 | 2.2 | 32798 | 4 | US-09-604-694B-1 | Sequence 11, Appl1 | 814 | 32.2 | 2.2 | 30780 | 4 | US-09-902-540-1243 | Sequence 1243, Ap |
| 742 | 32.4 | 2.2 | 34303 | 2 | US-08-735-609-4 | Sequence 4, Appl1 | 815 | 32.2 | 2.2 | 30922 | 4 | US-09-949-016-16700 | Sequence 16700, A |
| 743 | 32.4 | 2.2 | 34303 | 2 | US-08-735-609-4 | Sequence 4, Appl1 | 816 | 32.2 | 2.2 | 32223 | 4 | US-09-949-016-14417 | Sequence 14417, A |
| 744 | 32.4 | 2.2 | 34303 | 2 | US-09-315-372-4 | Sequence 4, Appl1 | 817 | 32.2 | 2.2 | 42276 | 4 | US-09-949-016-17218 | Sequence 17218, A |
| 745 | 32.4 | 2.2 | 34303 | 3 | US-09-244-752-4 | Sequence 4, Appl1 | 818 | 32.2 | 2.2 | 61158 | 4 | US-09-949-016-15041 | Sequence 15041, A |
| 746 | 32.4 | 2.2 | 34303 | 3 | US-09-245-497-4 | Sequence 4, Appl1 | 819 | 32.2 | 2.2 | 71989 | 3 | US-09-443-501A-2 | Sequence 2, Appl1 |
| 747 | 32.4 | 2.2 | 34303 | 3 | US-09-562-919-4 | Sequence 4, Appl1 | 820 | 32.2 | 2.2 | 72704 | 4 | US-09-902-540-1273 | Sequence 1273, Ap |
| 748 | 32.4 | 2.2 | 34303 | 3 | US-08-374-483-6 | Sequence 6, Appl1 | 821 | 32.2 | 2.2 | 75431 | 4 | US-09-949-016-15122 | Sequence 15122, A |
| 749 | 32.4 | 2.2 | 34308 | 2 | US-08-973-334-3 | Sequence 3, Appl1 | 822 | 32.2 | 2.2 | 97195 | 4 | US-09-949-016-12212 | Sequence 12212, A |
| 750 | 32.4 | 2.2 | 35408 | 3 | US-08-563-869A-3 | Sequence 3, Appl1 | 823 | 32.2 | 2.2 | 97196 | 4 | US-09-949-016-16971 | Sequence 16971, A |
| 751 | 32.4 | 2.2 | 35408 | 3 | US-09-956-335-2 | Sequence 2, Appl1 | 824 | 32.2 | 2.2 | 118136 | 4 | US-09-949-016-12439 | Sequence 12439, A |
| 752 | 32.4 | 2.2 | 35935 | 2 | US-08-735-609-1 | Sequence 1, Appl1 | 825 | 32.2 | 2.2 | 126982 | 4 | US-09-949-016-16597 | Sequence 16597, A |
| 753 | 32.4 | 2.2 | 35935 | 2 | US-08-379-452-43 | Sequence 43, Appl1 | 826 | 32.2 | 2.2 | 200 | 4 | US-09-513-999C-22029 | Sequence 22029, A |
| 754 | 32.4 | 2.2 | 35935 | 2 | US-09-315-372-1 | Sequence 1, Appl1 | 827 | 32.2 | 2.2 | 363 | 3 | US-09-060-756-159 | Sequence 159, App |
| 755 | 32.4 | 2.2 | 35935 | 2 | US-09-315-372-1 | Sequence 1, Appl1 | 828 | 32.2 | 2.2 | 363 | 3 | US-09-670-514-159 | Sequence 159, App |
| 756 | 32.4 | 2.2 | 35935 | 2 | US-09-315-372-1 | Sequence 1, Appl1 | 829 | 32.2 | 2.2 | 363 | 3 | US-09-670-514-159 | Sequence 159, App |
| 757 | 32.4 | 2.2 | 35935 | 3 | US-09-315-372-1 | Sequence 1, Appl1 | 830 | 32.2 | 2.2 | 434 | 4 | US-09-270-767-4804 | Sequence 4804, App |

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|-------|----|-----|--------|---|----------------------|--------------------|-------|------|-----|--------|---|----------------------|--------------------|
| 831 | 32 | 2.2 | 434 | 4 | US-09-270-767-20086 | Sequence 20086, A | 904 | 32 | 2.2 | 266748 | 4 | US-09-949-016-13188 | Sequence 13188, A |
| C 832 | 32 | 2.2 | 522 | 4 | US-09-253-991A-12063 | Sequence 12063, A | 905 | 32 | 2.2 | 283538 | 4 | US-09-949-016-13506 | Sequence 13506, A |
| 833 | 32 | 2.2 | 601 | 4 | US-09-949-016-16344 | Sequence 16344, A | 906 | 31.8 | 2.1 | 540 | 4 | US-09-252-991A-15565 | Sequence 15565, A |
| 834 | 32 | 2.2 | 601 | 4 | US-09-949-016-16345 | Sequence 16345, A | 907 | 31.8 | 2.1 | 564 | 4 | US-09-902-540-4648 | Sequence 4648, Ap |
| 835 | 32 | 2.2 | 601 | 4 | US-09-949-016-16839 | Sequence 16839, A | 908 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-19161 | Sequence 19161, A |
| 836 | 32 | 2.2 | 601 | 4 | US-09-949-016-19011 | Sequence 19011, A | 909 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-18412 | Sequence 18412, A |
| 837 | 32 | 2.2 | 601 | 4 | US-09-949-016-49183 | Sequence 49183, A | 910 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-11116 | Sequence 41116, A |
| 838 | 32 | 2.2 | 601 | 4 | US-09-949-016-49359 | Sequence 49359, A | C 911 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-13618 | Sequence 53618, A |
| 839 | 32 | 2.2 | 601 | 4 | US-09-949-016-86622 | Sequence 86622, A | C 912 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-13619 | Sequence 53619, A |
| 840 | 32 | 2.2 | 601 | 4 | US-09-949-016-86622 | Sequence 86622, A | C 913 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-13619 | Sequence 53619, A |
| 841 | 32 | 2.2 | 601 | 4 | US-09-949-016-163314 | Sequence 163314, A | C 914 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-163314 | Sequence 53619, A |
| C 842 | 32 | 2.2 | 622 | 4 | US-09-949-016-163315 | Sequence 163315, A | C 915 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-163315 | Sequence 53619, A |
| C 843 | 32 | 2.2 | 622 | 4 | US-09-311-021-161 | Sequence 161, Ap | C 916 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-19406 | Sequence 79406, A |
| C 844 | 32 | 2.2 | 630 | 4 | US-09-253-991A-15885 | Sequence 15885, Ap | C 917 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-19406 | Sequence 79406, A |
| C 845 | 32 | 2.2 | 693 | 4 | US-09-253-991A-12003 | Sequence 12003, A | C 918 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-19406 | Sequence 79406, A |
| C 846 | 32 | 2.2 | 1026 | 4 | US-09-902-540-4562 | Sequence 4562, Ap | C 919 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-19406 | Sequence 79406, A |
| 847 | 32 | 2.2 | 1071 | 4 | US-09-253-991A-1635 | Sequence 1635, Ap | C 920 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-144801 | Sequence 144801, A |
| 848 | 32 | 2.2 | 1290 | 4 | US-09-253-991A-15869 | Sequence 15869, A | C 921 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-144801 | Sequence 144801, A |
| C 849 | 32 | 2.2 | 1290 | 4 | US-09-902-540-5641 | Sequence 5641, Ap | C 922 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-144802 | Sequence 144802, A |
| C 850 | 32 | 2.2 | 1292 | 4 | US-09-902-540-127 | Sequence 127, Ap | C 923 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-144803 | Sequence 144803, A |
| C 851 | 32 | 2.2 | 1335 | 4 | US-09-253-991A-1685 | Sequence 1685, Ap | C 924 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-144803 | Sequence 144803, A |
| C 852 | 32 | 2.2 | 1422 | 4 | US-09-489-039A-4425 | Sequence 4425, Ap | C 925 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-144806 | Sequence 144806, A |
| C 853 | 32 | 2.2 | 1695 | 4 | US-09-253-991A-1686 | Sequence 1686, Ap | C 926 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-151512 | Sequence 151512, A |
| C 854 | 32 | 2.2 | 1704 | 4 | US-09-253-991A-11910 | Sequence 11910, A | C 927 | 31.8 | 2.1 | 601 | 4 | US-09-949-016-191381 | Sequence 191381, A |
| C 855 | 32 | 2.2 | 1740 | 4 | US-09-253-991A-1492 | Sequence 1492, Ap | C 928 | 31.8 | 2.1 | 663 | 4 | US-09-252-991A-12910 | Sequence 12910, A |
| C 856 | 32 | 2.2 | 1746 | 4 | US-09-902-540-2679 | Sequence 2679, Ap | C 929 | 31.8 | 2.1 | 918 | 4 | US-09-252-991A-9633 | Sequence 9633, Ap |
| C 857 | 32 | 2.2 | 1746 | 4 | US-09-489-039A-4325 | Sequence 4325, Ap | C 930 | 31.8 | 2.1 | 919 | 4 | US-09-902-540-6400 | Sequence 6400, Ap |
| C 858 | 32 | 2.2 | 1806 | 4 | US-09-253-991A-1534 | Sequence 1534, Ap | C 931 | 31.8 | 2.1 | 951 | 4 | US-09-252-991A-12576 | Sequence 12576, A |
| C 859 | 32 | 2.2 | 1916 | 4 | US-09-253-991A-12032 | Sequence 12032, A | C 932 | 31.8 | 2.1 | 1116 | 4 | US-09-902-540-3551 | Sequence 3551, Ap |
| C 860 | 32 | 2.2 | 2113 | 4 | US-09-573-080A-70 | Sequence 70, Ap | C 933 | 31.8 | 2.1 | 1422 | 4 | US-09-252-991A-15636 | Sequence 15636, A |
| 861 | 32 | 2.2 | 2481 | 4 | US-09-894-998A-35 | Sequence 35, Ap | C 934 | 31.8 | 2.1 | 1518 | 4 | US-09-252-991A-12883 | Sequence 12883, A |
| 862 | 32 | 2.2 | 2481 | 4 | US-10-237-551-35 | Sequence 35, Ap | C 935 | 31.8 | 2.1 | 1689 | 4 | US-09-902-540-6020 | Sequence 6020, Ap |
| 863 | 32 | 2.2 | 2560 | 4 | US-09-902-540-7617 | Sequence 7617, Ap | C 936 | 31.8 | 2.1 | 1692 | 4 | US-09-902-540-7344 | Sequence 7344, Ap |
| C 864 | 32 | 2.2 | 2566 | 4 | US-08-796-414B-6 | Sequence 6, Ap | C 937 | 31.8 | 2.1 | 1718 | 4 | US-09-962-665-10 | Sequence 10, Ap |
| 865 | 32 | 2.2 | 3066 | 4 | US-10-237-551-152 | Sequence 152, Ap | C 938 | 31.8 | 2.1 | 1718 | 4 | US-09-963-333-10 | Sequence 10, Ap |
| 866 | 32 | 2.2 | 3252 | 4 | US-09-902-540-9254 | Sequence 9254, Ap | C 939 | 31.8 | 2.1 | 1718 | 4 | US-09-962-677-10 | Sequence 10, Ap |
| 867 | 32 | 2.2 | 3293 | 4 | US-09-949-016-4658 | Sequence 4658, Ap | C 940 | 31.8 | 2.1 | 1722 | 4 | US-09-962-677-10 | Sequence 10, Ap |
| 868 | 32 | 2.2 | 3314 | 4 | US-09-949-016-836 | Sequence 836, Ap | C 941 | 31.8 | 2.1 | 2082 | 4 | US-09-818-780-67 | Sequence 67, Ap |
| 869 | 32 | 2.2 | 3372 | 4 | US-09-949-016-165 | Sequence 165, Ap | C 942 | 31.8 | 2.1 | 2453 | 4 | US-09-902-540-429 | Sequence 429, Ap |
| 870 | 32 | 2.2 | 3390 | 4 | US-09-253-991A-11961 | Sequence 11961, A | C 943 | 31.8 | 2.1 | 3592 | 4 | US-09-814-351-7 | Sequence 7, Ap |
| 871 | 32 | 2.2 | 3396 | 3 | US-08-974-549A-638 | Sequence 638, Ap | C 944 | 31.8 | 2.1 | 3654 | 4 | US-09-252-991A-9533 | Sequence 9533, Ap |
| 872 | 32 | 2.2 | 3396 | 4 | US-09-721-456-638 | Sequence 638, Ap | C 945 | 31.8 | 2.1 | 3957 | 4 | US-10-237-551-193 | Sequence 193, Ap |
| 873 | 32 | 2.2 | 3716 | 4 | US-09-949-016-4682 | Sequence 4682, Ap | C 946 | 31.8 | 2.1 | 4084 | 4 | US-09-949-016-570 | Sequence 570, Ap |
| 874 | 32 | 2.2 | 5017 | 4 | US-09-902-540-748 | Sequence 748, Ap | C 947 | 31.8 | 2.1 | 4085 | 4 | US-09-949-016-1163 | Sequence 1163, Ap |
| C 875 | 32 | 2.2 | 5773 | 4 | US-09-566-921-112 | Sequence 112, Ap | C 948 | 31.8 | 2.1 | 4561 | 4 | US-09-902-540-700 | Sequence 700, Ap |
| 876 | 32 | 2.2 | 10322 | 4 | US-09-902-540-989 | Sequence 989, Ap | C 949 | 31.8 | 2.1 | 5847 | 4 | US-09-962-665-11 | Sequence 11, Ap |
| C 877 | 32 | 2.2 | 17622 | 4 | US-09-902-540-1125 | Sequence 1125, Ap | C 950 | 31.8 | 2.1 | 5847 | 4 | US-09-963-333-11 | Sequence 11, Ap |
| C 878 | 32 | 2.2 | 20187 | 4 | US-09-902-540-1186 | Sequence 1187, Ap | C 951 | 31.8 | 2.1 | 5847 | 4 | US-09-962-677-11 | Sequence 11, Ap |
| C 879 | 32 | 2.2 | 24905 | 4 | US-09-902-540-1225 | Sequence 1225, Ap | C 952 | 31.8 | 2.1 | 8310 | 4 | US-09-902-540-1001 | Sequence 1001, Ap |
| C 880 | 32 | 2.2 | 28804 | 2 | US-08-593-874-1 | Sequence 1, Ap | C 953 | 31.8 | 2.1 | 8438 | 1 | US-07-945-283-1 | Sequence 1, Ap |
| C 881 | 32 | 2.2 | 28804 | 3 | US-09-056-942-2 | Sequence 2, Ap | C 954 | 31.8 | 2.1 | 11321 | 4 | US-09-949-016-13466 | Sequence 13466, A |
| C 882 | 32 | 2.2 | 28804 | 3 | US-09-096-867-2 | Sequence 2, Ap | C 955 | 31.8 | 2.1 | 12703 | 4 | US-09-949-016-16685 | Sequence 16685, A |
| 883 | 32 | 2.2 | 29927 | 4 | US-09-949-016-11814 | Sequence 11814, A | C 956 | 31.8 | 2.1 | 12787 | 4 | US-09-949-016-16339 | Sequence 16339, A |
| 884 | 32 | 2.2 | 29927 | 4 | US-09-949-016-17474 | Sequence 17474, A | C 957 | 31.8 | 2.1 | 16073 | 4 | US-09-949-016-12312 | Sequence 12312, A |
| 885 | 32 | 2.2 | 29927 | 4 | US-09-949-016-17475 | Sequence 17475, A | C 958 | 31.8 | 2.1 | 16073 | 4 | US-09-949-016-12312 | Sequence 12312, A |
| C 886 | 32 | 2.2 | 31111 | 4 | US-09-949-016-15628 | Sequence 15628, A | C 959 | 31.8 | 2.1 | 17228 | 4 | US-09-949-016-12905 | Sequence 12905, A |
| 887 | 32 | 2.2 | 31440 | 4 | US-09-949-016-12578 | Sequence 12578, A | C 960 | 31.8 | 2.1 | 20966 | 4 | US-09-902-540-1170 | Sequence 1170, Ap |
| 888 | 32 | 2.2 | 31444 | 4 | US-09-949-016-16400 | Sequence 16400, A | C 961 | 31.8 | 2.1 | 20966 | 4 | US-09-909-547-7 | Sequence 7, Ap |
| 889 | 32 | 2.2 | 37802 | 4 | US-09-949-016-12639 | Sequence 12639, A | C 962 | 31.8 | 2.1 | 22218 | 4 | US-09-949-016-14950 | Sequence 14950, A |
| C 890 | 32 | 2.2 | 38954 | 4 | US-09-949-016-12292 | Sequence 12292, A | C 963 | 31.8 | 2.1 | 22218 | 4 | US-09-949-016-14950 | Sequence 14950, A |
| C 891 | 32 | 2.2 | 53332 | 4 | US-09-801-861-3 | Sequence 3, Ap | C 964 | 31.8 | 2.1 | 24984 | 4 | US-09-949-016-14950 | Sequence 14950, A |
| C 892 | 32 | 2.2 | 53332 | 4 | US-10-224-562-3 | Sequence 3, Ap | C 965 | 31.8 | 2.1 | 26930 | 4 | US-09-902-540-1228 | Sequence 1228, Ap |
| C 893 | 32 | 2.2 | 100863 | 4 | US-09-949-016-17031 | Sequence 17031, A | C 966 | 31.8 | 2.1 | 32379 | 4 | US-09-949-016-15217 | Sequence 15217, A |
| C 894 | 32 | 2.2 | 102409 | 4 | US-09-949-016-15148 | Sequence 15148, A | C 967 | 31.8 | 2.1 | 32379 | 4 | US-09-949-016-15218 | Sequence 15218, A |
| C 895 | 32 | 2.2 | 119930 | 4 | US-09-949-016-12677 | Sequence 12677, A | C 968 | 31.8 | 2.1 | 32379 | 4 | US-09-949-016-15219 | Sequence 15219, A |
| C 896 | 32 | 2.2 | 119931 | 4 | US-09-949-016-16319 | Sequence 16319, A | C 969 | 31.8 | 2.1 | 32379 | 4 | US-09-949-016-15220 | Sequence 15220, A |
| C 897 | 32 | 2.2 | 125536 | 4 | US-09-949-016-14186 | Sequence 14186, A | C 970 | 31.8 | 2.1 | 32379 | 4 | US-09-949-016-15221 | Sequence 15221, A |
| C 898 | 32 | 2.2 | 141560 | 4 | US-09-949-016-16475 | Sequence 16475, A | C 971 | 31.8 | 2.1 | 32379 | 4 | US-09-949-016-15222 | Sequence 15222, A |
| 899 | 32 | 2.2 | 177251 | 4 | US-09-949-016-15841 | Sequence 15841, A | C 972 | 31.8 | 2.1 | 32379 | 4 | US-09-949-016-15223 | Sequence 15223, A |
| C 900 | 32 | 2.2 | 192302 | 4 | US-09-949-016-15270 | Sequence 15270, A | C 973 | 31.8 | 2.1 | 32379 | 4 | US-09-949-016-15224 | Sequence 15224, A |
| 901 | 32 | 2.2 | 251769 | 4 | US-09-949-016-13185 | Sequence 13185, A | C 974 | 31.8 | 2.1 | 32379 | 4 | US-09-949-016-15225 | Sequence 15225, A |
| 902 | 32 | 2.2 | 251769 | 4 | US-09-949-016-13186 | Sequence 13186, A | C 975 | 31.8 | 2.1 | 32379 | 4 | US-09-949-016-15226 | Sequence 15226, A |
| 903 | 32 | 2.2 | 266748 | 4 | US-09-949-016-13187 | Sequence 13187, A | C 976 | 31.8 | 2.1 | 45587 | 4 | US-09-949-016-15836 | Sequence 15836, A |

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|-------|------|-----|--------|---|----------------------|--------------------|------|------|-----|--------|---|---------------------|--------------------|
| 977 | 31.8 | 2.1 | 57392 | 4 | US-09-949-016-12070 | Sequence 12070, A | 1050 | 31.6 | 2.1 | 2795 | 4 | US-09-291-417D-25 | Sequence 25, Appl |
| 978 | 31.8 | 2.1 | 57400 | 4 | US-09-949-016-13293 | Sequence 13293, A | 1051 | 31.6 | 2.1 | 2962 | 4 | US-09-688-188B-106 | Sequence 106, App |
| 979 | 31.8 | 2.1 | 59240 | 4 | US-09-949-016-11933 | Sequence 11933, A | 1052 | 31.6 | 2.1 | 2962 | 4 | US-09-291-417D-106 | Sequence 106, App |
| 980 | 31.8 | 2.1 | 64377 | 4 | US-09-949-016-15212 | Sequence 15212, A | 1053 | 31.6 | 2.1 | 3664 | 4 | US-09-949-016-833 | Sequence 433, App |
| 981 | 31.8 | 2.1 | 64377 | 4 | US-09-949-016-15213 | Sequence 15213, A | 1054 | 31.6 | 2.1 | 3674 | 4 | US-09-902-540-9155 | Sequence 9155, App |
| 982 | 31.8 | 2.1 | 64377 | 4 | US-09-949-016-15214 | Sequence 15214, A | 1055 | 31.6 | 2.1 | 4056 | 4 | US-09-489-039A-3861 | Sequence 3861, App |
| 983 | 31.8 | 2.1 | 64377 | 4 | US-09-949-016-15215 | Sequence 15215, A | 1056 | 31.6 | 2.1 | 4221 | 4 | US-09-949-016-809 | Sequence 809, App |
| 984 | 31.8 | 2.1 | 64377 | 4 | US-09-949-016-15216 | Sequence 15216, A | 1057 | 31.6 | 2.1 | 4495 | 3 | US-09-417-822-6 | Sequence 6, Appl |
| 985 | 31.8 | 2.1 | 87350 | 3 | US-08-781-891-79 | Sequence 79, Appl | 1058 | 31.6 | 2.1 | 4495 | 3 | US-09-957-837A-6 | Sequence 6, Appl |
| 986 | 31.8 | 2.1 | 87350 | 3 | US-09-618-166-79 | Sequence 79, Appl | 1059 | 31.6 | 2.1 | 4534 | 3 | US-09-417-822-7 | Sequence 7, Appl |
| 987 | 31.8 | 2.1 | 87543 | 3 | US-09-791-211-3 | Sequence 3, Appl | 1060 | 31.6 | 2.1 | 4534 | 4 | US-09-957-837A-7 | Sequence 7, Appl |
| 988 | 31.8 | 2.1 | 113701 | 4 | US-09-949-016-13214 | Sequence 13214, A | 1061 | 31.6 | 2.1 | 4535 | 3 | US-09-417-822-8 | Sequence 8, Appl |
| 989 | 31.8 | 2.1 | 134890 | 4 | US-09-949-016-15602 | Sequence 15602, A | 1062 | 31.6 | 2.1 | 4808 | 4 | US-09-957-837A-8 | Sequence 8, Appl |
| 990 | 31.8 | 2.1 | 156324 | 4 | US-09-949-016-13749 | Sequence 13749, A | 1063 | 31.6 | 2.1 | 4808 | 4 | US-09-902-540-689 | Sequence 689, App |
| 991 | 31.8 | 2.1 | 187916 | 4 | US-09-949-016-12980 | Sequence 12980, A | 1064 | 31.6 | 2.1 | 4825 | 4 | US-09-902-540-692 | Sequence 692, App |
| 992 | 31.8 | 2.1 | 190078 | 4 | US-09-949-016-12707 | Sequence 12707, A | 1065 | 31.6 | 2.1 | 4944 | 1 | US-08-623-679-6 | Sequence 6, Appl |
| 993 | 31.8 | 2.1 | 190078 | 4 | US-09-949-016-17026 | Sequence 17026, A | 1066 | 31.6 | 2.1 | 4944 | 3 | US-08-933-774-6 | Sequence 6, Appl |
| 994 | 31.8 | 2.1 | 192956 | 4 | US-09-949-016-14382 | Sequence 14382, A | 1067 | 31.6 | 2.1 | 4944 | 3 | US-09-181-030-6 | Sequence 6, Appl |
| 995 | 31.8 | 2.1 | 237510 | 4 | US-09-949-016-14273 | Sequence 14273, A | 1068 | 31.6 | 2.1 | 4944 | 3 | US-09-534-242-6 | Sequence 6, Appl |
| 996 | 31.8 | 2.1 | 784019 | 4 | US-09-949-016-14033 | Sequence 14033, A | 1069 | 31.6 | 2.1 | 4944 | 3 | US-09-454-854-6 | Sequence 6, Appl |
| 997 | 31.8 | 2.1 | 828152 | 4 | US-09-949-016-12777 | Sequence 12777, A | 1070 | 31.6 | 2.1 | 4944 | 4 | US-09-154-671-6 | Sequence 6, Appl |
| 998 | 31.6 | 2.1 | 217 | 2 | US-08-332-766A-4 | Sequence 4, Appl | 1071 | 31.6 | 2.1 | 4944 | 4 | US-08-182-113-6 | Sequence 6, Appl |
| 999 | 31.6 | 2.1 | 284 | 2 | US-09-621-976-13655 | Sequence 13655, A | 1072 | 31.6 | 2.1 | 4944 | 4 | US-08-862-442-6 | Sequence 6, Appl |
| C 999 | 31.6 | 2.1 | 348 | 2 | US-08-623-906A-14 | Sequence 14, Appl | 1073 | 31.6 | 2.1 | 5055 | 1 | US-08-623-679-8 | Sequence 8, Appl |
| C1000 | 31.6 | 2.1 | 432 | 4 | US-09-252-991A-3530 | Sequence 3530, Ap | 1074 | 31.6 | 2.1 | 5055 | 3 | US-08-933-774-8 | Sequence 8, Appl |
| C1001 | 31.6 | 2.1 | 489 | 4 | US-09-902-540-3341 | Sequence 3341, Ap | 1075 | 31.6 | 2.1 | 5055 | 3 | US-09-181-030-8 | Sequence 8, Appl |
| 1002 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-19754 | Sequence 19754, A | 1076 | 31.6 | 2.1 | 5055 | 3 | US-09-534-242-8 | Sequence 8, Appl |
| 1003 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-28142 | Sequence 28142, A | 1077 | 31.6 | 2.1 | 5055 | 3 | US-09-454-854-8 | Sequence 8, Appl |
| C1004 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-28143 | Sequence 28143, A | 1078 | 31.6 | 2.1 | 5055 | 3 | US-09-164-671-8 | Sequence 8, Appl |
| C1005 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-29144 | Sequence 29144, A | 1079 | 31.6 | 2.1 | 5055 | 4 | US-09-182-113-8 | Sequence 8, Appl |
| C1006 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-29145 | Sequence 29145, A | 1080 | 31.6 | 2.1 | 5055 | 4 | US-08-862-442-8 | Sequence 8, Appl |
| C1007 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-41097 | Sequence 41097, A | 1081 | 31.6 | 2.1 | 5408 | 1 | US-08-441-139-15 | Sequence 15, Appl |
| C1008 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-41098 | Sequence 41098, A | 1082 | 31.6 | 2.1 | 7336 | 4 | US-09-949-016-13935 | Sequence 13935, A |
| C1009 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-41099 | Sequence 41099, A | 1083 | 31.6 | 2.1 | 8321 | 4 | US-09-902-540-979 | Sequence 979, App |
| C1010 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-41100 | Sequence 41100, A | 1084 | 31.6 | 2.1 | 8838 | 3 | US-09-417-822-1 | Sequence 1, Appl |
| C1011 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-81973 | Sequence 81973, A | 1085 | 31.6 | 2.1 | 8838 | 4 | US-09-957-837A-1 | Sequence 1, Appl |
| 1012 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-174173 | Sequence 174173, A | 1086 | 31.6 | 2.1 | 10280 | 4 | US-09-902-540-980 | Sequence 980, App |
| C1013 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-174174 | Sequence 174174, A | 1087 | 31.6 | 2.1 | 13335 | 4 | US-09-949-016-17476 | Sequence 1676, A |
| C1014 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-174365 | Sequence 174365, A | 1088 | 31.6 | 2.1 | 15535 | 4 | US-09-949-016-17225 | Sequence 17225, A |
| C1015 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-174366 | Sequence 174366, A | 1089 | 31.6 | 2.1 | 16073 | 4 | US-09-949-016-12312 | Sequence 12312, A |
| C1016 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-191466 | Sequence 191466, A | 1090 | 31.6 | 2.1 | 16073 | 4 | US-09-949-016-12905 | Sequence 12905, A |
| C1017 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-191467 | Sequence 191467, A | 1091 | 31.6 | 2.1 | 16387 | 4 | US-09-902-540-1156 | Sequence 1156, App |
| C1018 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-191468 | Sequence 191468, A | 1092 | 31.6 | 2.1 | 17125 | 4 | US-09-902-540-1166 | Sequence 1158, App |
| C1019 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-191469 | Sequence 191469, A | 1093 | 31.6 | 2.1 | 19237 | 4 | US-09-949-016-13568 | Sequence 13566, A |
| C1020 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-191470 | Sequence 191470, A | 1094 | 31.6 | 2.1 | 19383 | 4 | US-09-949-016-16031 | Sequence 16031, A |
| C1021 | 31.6 | 2.1 | 601 | 4 | US-09-949-016-191471 | Sequence 191471, A | 1095 | 31.6 | 2.1 | 19472 | 4 | US-09-949-016-13223 | Sequence 13223, A |
| C1022 | 31.6 | 2.1 | 601 | 4 | US-08-451-947-1 | Sequence 1, Appl | 1096 | 31.6 | 2.1 | 21196 | 4 | US-09-949-016-14670 | Sequence 14670, A |
| 1023 | 31.6 | 2.1 | 634 | 2 | US-08-424-826A-1 | Sequence 1, Appl | 1097 | 31.6 | 2.1 | 27150 | 4 | US-09-949-016-17378 | Sequence 17378, A |
| 1024 | 31.6 | 2.1 | 634 | 3 | US-08-928-694-1 | Sequence 1, Appl | 1098 | 31.6 | 2.1 | 27525 | 4 | US-09-949-016-16835 | Sequence 16835, A |
| 1025 | 31.6 | 2.1 | 634 | 4 | US-08-450-842-1 | Sequence 1, Appl | 1099 | 31.6 | 2.1 | 28862 | 4 | US-09-949-016-16793 | Sequence 16793, A |
| 1026 | 31.6 | 2.1 | 634 | 4 | US-08-451-390-1 | Sequence 1, Appl | 1100 | 31.6 | 2.1 | 30000 | 4 | US-10-007-010-10 | Sequence 10, Appl |
| 1027 | 31.6 | 2.1 | 634 | 5 | PCT-US91-06950-1 | Sequence 1, Appl | 1101 | 31.6 | 2.1 | 30001 | 1 | US-08-125-468-1 | Sequence 1, Appl |
| 1028 | 31.6 | 2.1 | 789 | 4 | US-09-902-540-3374 | Sequence 3374, Ap | 1102 | 31.6 | 2.1 | 30001 | 2 | US-08-474-933-1 | Sequence 1, Appl |
| 1029 | 31.6 | 2.1 | 867 | 4 | US-09-482-273-50 | Sequence 50, Appl | 1103 | 31.6 | 2.1 | 37224 | 4 | US-09-949-016-15973 | Sequence 15973, A |
| 1030 | 31.6 | 2.1 | 927 | 4 | US-09-252-991A-2499 | Sequence 2499, Ap | 1104 | 31.6 | 2.1 | 37875 | 4 | US-09-949-016-13182 | Sequence 13182, A |
| C1031 | 31.6 | 2.1 | 1149 | 4 | US-09-902-540-6250 | Sequence 6250, Ap | 1105 | 31.6 | 2.1 | 44499 | 4 | US-09-949-016-12711 | Sequence 12711, A |
| C1032 | 31.6 | 2.1 | 1207 | 3 | US-09-417-882-42 | Sequence 42, Appl | 1106 | 31.6 | 2.1 | 51967 | 4 | US-09-949-016-16982 | Sequence 16982, A |
| C1033 | 31.6 | 2.1 | 1207 | 4 | US-09-957-837A-42 | Sequence 42, Appl | 1107 | 31.6 | 2.1 | 53336 | 4 | US-09-949-016-12500 | Sequence 12500, A |
| C1034 | 31.6 | 2.1 | 1353 | 4 | US-09-902-540-9159 | Sequence 9159, Ap | 1108 | 31.6 | 2.1 | 53337 | 4 | US-09-949-016-16082 | Sequence 16092, A |
| C1035 | 31.6 | 2.1 | 1393 | 1 | US-07-602-824A-1 | Sequence 1, Appl | 1109 | 31.6 | 2.1 | 67911 | 4 | US-09-949-016-15976 | Sequence 15976, A |
| 1036 | 31.6 | 2.1 | 1393 | 1 | US-07-983-451-1 | Sequence 1, Appl | 1110 | 31.6 | 2.1 | 76124 | 4 | US-09-949-016-16937 | Sequence 16937, A |
| 1037 | 31.6 | 2.1 | 1493 | 1 | US-08-261-577-6 | Sequence 6, Appl | 1111 | 31.6 | 2.1 | 82494 | 4 | US-09-949-016-15243 | Sequence 15243, A |
| 1038 | 31.6 | 2.1 | 1493 | 1 | US-07-796-106-52 | Sequence 22, Appl | 1112 | 31.6 | 2.1 | 109159 | 4 | US-09-949-016-14169 | Sequence 14169, A |
| 1039 | 31.6 | 2.1 | 1408 | 3 | US-09-180-109A-5 | Sequence 5, Appl | 1113 | 31.6 | 2.1 | 109159 | 4 | US-09-949-016-14170 | Sequence 14170, A |
| C1040 | 31.6 | 2.1 | 1408 | 3 | US-09-902-540-271 | Sequence 7, Appl | 1114 | 31.6 | 2.1 | 113042 | 4 | US-09-949-016-12343 | Sequence 12343, A |
| C1041 | 31.6 | 2.1 | 1501 | 3 | US-09-902-540-271 | Sequence 21, App | 1115 | 31.6 | 2.1 | 113042 | 4 | US-09-949-016-15246 | Sequence 15246, A |
| C1042 | 31.6 | 2.1 | 1525 | 4 | US-09-964-895-3 | Sequence 3, Appl | 1116 | 31.6 | 2.1 | 152914 | 4 | US-09-949-016-11578 | Sequence 11578, A |
| C1043 | 31.6 | 2.1 | 1571 | 2 | US-08-145-658D-21 | Sequence 21, Appl | 1117 | 31.6 | 2.1 | 177797 | 4 | US-09-949-016-14125 | Sequence 14125, A |
| C1044 | 31.6 | 2.1 | 2351 | 4 | US-09-902-540-344 | Sequence 344, App | 1118 | 31.6 | 2.1 | 227979 | 4 | US-09-949-016-11842 | Sequence 11842, A |
| C1045 | 31.6 | 2.1 | 2412 | 4 | US-09-489-039A-5571 | Sequence 5571, App | 1119 | 31.6 | 2.1 | 260283 | 4 | US-09-949-016-17037 | Sequence 17037, A |
| C1046 | 31.6 | 2.1 | 2538 | 4 | US-09-488-039A-6419 | Sequence 6419, App | 1120 | 31.6 | 2.1 | 260283 | 4 | US-09-949-016-12106 | Sequence 12106, A |
| C1047 | 31.6 | 2.1 | 2567 | 4 | US-09-902-540-7310 | Sequence 7310, App | 1121 | 31.6 | 2.1 | 317366 | 4 | US-09-949-016-16001 | Sequence 16001, A |
| C1048 | 31.6 | 2.1 | 2795 | 4 | US-09-688-188B-25 | Sequence 25, Appl | 1122 | 31.6 | 2.1 | 336024 | 4 | US-09-949-016-12373 | Sequence 12373, A |

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|-------|------|-----|--------|---|----------------------|--------------------|-------|------|-----|--------|---|----------------------|--------------------|
| c1123 | 31.6 | 2.1 | 390416 | 4 | US-09-949-016-16923 | Sequence 16923, A | 1196 | 31.4 | 2.1 | 119982 | 4 | US-09-949-016-13606 | Sequence 13606, A |
| 1154 | 31.6 | 2.1 | 786431 | 4 | US-09-751-389-3 | Sequence 3, Appl1 | 1197 | 31.4 | 2.1 | 325034 | 4 | US-09-949-016-14957 | Sequence 14957, A |
| 1125 | 31.4 | 2.1 | 285 | 4 | US-09-902-540-1950 | Sequence 1950, Ap | 1198 | 31.4 | 2.1 | 389504 | 4 | US-09-949-016-11774 | Sequence 11774, A |
| c1126 | 31.4 | 2.1 | 336 | 4 | US-09-902-540-7416 | Sequence 7416, Ap | c1199 | 31.2 | 2.1 | 259 | 4 | US-09-313-294A-3922 | Sequence 3922, Ap |
| c1127 | 31.4 | 2.1 | 358 | 2 | US-08-454-557C-15 | Sequence 15, Appl1 | c1200 | 31.2 | 2.1 | 301 | 2 | US-08-333-766A-23 | Sequence 23, Appl1 |
| c1128 | 31.4 | 2.1 | 358 | 2 | US-08-340-426D-15 | Sequence 15, Appl1 | c1121 | 31.2 | 2.1 | 315 | 3 | US-09-060-756-46 | Sequence 46, Appl1 |
| c1129 | 31.4 | 2.1 | 358 | 2 | US-08-450-673C-15 | Sequence 15, Appl1 | c1202 | 31.2 | 2.1 | 315 | 4 | US-09-670-314-46 | Sequence 46, Appl1 |
| c1130 | 31.4 | 2.1 | 358 | 5 | PCR-US95-1711A-15 | Sequence 15, Appl1 | c1203 | 31.2 | 2.1 | 315 | 4 | US-09-248-796A-12307 | Sequence 12307, A |
| 1131 | 31.4 | 2.1 | 570 | 4 | US-09-266-965-20 | Sequence 20, Appl1 | c1204 | 31.2 | 2.1 | 324 | 3 | US-09-008-481A-5 | Sequence 5, Appl1 |
| 1132 | 31.4 | 2.1 | 601 | 4 | US-09-949-016-29160 | Sequence 29160, A | 1205 | 31.2 | 2.1 | 324 | 3 | US-09-008-481A-14 | Sequence 14, Appl1 |
| 1133 | 31.4 | 2.1 | 601 | 4 | US-09-949-016-41115 | Sequence 41115, A | 1206 | 31.2 | 2.1 | 324 | 3 | US-09-309-592-5 | Sequence 5, Appl1 |
| c1134 | 31.4 | 2.1 | 601 | 4 | US-09-949-016-41115 | Sequence 41115, A | 1207 | 31.2 | 2.1 | 324 | 3 | US-09-309-592-5 | Sequence 5, Appl1 |
| c1135 | 31.4 | 2.1 | 601 | 4 | US-09-949-016-77650 | Sequence 77650, A | 1208 | 31.2 | 2.1 | 324 | 3 | US-09-309-592-5 | Sequence 5, Appl1 |
| c1136 | 31.4 | 2.1 | 894 | 4 | US-09-902-540-4202 | Sequence 4202, Ap | c1209 | 31.2 | 2.1 | 399 | 4 | US-09-621-976-6976 | Sequence 6976, Ap |
| c1137 | 31.4 | 2.1 | 894 | 4 | US-09-902-540-6843 | Sequence 6843, Ap | c1210 | 31.2 | 2.1 | 420 | 4 | US-09-585-645A-3 | Sequence 3, Appl1 |
| c1138 | 31.4 | 2.1 | 1017 | 4 | US-09-252-991A-11927 | Sequence 11927, A | 1211 | 31.2 | 2.1 | 474 | 4 | US-09-252-991A-8385 | Sequence 8385, Ap |
| c1139 | 31.4 | 2.1 | 1071 | 2 | US-08-997-080-180 | Sequence 180, App | c1212 | 31.2 | 2.1 | 504 | 4 | US-09-252-991A-3681 | Sequence 3681, Ap |
| c1140 | 31.4 | 2.1 | 1071 | 2 | US-08-997-362-180 | Sequence 180, App | c1213 | 31.2 | 2.1 | 601 | 4 | US-09-949-016-81519 | Sequence 81519, A |
| c1141 | 31.4 | 2.1 | 1071 | 3 | US-09-095-885-180 | Sequence 180, App | c1214 | 31.2 | 2.1 | 601 | 4 | US-09-949-016-81519 | Sequence 81519, A |
| c1142 | 31.4 | 2.1 | 1071 | 3 | US-09-324-542-180 | Sequence 180, App | c1215 | 31.2 | 2.1 | 601 | 4 | US-09-949-016-81519 | Sequence 81519, A |
| c1143 | 31.4 | 2.1 | 1071 | 3 | US-09-205-426-180 | Sequence 180, App | c1216 | 31.2 | 2.1 | 601 | 4 | US-09-949-016-85245 | Sequence 85245, A |
| c1144 | 31.4 | 2.1 | 1110 | 4 | US-09-252-991A-12079 | Sequence 12079, A | c1217 | 31.2 | 2.1 | 601 | 4 | US-09-949-016-122719 | Sequence 122719, A |
| c1145 | 31.4 | 2.1 | 1281 | 4 | US-09-620-312D-849 | Sequence 849, App | c1218 | 31.2 | 2.1 | 601 | 4 | US-09-949-016-122731 | Sequence 122731, A |
| c1146 | 31.4 | 2.1 | 1305 | 4 | US-09-902-540-3710 | Sequence 3710, Ap | c1219 | 31.2 | 2.1 | 601 | 4 | US-09-949-016-165849 | Sequence 165849, A |
| c1147 | 31.4 | 2.1 | 1458 | 4 | US-09-252-991A-12019 | Sequence 12019, A | c1220 | 31.2 | 2.1 | 601 | 4 | US-09-949-016-173781 | Sequence 173781, A |
| c1148 | 31.4 | 2.1 | 1502 | 4 | US-09-902-540-6160 | Sequence 6160, Ap | 1221 | 31.2 | 2.1 | 601 | 4 | US-09-949-016-185608 | Sequence 185608, A |
| c1149 | 31.4 | 2.1 | 1608 | 4 | US-09-362-247-24 | Sequence 24, Appl1 | 1222 | 31.2 | 2.1 | 601 | 4 | US-09-949-016-407 | Sequence 407, App |
| c1150 | 31.4 | 2.1 | 1661 | 4 | US-09-436-521A-1 | Sequence 1, Appl1 | 1223 | 31.2 | 2.1 | 913 | 3 | US-09-298-731-16 | Sequence 46, Appl1 |
| c1151 | 31.4 | 2.1 | 1675 | 4 | US-09-902-540-302 | Sequence 302, App | 1224 | 31.2 | 2.1 | 925 | 4 | US-09-461-325-112 | Sequence 112, App |
| c1152 | 31.4 | 2.1 | 1686 | 4 | US-09-724-797-9 | Sequence 9, Appl1 | 1225 | 31.2 | 2.1 | 925 | 4 | US-10-012-542-112 | Sequence 112, App |
| c1153 | 31.4 | 2.1 | 1701 | 4 | US-09-902-540-9608 | Sequence 9608, Ap | 1226 | 31.2 | 2.1 | 925 | 4 | US-10-115-123-112 | Sequence 112, App |
| c1154 | 31.4 | 2.1 | 1869 | 4 | US-09-489-039A-4200 | Sequence 4200, Ap | c1227 | 31.2 | 2.1 | 954 | 4 | US-09-902-540-4253 | Sequence 4253, Ap |
| 1155 | 31.4 | 2.1 | 2328 | 4 | US-09-949-016-762 | Sequence 762, App | c1228 | 31.2 | 2.1 | 963 | 4 | US-09-902-540-4323 | Sequence 4323, Ap |
| c1156 | 31.4 | 2.1 | 2397 | 1 | US-07-891-942G-11 | Sequence 11, Appl1 | 1229 | 31.2 | 2.1 | 1188 | 4 | US-09-902-540-5280 | Sequence 9280, Ap |
| 1157 | 31.4 | 2.1 | 2561 | 4 | US-09-616-289-48 | Sequence 48, Appl1 | 1230 | 31.2 | 2.1 | 1242 | 4 | US-09-902-540-5329 | Sequence 5329, Ap |
| 1158 | 31.4 | 2.1 | 3899 | 4 | US-09-902-540-573 | Sequence 573, App | 1231 | 31.2 | 2.1 | 1260 | 3 | US-08-029-404-1 | Sequence 1, Appl1 |
| 1159 | 31.4 | 2.1 | 3934 | 3 | US-09-226-568-18 | Sequence 18, Appl1 | 1232 | 31.2 | 2.1 | 1260 | 3 | US-08-459-953A-1 | Sequence 1, Appl1 |
| 1160 | 31.4 | 2.1 | 3946 | 3 | US-08-077-848A-1 | Sequence 1, Appl1 | 1233 | 31.2 | 2.1 | 1260 | 4 | US-09-393-212-1 | Sequence 1, Appl1 |
| 1161 | 31.4 | 2.1 | 3946 | 3 | US-09-211-640-1 | Sequence 1, Appl1 | 1234 | 31.2 | 2.1 | 1284 | 3 | US-09-319-648-16 | Sequence 16, Appl1 |
| 1162 | 31.4 | 2.1 | 3946 | 3 | US-09-378-536-1 | Sequence 1, Appl1 | 1235 | 31.2 | 2.1 | 1284 | 3 | US-09-023-655-1182 | Sequence 1182, App |
| 1163 | 31.4 | 2.1 | 3946 | 4 | US-09-687-260-1 | Sequence 1, Appl1 | 1236 | 31.2 | 2.1 | 1293 | 2 | US-08-924-440-1 | Sequence 1, Appl1 |
| c1164 | 31.4 | 2.1 | 3946 | 5 | PCR-US94-03547-1 | Sequence 1, Appl1 | 1237 | 31.2 | 2.1 | 1371 | 4 | US-09-949-016-1236 | Sequence 3236, Ap |
| c1165 | 31.4 | 2.1 | 4852 | 1 | US-07-853-913-3 | Sequence 3, Appl1 | 1238 | 31.2 | 2.1 | 1385 | 4 | US-09-949-016-2373 | Sequence 2373, Ap |
| c1166 | 31.4 | 2.1 | 5245 | 4 | US-09-902-540-714 | Sequence 714, App | c1239 | 31.2 | 2.1 | 1385 | 4 | US-08-932-411A-17 | Sequence 17, Appl1 |
| c1167 | 31.4 | 2.1 | 5649 | 4 | US-09-949-016-14408 | Sequence 14408, A | c1240 | 31.2 | 2.1 | 1385 | 4 | US-08-585-645A-30 | Sequence 30, Appl1 |
| 1168 | 31.4 | 2.1 | 6436 | 4 | US-09-600-099-1 | Sequence 1, Appl1 | c1241 | 31.2 | 2.1 | 1412 | 4 | US-09-902-540-6637 | Sequence 6637, Ap |
| c1169 | 31.4 | 2.1 | 6757 | 4 | US-09-023-655-1087 | Sequence 1087, Ap | c1242 | 31.2 | 2.1 | 1412 | 4 | US-09-585-645A-6 | Sequence 6, Appl1 |
| c1170 | 31.4 | 2.1 | 12128 | 4 | US-09-949-016-12587 | Sequence 12587, A | c1243 | 31.2 | 2.1 | 1412 | 4 | US-09-585-645A-37 | Sequence 37, Appl1 |
| c1171 | 31.4 | 2.1 | 12129 | 4 | US-09-949-016-15713 | Sequence 15713, A | 1244 | 31.2 | 2.1 | 1446 | 2 | US-08-933-750C-91 | Sequence 91, Appl1 |
| 1172 | 31.4 | 2.1 | 12194 | 4 | US-09-902-540-1091 | Sequence 1091, Ap | 1245 | 31.2 | 2.1 | 1446 | 3 | US-09-234-613-91 | Sequence 91, Appl1 |
| 1173 | 31.4 | 2.1 | 12249 | 4 | US-09-266-965-74 | Sequence 74, Appl1 | c1246 | 31.2 | 2.1 | 1458 | 4 | US-09-902-540-3540 | Sequence 3540, Ap |
| c1174 | 31.4 | 2.1 | 12608 | 4 | US-09-949-016-15533 | Sequence 15533, A | c1247 | 31.2 | 2.1 | 1506 | 4 | US-09-902-540-3624 | Sequence 3624, Ap |
| c1175 | 31.4 | 2.1 | 17807 | 4 | US-09-949-016-12779 | Sequence 12779, A | 1248 | 31.2 | 2.1 | 1515 | 4 | US-09-252-991A-3746 | Sequence 3746, Ap |
| c1176 | 31.4 | 2.1 | 17864 | 4 | US-09-949-016-15511 | Sequence 15511, A | 1249 | 31.2 | 2.1 | 1524 | 4 | US-09-795-927-9 | Sequence 9, Appl1 |
| 1177 | 31.4 | 2.1 | 18031 | 4 | US-09-902-540-1180 | Sequence 1180, Ap | c1250 | 31.2 | 2.1 | 1587 | 4 | US-09-010-147B-19 | Sequence 19, Appl1 |
| 1178 | 31.4 | 2.1 | 18331 | 4 | US-09-266-965-96 | Sequence 96, Appl1 | 1251 | 31.2 | 2.1 | 1649 | 2 | US-08-845-566-2 | Sequence 2, Appl1 |
| c1179 | 31.4 | 2.1 | 21330 | 4 | US-09-902-540-1109 | Sequence 1209, Ap | 1252 | 31.2 | 2.1 | 1673 | 4 | US-09-949-016-2544 | Sequence 2544, Ap |
| c1180 | 31.4 | 2.1 | 21356 | 4 | US-09-949-016-16646 | Sequence 16646, A | 1253 | 31.2 | 2.1 | 1673 | 4 | US-09-949-016-2921 | Sequence 2921, Ap |
| 1181 | 31.4 | 2.1 | 23858 | 4 | US-09-949-016-15732 | Sequence 15732, A | 1254 | 31.2 | 2.1 | 1677 | 3 | US-09-153-804-10 | Sequence 10, Appl1 |
| 1182 | 31.4 | 2.1 | 28560 | 4 | US-09-949-016-16281 | Sequence 16281, A | 1255 | 31.2 | 2.1 | 1708 | 4 | US-09-919-172-30 | Sequence 30, Appl1 |
| c1183 | 31.4 | 2.1 | 43267 | 4 | US-09-949-016-17117 | Sequence 17117, A | 1256 | 31.2 | 2.1 | 1709 | 2 | US-09-010-398-2 | Sequence 2, Appl1 |
| 1184 | 31.4 | 2.1 | 77536 | 4 | US-09-410-551B-1 | Sequence 1, Appl1 | 1257 | 31.2 | 2.1 | 1709 | 3 | US-09-366-260-2 | Sequence 2, Appl1 |
| 1185 | 31.4 | 2.1 | 77536 | 4 | US-09-940-316B-1 | Sequence 1, Appl1 | 1258 | 31.2 | 2.1 | 1709 | 3 | US-09-153-804-11 | Sequence 11, Appl1 |
| 1186 | 31.4 | 2.1 | 85850 | 4 | US-09-949-016-13424 | Sequence 13424, A | c1259 | 31.2 | 2.1 | 1720 | 4 | US-09-148-545-53 | Sequence 53, Appl1 |
| 1187 | 31.4 | 2.1 | 88245 | 4 | US-09-949-016-11835 | Sequence 11835, A | 1260 | 31.2 | 2.1 | 1724 | 4 | US-09-620-312D-650 | Sequence 650, App |
| 1188 | 31.4 | 2.1 | 94133 | 4 | US-09-949-016-11901 | Sequence 11901, A | c1261 | 31.2 | 2.1 | 1761 | 4 | US-09-252-991A-8423 | Sequence 8423, App |
| 1189 | 31.4 | 2.1 | 94133 | 4 | US-09-949-016-12713 | Sequence 12713, A | 1262 | 31.2 | 2.1 | 1825 | 4 | US-09-976-594-573 | Sequence 673, App |
| 1190 | 31.4 | 2.1 | 94133 | 4 | US-09-949-016-15934 | Sequence 15934, A | c1263 | 31.2 | 2.1 | 1854 | 4 | US-09-902-540-340 | Sequence 340, App |
| 1191 | 31.4 | 2.1 | 94135 | 4 | US-09-949-016-15935 | Sequence 15935, A | 1264 | 31.2 | 2.1 | 1859 | 3 | US-09-399-913-33 | Sequence 23, Appl1 |
| 1192 | 31.4 | 2.1 | 94135 | 4 | US-09-949-016-15936 | Sequence 15936, A | 1265 | 31.2 | 2.1 | 1859 | 3 | US-09-298-711-23 | Sequence 23, Appl1 |
| 1193 | 31.4 | 2.1 | 94135 | 4 | US-09-949-016-15937 | Sequence 15937, A | 1266 | 31.2 | 2.1 | 1896 | 4 | US-09-350-694-73 | Sequence 37, Appl1 |
| c1194 | 31.4 | 2.1 | 105055 | 4 | US-09-949-016-14001 | Sequence 14001, A | 1267 | 31.2 | 2.1 | 1896 | 4 | US-09-461-325-17 | Sequence 37, Appl1 |
| 1195 | 31.4 | 2.1 | 119981 | 4 | US-09-949-016-11844 | Sequence 11844, A | 1268 | 31.2 | 2.1 | 1896 | 4 | US-10-012-542-37 | Sequence 37, Appl1 |

| | | | | | | | | | | | | | |
|-------|------|-----|--------|---|---------------------|--------------------|-------|------|-----|--------|---|----------------------|---------------------|
| 1269 | 31.2 | 2.1 | 1896 | 4 | US-10-115-123-37 | Sequence 37, Appl | c1342 | 31.2 | 2.1 | 248968 | 4 | US-09-949-016-12614 | Sequence 12614, A |
| c1270 | 31.2 | 2.1 | 1908 | 3 | US-09-252-991A-1727 | Sequence 3727, Ap | c1343 | 31.2 | 2.1 | 278866 | 4 | US-09-949-016-13922 | Sequence 13922, A |
| 1271 | 31.2 | 2.1 | 1955 | 3 | US-09-399-913-19 | Sequence 19, Appl | c1344 | 31.2 | 2.1 | 278866 | 4 | US-09-949-016-13923 | Sequence 13923, A |
| 1272 | 31.2 | 2.1 | 1955 | 3 | US-09-298-731-19 | Sequence 19, Appl | c1345 | 31.2 | 2.1 | 278866 | 4 | US-09-949-016-13924 | Sequence 13924, A |
| 1273 | 31.2 | 2.1 | 1955 | 4 | US-09-350-614-19 | Sequence 19, Appl | c1346 | 31.2 | 2.1 | 278866 | 4 | US-09-949-016-13925 | Sequence 13925, A |
| 1274 | 31.2 | 2.1 | 1962 | 4 | US-09-148-545-111 | Sequence 111, App | c1347 | 31.2 | 2.1 | 278866 | 4 | US-09-949-016-13926 | Sequence 13926, A |
| 1275 | 31.2 | 2.1 | 2009 | 3 | US-09-399-913-13 | Sequence 13, Appl | c1348 | 31.2 | 2.1 | 278866 | 4 | US-09-949-016-14659 | Sequence 14659, A |
| 1276 | 31.2 | 2.1 | 2009 | 3 | US-09-298-731-13 | Sequence 13, Appl | c1349 | 31.2 | 2.1 | 278866 | 4 | US-09-949-016-14700 | Sequence 14700, A |
| 1277 | 31.2 | 2.1 | 2009 | 4 | US-09-350-614-13 | Sequence 13, Appl | c1350 | 31.2 | 2.1 | 278866 | 4 | US-09-949-016-14701 | Sequence 14701, A |
| c1278 | 31.2 | 2.1 | 2037 | 4 | US-09-252-991A-1631 | Sequence 1631, Ap | c1351 | 31.2 | 2.1 | 278866 | 4 | US-09-949-016-14702 | Sequence 14702, A |
| 1279 | 31.2 | 2.1 | 2131 | 4 | US-09-949-016-4671 | Sequence 4671, Ap | c1352 | 31.2 | 2.1 | 278866 | 4 | US-09-949-016-14703 | Sequence 14703, A |
| c1280 | 31.2 | 2.1 | 2187 | 4 | US-09-902-540-3500 | Sequence 3500, Ap | c1353 | 31.2 | 2.1 | 304533 | 4 | US-09-949-016-15371 | Sequence 15371, A |
| c1281 | 31.2 | 2.1 | 2207 | 4 | US-09-949-016-5071 | Sequence 5071, Ap | c1354 | 31.2 | 2.1 | 304533 | 4 | US-09-949-016-15372 | Sequence 15372, A |
| 1282 | 31.2 | 2.1 | 2222 | 4 | US-09-795-927-11 | Sequence 11, Appl | c1355 | 31.2 | 2.1 | 312957 | 4 | US-09-949-001-31 | Sequence 31, Appl |
| 1283 | 31.2 | 2.1 | 2222 | 4 | US-09-731-030A-10 | Sequence 10, Appl | c1356 | 31.2 | 2.1 | 312957 | 4 | US-09-949-001-34 | Sequence 34, Appl |
| 1284 | 31.2 | 2.1 | 2341 | 4 | US-09-902-540-395 | Sequence 395, App | c1357 | 31.2 | 2.1 | 421494 | 4 | US-09-949-016-12805 | Sequence 12805, A |
| c1285 | 31.2 | 2.1 | 2348 | 4 | US-09-658-688A-3 | Sequence 3, Appl1 | c1358 | 31.2 | 2.1 | 421494 | 4 | US-09-949-016-14060 | Sequence 14060, A |
| c1286 | 31.2 | 2.1 | 2444 | 4 | US-09-482-273-100 | Sequence 100, App | c1359 | 31.2 | 2.1 | 211 | 4 | US-09-902-540-6919 | Sequence 6919, Ap |
| c1287 | 31.2 | 2.1 | 2621 | 4 | US-09-799-451-743 | Sequence 743, App | c1360 | 31 | 2.1 | 251 | 4 | US-09-621-976-14639 | Sequence 14639, Ap |
| 1288 | 31.2 | 2.1 | 2712 | 4 | US-09-902-540-4301 | Sequence 4301, Ap | c1361 | 31 | 2.1 | 270 | 4 | US-09-313-294A-1739 | Sequence 1739, Ap |
| c1289 | 31.2 | 2.1 | 2911 | 3 | US-08-981-825-5 | Sequence 5, Appl1 | c1362 | 31 | 2.1 | 445 | 2 | US-08-332-766A-16 | Sequence 16, Appl |
| c1290 | 31.2 | 2.1 | 2911 | 3 | US-09-480-784-5 | Sequence 5, Appl1 | c1363 | 31 | 2.1 | 549 | 4 | US-09-792-568-3 | Sequence 15507, A |
| c1291 | 31.2 | 2.1 | 3049 | 4 | US-09-300-958A-42 | Sequence 42, Appl | c1364 | 31 | 2.1 | 570 | 4 | US-09-501-115-39 | Sequence 3, Appl1 |
| c1292 | 31.2 | 2.1 | 3049 | 4 | US-09-949-016-991 | Sequence 991, App | c1365 | 31 | 2.1 | 580 | 4 | US-09-252-991A-15455 | Sequence 15455, A |
| 1293 | 31.2 | 2.1 | 3169 | 4 | US-09-620-312D-713 | Sequence 713, App | c1366 | 31 | 2.1 | 591 | 4 | US-09-949-016-58398 | Sequence 58398, A |
| c1294 | 31.2 | 2.1 | 3300 | 4 | US-09-482-273-68 | Sequence 68, Appl | c1367 | 31 | 2.1 | 601 | 4 | US-09-949-016-58398 | Sequence 58398, A |
| 1295 | 31.2 | 2.1 | 3778 | 4 | US-09-799-451-160 | Sequence 160, App | c1368 | 31 | 2.1 | 601 | 4 | US-09-949-016-58399 | Sequence 58399, A |
| c1296 | 31.2 | 2.1 | 3893 | 4 | US-09-799-451-21 | Sequence 21, Appl | c1369 | 31 | 2.1 | 601 | 4 | US-09-949-016-60104 | Sequence 60104, A |
| 1297 | 31.2 | 2.1 | 5919 | 4 | US-08-875-435B-2 | Sequence 9, Appl1 | c1370 | 31 | 2.1 | 601 | 4 | US-09-949-016-80104 | Sequence 80104, A |
| 1298 | 31.2 | 2.1 | 6043 | 4 | US-09-989-981A-9 | Sequence 9, Appl1 | c1371 | 31 | 2.1 | 601 | 4 | US-09-949-016-87648 | Sequence 87648, A |
| c1299 | 31.2 | 2.1 | 6507 | 4 | US-09-949-016-15053 | Sequence 15053, A | c1372 | 31 | 2.1 | 601 | 4 | US-09-949-016-87648 | Sequence 87648, A |
| 1300 | 31.2 | 2.1 | 7201 | 4 | US-09-902-540-914 | Sequence 914, App | c1373 | 31 | 2.1 | 684 | 4 | US-09-949-016-883033 | Sequence 883033, A |
| 1301 | 31.2 | 2.1 | 8009 | 4 | US-09-949-016-14978 | Sequence 14978, A | c1374 | 31 | 2.1 | 702 | 4 | US-09-902-540-6341 | Sequence 6341, Ap |
| 1302 | 31.2 | 2.1 | 9818 | 4 | US-09-902-540-967 | Sequence 967, App | c1375 | 31 | 2.1 | 748 | 3 | US-09-902-540-6731 | Sequence 6731, Ap |
| c1303 | 31.2 | 2.1 | 10321 | 4 | US-09-949-016-13587 | Sequence 13587, A | c1376 | 31 | 2.1 | 748 | 3 | US-08-998-416-434 | Sequence 416, App |
| c1304 | 31.2 | 2.1 | 10717 | 4 | US-09-902-540-991 | Sequence 991, App | c1377 | 31 | 2.1 | 945 | 3 | US-09-949-016-5170 | Sequence 5170, Appl |
| 1305 | 31.2 | 2.1 | 11280 | 4 | US-09-949-016-15203 | Sequence 15203, A | c1378 | 31 | 2.1 | 945 | 3 | US-09-268-364-3 | Sequence 3, Appl |
| 1306 | 31.2 | 2.1 | 11280 | 4 | US-09-949-016-15204 | Sequence 15204, A | c1379 | 31 | 2.1 | 1011 | 4 | US-09-902-540-1143 | Sequence 1143, App |
| 1307 | 31.2 | 2.1 | 11585 | 2 | US-08-687-080-105 | Sequence 105, App | c1380 | 31 | 2.1 | 1044 | 4 | US-09-640-211A-154 | Sequence 154, App |
| 1308 | 31.2 | 2.1 | 11631 | 4 | US-09-902-540-1092 | Sequence 1092, App | c1381 | 31 | 2.1 | 1281 | 4 | US-09-620-312D-849 | Sequence 849, App |
| c1309 | 31.2 | 2.1 | 17228 | 4 | US-09-902-540-1170 | Sequence 1170, App | c1382 | 31 | 2.1 | 1344 | 4 | US-09-902-540-2519 | Sequence 2519, App |
| 1310 | 31.2 | 2.1 | 17896 | 4 | US-09-949-016-11986 | Sequence 11986, A | c1383 | 31 | 2.1 | 1353 | 4 | US-09-902-540-7306 | Sequence 7306, App |
| c1311 | 31.2 | 2.1 | 18034 | 4 | US-09-266-965-75 | Sequence 75, Appl | c1384 | 31 | 2.1 | 1371 | 4 | US-09-252-991A-12349 | Sequence 12349, A |
| 1312 | 31.2 | 2.1 | 18034 | 4 | US-09-949-016-16413 | Sequence 16413, A | c1385 | 31 | 2.1 | 1392 | 4 | US-09-252-991A-12349 | Sequence 12349, A |
| 1313 | 31.2 | 2.1 | 18471 | 4 | US-09-902-540-1167 | Sequence 1167, App | c1386 | 31 | 2.1 | 1407 | 4 | US-09-252-991A-12361 | Sequence 12361, A |
| c1314 | 31.2 | 2.1 | 20347 | 4 | US-09-949-016-16752 | Sequence 16752, A | c1387 | 31 | 2.1 | 1479 | 4 | US-09-270-767-10543 | Sequence 10543, A |
| 1315 | 31.2 | 2.1 | 20840 | 4 | US-09-949-016-14115 | Sequence 14115, A | c1388 | 31 | 2.1 | 1480 | 4 | US-09-501-115-9 | Sequence 9, Appl1 |
| c1316 | 31.2 | 2.1 | 22339 | 4 | US-09-949-016-12411 | Sequence 12411, A | c1389 | 31 | 2.1 | 2091 | 4 | US-09-252-991A-12312 | Sequence 12312, A |
| c1317 | 31.2 | 2.1 | 22339 | 4 | US-09-949-016-16154 | Sequence 16154, A | c1390 | 31 | 2.1 | 2112 | 4 | US-09-902-540-539 | Sequence 539, App |
| 1318 | 31.2 | 2.1 | 22807 | 4 | US-09-902-540-1214 | Sequence 1215, App | c1391 | 31 | 2.1 | 2147 | 4 | US-09-949-016-5245 | Sequence 5245, App |
| c1319 | 31.2 | 2.1 | 25733 | 4 | US-09-902-540-1215 | Sequence 1215, App | c1392 | 31 | 2.1 | 2149 | 4 | US-09-949-016-556 | Sequence 456, App |
| 1320 | 31.2 | 2.1 | 26510 | 4 | US-09-949-016-1408 | Sequence 12408, A | c1393 | 31 | 2.1 | 2186 | 2 | US-08-878-546-8 | Sequence 9, Appl1 |
| c1321 | 31.2 | 2.1 | 31350 | 4 | US-09-949-016-15697 | Sequence 16967, A | c1394 | 31 | 2.1 | 2208 | 4 | US-09-252-991A-13675 | Sequence 13675, A |
| c1322 | 31.2 | 2.1 | 35542 | 4 | US-09-949-016-12149 | Sequence 12149, A | c1395 | 31 | 2.1 | 2235 | 4 | US-09-252-991A-12994 | Sequence 12994, A |
| c1323 | 31.2 | 2.1 | 36544 | 4 | US-09-949-016-13434 | Sequence 13434, A | c1396 | 31 | 2.1 | 2261 | 4 | US-09-252-991A-15884 | Sequence 15884, A |
| c1324 | 31.2 | 2.1 | 40576 | 4 | US-09-949-016-12329 | Sequence 12329, A | c1397 | 31 | 2.1 | 2319 | 4 | US-09-252-991A-13870 | Sequence 13870, A |
| c1325 | 31.2 | 2.1 | 40577 | 4 | US-09-949-016-16663 | Sequence 16663, A | c1398 | 31 | 2.1 | 2427 | 4 | US-09-252-991A-15396 | Sequence 15396, A |
| 1326 | 31.2 | 2.1 | 41318 | 4 | US-09-949-016-16225 | Sequence 16225, A | c1399 | 31 | 2.1 | 2628 | 4 | US-09-252-991A-13485 | Sequence 13485, A |
| c1327 | 31.2 | 2.1 | 43353 | 4 | US-09-949-016-15302 | Sequence 15302, A | c1400 | 31 | 2.1 | 2862 | 4 | US-09-252-991A-13485 | Sequence 13485, A |
| c1328 | 31.2 | 2.1 | 44554 | 4 | US-09-949-016-12043 | Sequence 12043, A | c1401 | 31 | 2.1 | 2905 | 4 | US-09-949-016-110 | Sequence 410, App |
| c1329 | 31.2 | 2.1 | 44555 | 4 | US-09-949-016-17877 | Sequence 12787, A | c1402 | 31 | 2.1 | 2906 | 4 | US-09-949-016-1249 | Sequence 5249, App |
| 1330 | 31.2 | 2.1 | 62908 | 4 | US-09-949-016-17554 | Sequence 17554, A | c1403 | 31 | 2.1 | 3000 | 1 | US-08-393-985-3 | Sequence 3, Appl1 |
| c1331 | 31.2 | 2.1 | 67907 | 4 | US-09-949-016-11804 | Sequence 11804, A | c1404 | 31 | 2.1 | 3070 | 4 | US-09-902-540-593 | Sequence 593, App |
| c1332 | 31.2 | 2.1 | 67919 | 4 | US-09-949-016-14555 | Sequence 12455, A | c1405 | 31 | 2.1 | 3157 | 2 | US-08-939-002A-1 | Sequence 1, Appl1 |
| c1333 | 31.2 | 2.1 | 69813 | 4 | US-09-949-016-13905 | Sequence 13905, A | c1406 | 31 | 2.1 | 3171 | 4 | US-09-016-434-1348 | Sequence 1348, App |
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| c1337 | 31.2 | 2.1 | 121982 | 4 | US-09-949-016-12085 | Sequence 12085, A | c1410 | 31 | 2.1 | 4998 | 4 | US-09-501-171-5 | Sequence 591, App |
| c1338 | 31.2 | 2.1 | 121982 | 4 | US-09-949-016-14105 | Sequence 14105, A | c1411 | 31 | 2.1 | 5074 | 4 | US-09-902-540-691 | Sequence 691, App |
| 1339 | 31.2 | 2.1 | 123463 | 4 | US-09-949-016-11078 | Sequence 11078, A | c1412 | 31 | 2.1 | 7398 | 4 | US-09-949-016-15901 | Sequence 15901, App |
| c1340 | 31.2 | 2.1 | 190078 | 4 | US-09-949-016-12707 | Sequence 12707, A | c1413 | 31 | 2.1 | 7610 | 4 | US-09-949-016-5516 | Sequence 5516, App |
| c1341 | 31.2 | 2.1 | 190078 | 4 | US-09-949-016-17026 | Sequence 17026, A | c1414 | 31 | 2.1 | 7654 | 4 | US-09-949-016-584 | Sequence 384, App |

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| c1415 | 1415 | 31 | 2.1 | 8578 | 4 | US-09-902-540-871 |
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| c1417 | 1417 | 31 | 2.1 | 8931 | 3 | US-09-028-934-28 |
| c1418 | 1418 | 31 | 2.1 | 10733 | 4 | US-09-902-540-1021 |
| c1419 | 1419 | 31 | 2.1 | 11973 | 4 | US-09-792-568-8 |
| c1420 | 1420 | 31 | 2.1 | 18228 | 4 | US-09-949-016-11964 |
| c1421 | 1421 | 31 | 2.1 | 18229 | 4 | US-09-949-016-11965 |
| c1422 | 1422 | 31 | 2.1 | 18469 | 4 | US-09-949-016-11966 |
| c1423 | 1423 | 31 | 2.1 | 18518 | 4 | US-09-949-016-11967 |
| c1424 | 1424 | 31 | 2.1 | 19818 | 4 | US-09-949-016-11968 |
| c1425 | 1425 | 31 | 2.1 | 19819 | 4 | US-09-949-016-11969 |
| c1426 | 1426 | 31 | 2.1 | 20634 | 4 | US-09-949-016-11970 |
| c1427 | 1427 | 31 | 2.1 | 26086 | 4 | US-09-949-016-11971 |
| c1428 | 1428 | 31 | 2.1 | 26288 | 4 | US-09-949-016-11972 |
| c1429 | 1429 | 31 | 2.1 | 30330 | 4 | US-09-949-016-11973 |
| c1430 | 1430 | 31 | 2.1 | 31797 | 4 | US-09-949-016-11974 |
| c1431 | 1431 | 31 | 2.1 | 36582 | 4 | US-09-949-016-11975 |
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| c1436 | 1436 | 31 | 2.1 | 71645 | 4 | US-09-949-016-11980 |
| c1437 | 1437 | 31 | 2.1 | 71651 | 4 | US-09-949-016-11981 |
| c1438 | 1438 | 31 | 2.1 | 76868 | 4 | US-09-949-016-11982 |
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| c1440 | 1440 | 31 | 2.1 | 178883 | 4 | US-09-949-016-11984 |
| c1441 | 1441 | 31 | 2.1 | 178884 | 4 | US-09-949-016-11985 |
| c1442 | 1442 | 31 | 2.1 | 250958 | 4 | US-09-949-016-11986 |
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| c1446 | 1446 | 31 | 2.1 | 336204 | 4 | US-09-949-016-11990 |
| c1447 | 1447 | 31 | 2.1 | 767677 | 4 | US-09-949-016-11991 |
| c1448 | 1448 | 31 | 2.1 | 767677 | 4 | US-09-949-016-11992 |
| c1449 | 1449 | 30.8 | 2.1 | 262 | 4 | US-09-513-999C-307171A |
| c1450 | 1450 | 30.8 | 2.1 | 277 | 3 | US-09-007-005-3 |
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| c1452 | 1452 | 30.8 | 2.1 | 279 | 2 | US-09-623-906A-3 |
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[illegible]


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; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,013
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION/DOCKET NUMBER: 36,749
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 658 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: OVAR1UT01
; CLONE: 815614
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; US-08-792-013-5
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Query Match      12.9%; Score 192.2; DB 3; Length 658;
Best Local Similarity 67.1%; Pred. No. 1.1e-43;
Matches 288; Conservative 0; Mismatches 138; Indels 3; Gaps 1;

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QY 250 CTCACAGCTTCAAGAGAGTACATGAGATTTGACCTGAAACATGAAAGCGAGATTGAC 309
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DB 531 TTGCCCTGA 539
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RESULT 5
US-09-513-999C-3906
; Sequence 3906, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3906
; LENGTH: 658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..624
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; NAME/KEY: misc_feature
; LOCATION: 525
; OTHER INFORMATION: n=a, y, c or t
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; US-09-513-999C-3906
;
Query Match      12.5%; Score 186; DB 4; Length 658;
Best Local Similarity 66.2%; Pred. No. 6.1e-42;
Matches 284; Conservative 0; Mismatches 141; Indels 4; Gaps 1;

QY 130 TTCCAAGGAGGAGAGGCTTGGCTTCAAGCCCGGAGAGAGAGGCTGCGCGAG 189
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DB 543 TTGCCCTGA 551
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RESULT 6
US-09-513-999C-14979
; Sequence 14979, Application US/09513999C
; Patent No. 6783961
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GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Ducierte, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 14979
LENGTH: 597
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 464
OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-14979

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Best Local Similarity 66.2% Pred. No. 3.6e-41;
Matches 280; Conservative 0; Mismatches 139; Indels 4; Gaps 1;

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DB 312 TTAATGAGAGAGATGAG 371
QY 436 ATGATCTGAG 495
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QY 496 AAGCAG 555
DB 430 --CGAG 487
QY 556 TGA 558
DB 488 TGA 490

RESULT 7

US-08-361-441B-4
Sequence 4, Application US/08361441B
Patent No. 6077948
GENERAL INFORMATION:
APPLICANT: Russell, Mary E.
APPLICANT: Ureans, Ulrike
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston

STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,441B
FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171,385
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-361-441B-4

Query Match 12.1% Score 180.4; DB 3 Length 627,
Best Local Similarity 64.8% Pred. No. 2.2e-40;
Matches 284; Conservative 0; Mismatches 151; Indels 3; Gaps 1;

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DB 80 AGCAAGAGATTTGAG 139
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QY 541 ATTGCTAGCTGCTGCTGA 558
DB 497 ATTCTGAGTGCCTTAA 514

RESULT 8

US-08-171-385-4
Sequence 4, Application US/08171385
Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: Mary E. Russell

APPLICANT: Unlike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
NUMBER OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,385
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Javis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEX: 200154
FAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 651
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-171-385-4
Query Match 12.1%; Score 180.4; DB 1; Length 651;
Best Local Similarity 64.8%; Pred. No. 2.3e-40;
Matches 284; Conservative 0; Mismatches 151; Indels 3; Gaps 1;
QY 121 AGCAAGGTCCTCAAGAGGGAAGGCTTGGCTTGTCTCAAGAGGAGGAGGAGGAGG 180
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QY 481 TTTGAAGAAAGCCCAAG 540
DB 440 TATGAG 496
QY 541 ATTGCTAGCTGCTGAG 558
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DB 497 ATTTCTGAGTTGCCCTAA 514
RESULT 9
US-09-513-999C-10617
Sequence 10617, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59,US2,REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 10617
LENGTH: 507
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: msec_feature
LOCATION: 443
OTHER INFORMATION: k=g or t
US-09-513-999C-10617
Query Match 8.8%; Score 131.4; DB 4; Length 507;
Best Local Similarity 66.3%; Pred. No. 1.2e-26;
Matches 205; Conservative 0; Mismatches 101; Indels 3; Gaps 1;
QY 250 CTCACAGCTTCAAGAGAGTACATGAGATTTGACCTGTAACATGAGAGAGAGAGAGAG 309
DB 95 CTCTCCCTCAACCAAGAGATACATGAGATTTGACCTTATGAGAAATGGCATTTGAT 154
QY 310 CTGATGCTTTTAAAGAGATGATGAGAGAGCTTGTGTCCCAAGAGAGAGAGAGAGAGATG 369
DB 155 ATCATGTCCTCGAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 214
QY 370 AAGAGATGATCTCAAGAGTGAACAAGGAGGCTCATGATCATATCTTACCGAGACTTT 429
DB 215 AAGAAATTAATGAGAGAGTGTCCAGTGGCTCCGAGAGAGAGTCACTACCTGACTTT 274
QY 430 GTGAACATGATGAGGAG 489
DB 275 CTCAGATGATGCTGGAGAGAGATCTGCTCATCTTAAGATGATCTGATGATGAGAGAA 334
QY 490 AAAGCCAAAG 549
DB 335 AAAG 391
QY 550 CTGCCCTGA 558
DB 392 TTGCCCTGA 400
RESULT 10
US-08-171-385-1/c
Sequence 1, Application US/08171385
Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: Mary E. Russell
APPLICANT: Unlike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston

STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171.385
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraezer, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 331
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-171-385-1

Query Match 6.4%; Score 94.8; DB 1; Length 331;
Best Local Similarity 63.7%; Pred. No. 1.7e-16;
Matches 177; Conservative 0; Mismatches 97; Indels 4; Gaps 2;
QY 281 TTGACCTGGAACATGAGGCGGAGATTGACCTGATGCTTTAAAGAGATGATGAGAAAGC 340
DB 325 TTGATCTGAATGCGCAATGGAATATCGATTAATGCTTTGAAGGAAATGCTGAGAAAC 266
QY 341 TTGGTGTCCTCCAGAACCCCACTGAGATGAAGAAATATCTCAGAGGTGAACAGAGGG 400
DB 265 TTGG-GTTCCTCAAGACCCATCTAGAGCTGAAGAAATTAATTAGAGAGGTGTCAGTGCT 207
QY 401 TCAGTACACTATATCTTACCGAGACTTTTGAACATGATCTGGGGAAGGTCGGCTG 460
DB 206 CCGAGGAGACGTTCACTGCTGCTTCTCAGATATGCTGGCAAGATCTGCCA 147
QY 461 TCTCAAGTTAGTATGATGTTTGAAGAAAAGCAAGAGAGAGCCCAAGCCAGTTG 520
DB 146 TCTTGAAGATGATTTCTGATGTGTGAGAGAAAACAAAGA---ACACCGAAGCCACTG 90
QY 521 GCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCTGA 558
DB 89 GTCCCCCAGCAAGAAAGCTATTCTGTATTGCCCTTA 52

RESULT 11
US-08-361-441B-1/c
Sequence 1, Application US/08361441B
Patent No. 6077948
GENERAL INFORMATION:
APPLICANT: Ruseell, Mary E.
APPLICANT: Uman, Ulrike
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361.441B
FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171.385
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraezer, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-361-441B-1

Query Match 6.4%; Score 94.8; DB 3; Length 331;
Best Local Similarity 63.7%; Pred. No. 1.7e-16;
Matches 177; Conservative 0; Mismatches 97; Indels 4; Gaps 2;
QY 281 TTGACCTGGAACATGAGGCGGAGATTGACCTGATGCTTTAAAGAGATGATGAGAAAGC 340
DB 325 TTGATCTGAATGCGCAATGGAATATCGATTAATGCTTTGAAGGAAATGCTGAGAAAC 266
QY 341 TTGGTGTCCTCCAGAACCCCACTGAGATGAAGAAATATCTCAGAGGTGAACAGAGGG 400
DB 265 TTGG-GTTCCTCAAGACCCATCTAGAGCTGAAGAAATTAATTAGAGAGGTGTCAGTGCT 207
QY 401 TCAGTACACTATATCTTACCGAGACTTTTGAACATGATCTGGGGAAGGTCGGCTG 460
DB 206 CCGAGGAGACGTTCACTGCTGCTTCTCAGATATGCTGGCAAGATCTGCCA 147
QY 461 TCTCAAGTTAGTATGATGTTTGAAGAAAAGCAAGAGAGAGCCCAAGCCAGTTG 520
DB 146 TCTTGAAGATGATTTCTGATGTGTGAGAGAAAACAAAGA---ACACCGAAGCCACTG 90
QY 521 GCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCTGA 558
DB 89 GTCCCCCAGCAAGAAAGCTATTCTGTATTGCCCTTA 52

RESULT 12
US-09-949-016-5139
Sequence 5139, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5139
LENGTH: 1363
TYPE: DNA

ORGANISM: Human
US-09-949-016-5139

Query Match 5.3%; Score 79.4; DB 4; Length 1363;
Best Local Similarity 68.3%; Pred. No. 7.7e-12;
Matches 110; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 307 GACCTGATGCTTTTAAAGAGATGATGAGAAAGCTTGAGTCCCAAGACCACCTGGAG 366
Db GATATCATGTCCTTAAAGCAATGCTGAGAAACTTGGAGTCCCAAGACTTACCTTAGAG 744
Qy 367 ATGAAGAAGATGATCTCAGAGGTGACAGAGGGGTCACTGACACTATATCTTACCGAGAC 426
Db CTAAGAATAATTAATTGAGAGGTGTCCAGTGGCTCCGGGAGACGTTCACTACCTGAC 804
Qy 427 TTGTGAACATGATGCTGGGAAACGGTCCGCTGCTCTCAA 467
Db TTCTCAGATGATGCTGGGCAAGATCTGCCATCTTAA 845

RESULT 13

US-09-949-016-5140
Sequence 5140; Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5140

LENGTH: 1363

TYPE: DNA

ORGANISM: Human

US-09-949-016-5140

Query Match 5.3%; Score 79.4; DB 4; Length 1363;
Best Local Similarity 68.3%; Pred. No. 7.7e-12;
Matches 110; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 307 GACCTGATGCTTTTAAAGAGATGATGAGAAAGCTTGAGTCCCAAGACCACCTGGAG 366
Db GATATCATGTCCTTAAAGCAATGCTGAGAAACTTGGAGTCCCAAGACTTACCTTAGAG 744
Qy 367 ATGAAGAAGATGATCTCAGAGGTGACAGAGGGGTCACTGACACTATATCTTACCGAGAC 426
Db CTAAGAATAATTAATTGAGAGGTGTCCAGTGGCTCCGGGAGACGTTCACTACCTGAC 804
Qy 427 TTGTGAACATGATGCTGGGAAACGGTCCGCTGCTCTCAA 467
Db TTCTCAGATGATGCTGGGCAAGATCTGCCATCTTAA 845

RESULT 14

US-09-949-016-16881
Sequence 16881; Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16881
LENGTH: 5502
TYPE: DNA
ORGANISM: Human
US-09-949-016-16881

Query Match 5.3%; Score 79.4; DB 4; Length 5502;
Best Local Similarity 68.3%; Pred. No. 1.6e-11;
Matches 110; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 307 GACCTGATGCTTTTAAAGAGATGATGAGAAAGCTTGAGTCCCAAGACCACCTGGAG 366
Db GATATCATGTCCTTAAAGCAATGCTGAGAAACTTGGAGTCCCAAGACTTACCTTAGAG 2882
Qy 367 ATGAAGAAGATGATCTCAGAGGTGACAGAGGGGTCACTGACACTATATCTTACCGAGAC 426
Db CTAAGAATAATTAATTGAGAGGTGTCCAGTGGCTCCGGGAGACGTTCACTACCTGAC 2942
Qy 427 TTGTGAACATGATGCTGGGAAACGGTCCGCTGCTCTCAA 467
Db TTCTCAGATGATGCTGGGCAAGATCTGCCATCTTAA 2983

RESULT 15

US-09-949-016-16882
Sequence 16882; Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 16882

LENGTH: 5502

TYPE: DNA

ORGANISM: Human

US-09-949-016-16882

Query Match 5.3%; Score 79.4; DB 4; Length 5502;
Best Local Similarity 68.3%; Pred. No. 1.6e-11;
Matches 110; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 307 GACCTGATGCTTTTAAAGAGATGATGAGAAAGCTTGAGTCCCAAGACCACCTGGAG 366
Db GATATCATGTCCTTAAAGCAATGCTGAGAAACTTGGAGTCCCAAGACTTACCTTAGAG 2882
Qy 367 ATGAAGAAGATGATCTCAGAGGTGACAGAGGGGTCACTGACACTATATCTTACCGAGAC 426
Db CTAAGAATAATTAATTGAGAGGTGTCCAGTGGCTCCGGGAGACGTTCACTACCTGAC 2942
Qy 427 TTGTGAACATGATGCTGGGAAACGGTCCGCTGCTCTCAA 467
Db TTCTCAGATGATGCTGGGCAAGATCTGCCATCTTAA 2983

Search completed: March 29, 2005, 03:26:36
Job time : 370 secs

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GenCore version 5.1.6
Run on: March 28, 2005, 23:56:39 ; Search time 869 Seconds
(without alignments)
10116.014 Million cell updates/sec

Title: US-10-015-610A-195
Perfect score: 1485
Sequence: 1 gcggccacagcagctagcc.....tgaaaaaaaaaaaaaaaaaa 1485
Scoring table: IDENTITY NUC
Gapop 10-0, Gapext 1.0
4390206 segs, 2359870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn19808:*
- 2: geneseqn19908:*
- 3: geneseqn20008:*
- 4: geneseqn20018:*
- 5: geneseqn20018s:*
- 6: geneseqn20028s:*
- 7: geneseqn20038s:*
- 8: geneseqn20038s:*
- 9: geneseqn20038s:*
- 10: geneseqn20038s:*
- 11: geneseqn20038s:*
- 12: geneseqn20048s:*
- 13: geneseqn20048s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| No. | Score | Match | Length | DB | ID | Description |
|-----------------------|------------------------|----------------|--------------|----------------|-----------------|-------------|
| RESULT 1 | | | | | | |
| ID | AA337076 | standard; | CDNA; | 1485 | BP. | |
| DE | Human PRO1306 | (UNQ672) | CDNA | sequence | SEQ ID NO:195. | |
| PN | WO200012708-A2. | | | | | |
| PD | 09-MAR-2000. | | | | | |
| PA | (GETH) GENENTECH INC. | | | | | |
| Query Match | | 100.0%; | Score 1485; | DB 3; | Length 1485; | |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | | |
| RESULT 2 | | | | | | |
| ID | AA54342 | standard; | DNA; | 1485 | BP. | |
| DE | DNA encoding | protein of the | invention | #55. | | |
| PN | WO200078961-A1. | | | | | |
| PD | 28-DEC-2000. | | | | | |
| PA | (GETH) GENENTECH INC. | | | | | |
| Query Match | | 100.0%; | Score 1485; | DB 4; | Length 1485; | |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | | |
| RESULT 3 | | | | | | |
| ID | AEK3590 | standard; | CDNA; | 1485 | BP. | |
| DE | CDNA encoding | human PRO | protein, | Seq ID NO | 109. | |
| PN | WO200208288-A2. | | | | | |
| PD | 31-JAN-2002. | | | | | |
| PA | (GETH) GENENTECH INC. | | | | | |
| Query Match | | 100.0%; | Score 1485; | DB 6; | Length 1485; | |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | | |
| RESULT 4 | | | | | | |
| ID | ABL89176 | standard; | CDNA; | 1485 | BP. | |
| DE | Human PRO1306 | CDNA | sequence | SEQ ID NO:209. | | |
| PN | WO200200690-A2. | | | | | |
| PD | 03-JAN-2002. | | | | | |
| PA | (GETH) GENENTECH INC. | | | | | |
| Query Match | | 100.0%; | Score 1485; | DB 6; | Length 1485; | |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | | |
| RESULT 5 | | | | | | |
| ID | AB195665 | standard; | CDNA; | 1485 | BP. | |
| DE | Human angiotensin | related | CDNA | PRO1306 | SEQ ID NO: 209. | |
| PN | WO200208284-A2. | | | | | |
| PD | 31-JAN-2002. | | | | | |
| PA | (GETH) GENENTECH INC. | | | | | |

| | | | | | |
|-----------------------|------------------------|------------------------|------------------------|----------|---------------|
| PA | (BAKE/) | BAKER K P. | | | |
| PA | (FERB/) | FERRARA N. | | | |
| PA | (GERB/) | GERBER H. | | | |
| PA | (GERR/) | GERRITSEN M E. | | | |
| PA | (GODD/) | GODDARD A. | | | |
| PA | (GODD/) | GODOWSKI P J. | | | |
| PA | (GURN/) | GURNEY A L. | | | |
| PA | (HILL/) | HILLAN K J. | | | |
| PA | (MARS/) | MARSTERS S A. | | | |
| PA | (PANU/) | PAN J. | | | |
| PA | (PAON/) | PAONT N F. | | | |
| PA | (STEP/) | STEPHAN J P. | | | |
| PA | (WATA/) | WATANABE C K. | | | |
| PA | (WILL/) | WILLIAMS P M. | | | |
| PA | (WOOD/) | WOOD W I. | | | |
| Query Match | | 100.0%; | Score 1485; | DB 6; | Length 1485; |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | |
| RESULT 6 | | | | | |
| ID | ACA68551 | standard; | CDNA; | 1485 | BP. |
| DE | Novel human | secreted and | transmembrane | protein | PRO1306 CDNA. |
| PN | US2003088063-A1. | | | | |
| PD | 08-MAY-2003. | | | | |
| PA | (GETH) GENENTECH INC. | | | | |
| Query Match | | 100.0%; | Score 1485; | DB 8; | Length 1485; |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | |
| RESULT 7 | | | | | |
| ID | ABT44280 | standard; | CDNA; | 1485 | BP. |
| DE | Human PRO1306 | CDNA. | | | |
| PN | US2003050448-A1. | | | | |
| PD | 13-MAR-2003. | | | | |
| PA | (GETH) GENENTECH INC. | | | | |
| Query Match | | 100.0%; | Score 1485; | DB 9; | Length 1485; |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | |
| RESULT 8 | | | | | |
| ID | ACD68379 | standard; | CDNA; | 1485 | BP. |
| DE | Novel human | secreted and | transmembrane | protein | PRO1306 CDNA. |
| PN | US2003073130-A1. | | | | |
| PD | 17-APR-2003. | | | | |
| PA | (GETH) GENENTECH INC. | | | | |
| Query Match | | 100.0%; | Score 1485; | DB 9; | Length 1485; |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | |
| RESULT 9 | | | | | |
| ID | ABT44563 | standard; | CDNA; | 1485 | BP. |
| DE | Human PRO1306 | CDNA. | | | |
| PN | US2003027988-A1. | | | | |
| PD | 06-FEB-2003. | | | | |
| PA | (GETH) GENENTECH INC. | | | | |
| Query Match | | 100.0%; | Score 1485; | DB 9; | Length 1485; |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | |
| RESULT 10 | | | | | |
| ID | ACD82230 | standard; | CDNA; | 1485 | BP. |
| DE | Human | secreted/transmembrane | polypeptide | PRO 1306 | CDNA. |
| PN | US2003044934-A1. | | | | |
| PD | 06-MAR-2003. | | | | |
| PA | (GETH) GENENTECH INC. | | | | |
| Query Match | | 100.0%; | Score 1485; | DB 9; | Length 1485; |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | |
| RESULT 11 | | | | | |
| ID | ACH04481 | standard; | CDNA; | 1485 | BP. |
| DE | Human CDNA | encoding | secreted/transmembrane | protein | PRO1306. |
| PN | US2003044841-A1. | | | | |
| PD | 06-MAR-2003. | | | | |
| PA | (GETH) GENENTECH INC. | | | | |
| Query Match | | 100.0%; | Score 1485; | DB 9; | Length 1485; |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | |
| RESULT 12 | | | | | |
| ID | ACD68025 | standard; | CDNA; | 1485 | BP. |
| DE | Novel human | secreted and | transmembrane | protein | PRO1306 CDNA. |
| PN | US2003073129-A1. | | | | |
| PD | 17-APR-2003. | | | | |
| PA | (GETH) GENENTECH INC. | | | | |
| Query Match | | 100.0%; | Score 1485; | DB 9; | Length 1485; |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | |

```
RESULT 13
ID ADB13936 standard; cDNA; 1485 BP.
DE Human membrane bound receptor/protein PRO1306 cDNA sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 9; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 14
ID ADB83599 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 9; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 15
ID ADB80705 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 9; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 16
ID ADB73246 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 9; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 17
ID ADB78328 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 9; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 18
ID ADB84976 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 19
ID ADB78082 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 20
ID ADB87148 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 21
ID ADB84730 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 22
ID ADB83845 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 23
ID ADB73000 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 24
ID ADC18064 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 25
ID ADC36838 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 26
ID ADC21828 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 27
ID ADC49859 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 28
ID ADC49058 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 29
ID ADC49575 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 30
ID ADC47436 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 31
ID ADC47181 standard; cDNA; 1485 BP.
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DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 32
ID ADC78056 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 33
ID ADD06291 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 34
ID ADD10498 standard; cDNA; 1485 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #105.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 35
ID ADC77810 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 36
ID ADD11458 standard; cDNA; 1485 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #105.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 37
ID ADD50773 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 38
ID ADD51019 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 39
ID ADD70710 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003096625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 40
ID ADD39787 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.

PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 41
ID ADD70233 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 42
ID ADD37251 standard; cDNA; 1485 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #105.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 43
ID ADD38354 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 44
ID ADD39310 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 45
ID ADD50500 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 46
ID ADD50254 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 47
ID ADD38833 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 48
ID ADD40264 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 49
ID ADD51265 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003105289-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 50
ID ADB50485 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 51
ID ADB20097 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 52
ID ADB50008 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 53
ID ADB21566 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ADB29991 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ADB55884 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 56
ID ADB99388 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 57
ID ACA66895 standard; cDNA; 1485 BP.
DE cDNA encoding human PRO polypeptide #55.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 58
ID ACD68647 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 59
ID ADC48812 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 60
ID ADB20983 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 61
ID ADB05827 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 62
ID ADB75056 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 63
ID ADB75802 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 64
ID ADB85034 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 65
ID ADB6660 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 66
ID ADB20737 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 67
ID ADB39034 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 68
ID ADE05581 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 69
ID ADD73566 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ADD78406 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID ADE41459 standard; cDNA; 1485 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #105.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 72
ID ADE21229 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 73
ID ADD77344 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 74
ID ADE20491 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 75
ID ADD75556 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 76
ID ADD74072 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 77
ID ADD74318 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ADD76048 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ADE85540 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ADE05089 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID ADD75302 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID ADD76846 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID ADE86614 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID ADD78082 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID ADD77590 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 86
ID ADP7836 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 87
ID ADP85294 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 88
ID ADP7826 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 89
ID ADP74564 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 90
ID ADP7092 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 91
ID ADP85786 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 92
ID ADE05335 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 93
ID ADP74810 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 94
ID ADP86568 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 95

ID ADP25879 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US200319675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 96
ID ADP24778 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US200319893-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 97
ID ADP29514 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 98
ID ADP37045 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 99
ID ADG05622 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003096859-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 100
ID ADG27176 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 101
ID ADG11239 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 102
ID ADG12018 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 103
ID ADP94575 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 104
ID ADG06671 standard; cDNA; 1485 BP.

DE Human PRO polynucleotide #55.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 105
ID ADH03083 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2003216662-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 106
ID ADH04037 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 107
ID ADH03560 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 108
ID ADH39015 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 CDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 109
ID ADH43642 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #105.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 110
ID ADG34105 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 CDNA.
PN US2004006306-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 111
ID ADH04514 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 112
ID ADI33575 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 113
ID ADH69669 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 114
ID ADH61515 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 115
ID ADI29830 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 CDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 116
ID ADM27227 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 CDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 117
ID ADK82987 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #105.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 118
ID ADK66585 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 119
ID ADL94714 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 120
ID ADH17625 standard; cDNA; 3375 BP.
DE Human CDNA Sequence SEQ ID NO:117244.
PN BE1074617-A2.
PD 07-FEB-2001.
PA (HSEI-) HELIX RES INST.
Query Match 98.5%; Score 1462.4; DB 4; Length 3375;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 121
ID ABK05007 standard; cDNA; 3385 BP.
DE Human novel polynucleotide #22.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HSEI-) HYSEQ INC.
Query Match 98.5%; Score 1462.4; DB 8; Length 3385;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 122
ID ABA93720 standard; cDNA; 3381 BP.
DE Human differentiation/development CDNA clone amy2_1j19.
PN WO200198454-A2.

PD 27-DEC-2001.
PA (GHRU-) GERMAN HUMAN GENOME PROJECT.
Query Match 97.8%; Score 1453; DB 6; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 123
ID ACN38972 standard; cDNA; 3362 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325244, SEQ ID NO:2818.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GERTH) GENENTECH INC.
Query Match 97.4%; Score 1446.6; DB 13; Length 3362;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 124
ID AAC66521 standard; cDNA; 3449 BP.
DE Human immune system associated protein HISA-3 coding sequence.
PN US6135941-A.
PD 24-OCT-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 97.3%; Score 1445.6; DB 4; Length 3449;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 125
ID AAI58050 standard; cDNA; 1731 BP.
DE Human polynucleotide SEQ ID NO 253.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 96.4%; Score 1430.8; DB 4; Length 1731;
Best Local Similarity 99.1%; Pred. No. 0;
RESULT 126
ID AAI59836 standard; cDNA; 1743 BP.
DE Human polynucleotide SEQ ID NO 3825.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 96.4%; Score 1430.8; DB 4; Length 1743;
Best Local Similarity 99.1%; Pred. No. 0;
RESULT 127
ID APT03024 standard; DNA; 3470 BP.
DE Human breast specific coding sequence SEQ ID NO: 29.
PN WO200240672-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 95.8%; Score 1423.2; DB 6; Length 3470;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 128
ID AD080255 standard; cDNA; 3451 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1761.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 92.6%; Score 1374.4; DB 13; Length 3451;
Best Local Similarity 94.9%; Pred. No. 0;
RESULT 129
ID ADR26679 standard; DNA; 1343 BP.
DE Breast cancer prognosis marker #2540.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Query Match 83.2%; Score 1236; DB 13; Length 1343;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 130
ID AAI96212 standard; cDNA; 781 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2287.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 43.4%; Score 644.4; DB 4; Length 781;
Best Local Similarity 97.0%; Pred. No. 5.3e-169;
RESULT 131
ID AAI96213 standard; cDNA; 766 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2288.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 43.4%; Score 644.4; DB 4; Length 781;
Best Local Similarity 97.0%; Pred. No. 5.3e-169;
RESULT 132
ID AAH05908 standard; cDNA; 857 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:2743.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 41.5%; Score 616; DB 4; Length 857;
Best Local Similarity 92.0%; Pred. No. 4.7e-161;
RESULT 133
ID AAV41919 standard; cDNA; 632 BP.
DE Nucleotide sequence of the cDNA clone AIF-2 (HEBGM49).
PN WO9831800-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 40.6%; Score 602.8; DB 2; Length 632;
Best Local Similarity 99.5%; Pred. No. 1.9e-157;
RESULT 134
ID ACH39813 standard; cDNA; 593 BP.
DE Human foetal brain cDNA #1180.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABART I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 32.1%; Score 476.2; DB 9; Length 593;
Best Local Similarity 96.4%; Pred. No. 4.1e-122;
RESULT 135
ID ABU49913 standard; DNA; 453 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:33.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 30.4%; Score 451.4; DB 6; Length 453;
Best Local Similarity 99.8%; Pred. No. 3e-115;
RESULT 136
ID AAV62798 standard; cDNA; 453 BP.
DE cDNA encoding a ATG-117 (allograft inflammatory factor, AIF3) protein.
PN EP879880-A1.
PD 25-NOV-1998.
PA (SMIK) SMITHLINE BECHAM CORP.
Query Match 30.2%; Score 448.2; DB 2; Length 453;
Best Local Similarity 99.3%; Pred. No. 2.3e-114;
RESULT 137
ID ABX74821 standard; cDNA; 437 BP.
DE Human cDNA sequence #121 down-regulated in CC-RCC patients.
PN WO200279411-A2.
PD 10-OCT-2002.
PA (VAND-) VAN ANDEL INST.
Query Match 23.4%; Score 348; DB 10; Length 437;
Best Local Similarity 94.4%; Pred. No. 2.1e-86;
RESULT 138
ID APT03023 standard; DNA; 393 BP.
DE Human breast specific coding sequence SEQ ID NO: 28.
PN WO200240672-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 18.7%; Score 278.4; DB 6; Length 393;
Best Local Similarity 99.3%; Pred. No. 5.3e-67;
RESULT 139
ID ABL49912 standard; DNA; 444 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:32.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.

Query Match 12.9%; Score 192.2; DB 6; Length 444;
Best Local Similarity 67.1%; Pred. No. 6.4e-43;
RESULT 140
ID AAG9369 standard; cDNA; 491 BP.
DE Human allograft inflammatory factor 1 (AIF-1) cDNA.
PN W05017506-A1.
PD 29-JUN-1995.
PA (HARD) HARVARD COLLEGE.
Query Match 12.9%; Score 192.2; DB 2; Length 491;
Best Local Similarity 67.1%; Pred. No. 6.8e-43;
RESULT 141
ID AA65628 standard; cDNA; 491 BP.
DE Human allograft inflammatory factor 1 (AIF-1) encoding cDNA SEQ ID NO:43.
PN US6077948-A.
PD 20-JUN-2000.
PA (HARD) HARVARD COLLEGE.
Query Match 12.9%; Score 192.2; DB 3; Length 491;
Best Local Similarity 67.1%; Pred. No. 6.8e-43;
RESULT 142
ID AAT64809 standard; cDNA; 635 BP.
DE Human RC-9 cDNA useful in proliferative arterial disease diagnosis.
PN W09722880-A1.
PD 26-JUN-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 12.9%; Score 192.2; DB 2; Length 635;
Best Local Similarity 67.1%; Pred. No. 7.7e-43;
RESULT 143
ID AAV82800 standard; cDNA; 635 BP.
DE ATG-750/RC-9 (allograft inflammatory factor-1) cDNA.
PN EP879883-A1.
PD 25-NOV-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 12.9%; Score 192.2; DB 2; Length 635;
Best Local Similarity 67.1%; Pred. No. 7.7e-43;
RESULT 144
ID AAV82802 standard; cDNA; 635 BP.
DE ATG-750/RC-9 (allograft inflammatory factor-1) cDNA.
PN EP879883-A1.
PD 25-NOV-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 12.9%; Score 192.2; DB 2; Length 635;
Best Local Similarity 67.1%; Pred. No. 7.7e-43;
RESULT 145
ID ADA19323 standard; cDNA; 639 BP.
DE Human insulin resistance marker IRM228 (AIF1) cDNA.
PN W0200298355-A2.
PD 12-DEC-2002.
PA (CLIN-) CLINGENIX INC.
Query Match 12.9%; Score 192.2; DB 10; Length 639;
Best Local Similarity 67.1%; Pred. No. 7.7e-43;
RESULT 146
ID AAD05035 standard; cDNA; 659 BP.
DE Novel human cytokine-2 (NHC-2) cDNA.
PN US6204021-B1.
PD 20-MAR-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.9%; Score 192.2; DB 4; Length 659;
Best Local Similarity 67.1%; Pred. No. 7.9e-43;
RESULT 147
ID ABR15589 standard; cDNA; 659 BP.
DE DNA encoding novel human cytokine-2 (NHC-2), version #2.
PN US200201827-A1.
PD 03-JAN-2002.
PA (INCY-) INCYTE PHARM INC.
Query Match 12.9%; Score 192.2; DB 6; Length 659;
Best Local Similarity 67.1%; Pred. No. 7.9e-43;
RESULT 148
ID ADA67731 standard; DNA; 659 BP.
DE Novel human cytokine 2, NHC-2, DNA #2.
PN US2003096371-A1.
PD 22-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.9%; Score 192.2; DB 9; Length 659;

Best Local Similarity 67.1%; Pred. No. 7.9e-43;
RESULT 149
ID ADQ22610 standard; DNA; 760 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5430.
PN W0200404838-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 12.9%; Score 192.2; DB 12; Length 760;
Best Local Similarity 67.1%; Pred. No. 8.4e-43;
RESULT 150
ID ABK84357 standard; cDNA; 639 BP.
DE Human cDNA differentially expressed in granulocytic cells #928.
PN W0200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 12.9%; Score 191; DB 6; Length 639;
Best Local Similarity 68.7%; Pred. No. 1.7e-42;
RESULT 151
ID ACA89946 standard; cDNA; 639 BP.
DE Gene differentially regulated in cardiovascular disease #67.
PN W02003031650-A2.
PD 17-APR-2003.
PA (FARB) BAYER AG.
Query Match 12.9%; Score 191; DB 8; Length 639;
Best Local Similarity 68.7%; Pred. No. 1.7e-42;
RESULT 152
ID ADR24778 standard; DNA; 639 BP.
DE Breast cancer prognosis marker #639.
PN W02004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 12.9%; Score 191; DB 13; Length 639;
Best Local Similarity 68.7%; Pred. No. 1.7e-42;
RESULT 153
ID ADR52830 standard; DNA; 639 BP.
DE Drug therapy altered expressed gene #181.
PN W02004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 12.9%; Score 191; DB 13; Length 639;
Best Local Similarity 68.7%; Pred. No. 1.7e-42;
RESULT 154
ID AAH25798 standard; DNA; 441 BP.
DE Human Mpi type ibai DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKAI CENT SOCHO.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 12.7%; Score 189.2; DB 4; Length 441;
Best Local Similarity 66.9%; Pred. No. 4.4e-42;
RESULT 155
ID ABR15587 standard; cDNA; 658 BP.
DE DNA encoding novel human cytokine-2 (NHC-2) version #1.
PN US2002001827-A1.
PD 03-JAN-2002.
PA (INCY-) INCYTE PHARM INC.
Query Match 12.6%; Score 186.8; DB 6; Length 658;
Best Local Similarity 65.2%; Pred. No. 2.5e-41;
RESULT 156
ID AAC03908 standard; cDNA; 658 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 3906.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 12.5%; Score 186; DB 3; Length 658;
Best Local Similarity 66.2%; Pred. No. 4.2e-41;
RESULT 157

ID AAC10904 standard; cDNA; 597 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 14979.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GENSET) GENSET.
Query Match 12.3%; Score 183.2; DB 3; Length 597;
Best Local Similarity 66.2%; Pred. No. 2.4e-40;
RESULT 158
ID AAH25799 standard; DNA; 441 BP.
DE Murine Mpi1 cype Ibai DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 12.3%; Score 182.2; DB 4; Length 441;
Best Local Similarity 65.3%; Pred. No. 4e-40;
RESULT 159
ID AAG99370 standard; cDNA; 627 BP.
DE Rat allograft inflammatory factor 1 (AIF-1) cDNA.
PN WO9517506-A1.
PD 29-JUN-1995.
PA (HARD) HARVARD COLLEGE.
Query Match 12.3%; Score 182; DB 2; Length 627;
Best Local Similarity 65.1%; Pred. No. 5.4e-40;
RESULT 160
ID ADB58279 standard; DNA; 653 BP.
DE Toxicity-related gene, SEQ ID 3305.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 12.3%; Score 182; DB 10; Length 653;
Best Local Similarity 65.1%; Pred. No. 5.5e-40;
RESULT 161
ID AAA65591 standard; cDNA; 627 BP.
DE Rat allograft inflammatory factor 1 (AIF-1) encoding cDNA SEQ ID NO:4.
PN US6077948-A.
PD 20-JUN-2000.
PA (HARD) HARVARD COLLEGE.
Query Match 12.1%; Score 180.4; DB 3; Length 627;
Best Local Similarity 64.8%; Pred. No. 1.5e-39;
RESULT 162
ID ADA19322 standard; cDNA; 536 BP.
DE Human insulin resistance marker IM228 (AIF1) EST.
PN WO200298355-A2.
PD 12-DEC-2002.
PA (CLIN-) CLINGENIX INC.
Query Match 12.0%; Score 177.8; DB 10; Length 536;
Best Local Similarity 66.5%; Pred. No. 7.4e-39;
RESULT 163
ID AAT64808 standard; cDNA; 696 BP.
DE Rat RC-9 cDNA useful in proliferative arterial disease diagnosis.
PN WO9722880-A1.
PD 26-JUN-1997.
PA (SMK) SMITHKLINE BEECHAM CORP.
Query Match 11.9%; Score 176; DB 2; Length 696;
Best Local Similarity 65.1%; Pred. No. 2.7e-38;
RESULT 164
ID AAH25804 standard; DNA; 441 BP.
DE Murine Ibai (EP1-EF1) DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 11.3%; Score 167.8; DB 4; Length 441;
Best Local Similarity 63.2%; Pred. No. 4.2e-36;
RESULT 165
ID AAH25805 standard; DNA; 360 BP.
DE Murine Ibai (1-120) DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.

PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 11.2%; Score 166.8; DB 4; Length 360;
Best Local Similarity 67.6%; Pred. No. 7.1e-36;
RESULT 166
ID AAH25800 standard; DNA; 345 BP.
DE Murine Ibai (1-115) DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 11.0%; Score 163.8; DB 4; Length 345;
Best Local Similarity 68.1%; Pred. No. 4.8e-35;
RESULT 167
ID AAH25803 standard; DNA; 441 BP.
DE Murine Ibai (EP2-EF2) DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 10.8%; Score 159.8; DB 4; Length 441;
Best Local Similarity 62.1%; Pred. No. 7.1e-34;
RESULT 168
ID AAH25801 standard; DNA; 354 BP.
DE Murine Ibai (30-147) DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 9.6%; Score 143.2; DB 4; Length 354;
Best Local Similarity 64.6%; Pred. No. 2.7e-29;
RESULT 169
ID AAC06542 standard; cDNA; 507 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 10617.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GENSET) GENSET.
Query Match 8.8%; Score 131.4; DB 3; Length 507;
Best Local Similarity 66.3%; Pred. No. 6.4e-26;
RESULT 170
ID AAV62799 standard; cDNA; 579 BP.
DE ATG-1100 (allograft inflammatory factor-1gamma) cDNA.
PN EP879882-A1.
PD 25-NOV-1998.
PA (SMK) SMITHKLINE BEECHAM CORP.
Query Match 8.8%; Score 131.4; DB 2; Length 579;
Best Local Similarity 66.3%; Pred. No. 6.9e-26;
RESULT 171
ID AAH25802 standard; DNA; 273 BP.
DE Murine Ibai (30-120) DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 8.6%; Score 127.8; DB 4; Length 273;
Best Local Similarity 67.4%; Pred. No. 4.8e-25;
RESULT 172
ID ADA67729 standard; DNA; 639 BP.
DE Novel human cytokine 2, NHC-2, DNA #1.
PN US2003096371-A1.
PD 22-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.5%; Score 126.4; DB 9; Length 639;
Best Local Similarity 65.2%; Pred. No. 1.8e-24;
RESULT 173
ID AAT64807 standard; DNA; 1678 BP.
DE Rat RC-9 gene useful in proliferative arterial disease diagnosis.
PN WO9722880-A1.
PD 26-JUN-1997.

PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 8.4%; Score 124; DB 2; Length 1678;
Best Local Similarity 64.8%; Pred. No. 1.4e-23;
RESULT 174
ID AA190746 standard; cDNA; 351 BP.
DE Human polynucleotide SEQ ID NO 10806.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 123.2; DB 4; Length 351;
Best Local Similarity 62.8%; Pred. No. 1e-23;
RESULT 175
ID ACH42742 standard; cDNA; 379 BP.
DE Human foetal kidney cDNA #276.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 7.9%; Score 117.8; DB 9; Length 379;
Best Local Similarity 66.2%; Pred. No. 3.5e-22;
RESULT 176
ID AAT64806 standard; DNA; 424 BP.
DE Rat RC-9 DNA useful in proliferative arterial disease diagnosis.
PN WO9722880-A1.
PD 26-JUN-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 7.9%; Score 117.8; DB 2; Length 424;
Best Local Similarity 64.6%; Pred. No. 3.7e-22;
RESULT 177
ID ADP2830 standard; DNA; 424 BP.
DE Renal toxin progression gene marker #1419.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 7.9%; Score 117.8; DB 12; Length 424;
Best Local Similarity 64.6%; Pred. No. 3.7e-22;
RESULT 178
ID ABL4989 standard; DNA; 117 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:14.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 7.9%; Score 117; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
RESULT 179
ID AAV82801 standard; cDNA; 631 BP.
DE ATG-1120 (allograft inflammatory factor-1-delta) cDNA.
PN EP979883-A1.
PD 25-NOV-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 7.7%; Score 114.2; DB 2; Length 631;
Best Local Similarity 59.7%; Pred. No. 4.5e-21;
RESULT 180
ID ABL49900 standard; DNA; 117 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:15.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 7.0%; Score 104.2; DB 6; Length 117;
Best Local Similarity 93.2%; Pred. No. 1.2e-18;
RESULT 181
ID AAQ9371 standard; cDNA; 331 BP.
DE Rat allograft inflammatory factor 1 (AIF-1) partial cDNA sequence.
PN WO9517506-A1.
PD 29-JUN-1995.
PA (HARD) HARVARD COLLEGE.
Query Match 6.4%; Score 94.8; DB 2; Length 331;
Best Local Similarity 63.7%; Pred. No. 8.5e-16;
RESULT 182
ID AA65568 standard; cDNA; 331 BP.

DE Rat allograft inflammatory factor 1 (AIF-1) cDNA sequence SEQ ID NO:1.
PN US607948-A.
PD 20-JUN-2000.
PA (HARD) HARVARD COLLEGE.
Query Match 6.4%; Score 94.8; DB 3; Length 331;
Best Local Similarity 63.7%; Pred. No. 8.5e-16;
RESULT 183
ID ABL49901 standard; DNA; 117 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:16.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 6.0%; Score 88.8; DB 6; Length 117;
Best Local Similarity 85.3%; Pred. No. 2.4e-14;
RESULT 184
ID ADP10331 standard; DNA; 1363 BP.
DE Reference mRNA sequences for marker probe #8.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 5.3%; Score 79.4; DB 12; Length 1363;
Best Local Similarity 68.3%; Pred. No. 3.4e-11;
RESULT 185
ID ADP10462 standard; DNA; 1363 BP.
DE Reference mRNA sequences for marker probe #139.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 5.3%; Score 79.4; DB 12; Length 1363;
Best Local Similarity 68.3%; Pred. No. 3.4e-11;
RESULT 186
ID ADQ84989 standard; cDNA; 1363 BP.
DE Human tumor-associated antigenic target (TAT) cDNA sequence #1803.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 5.3%; Score 79.4; DB 12; Length 1363;
Best Local Similarity 68.3%; Pred. No. 3.4e-11;
RESULT 187
ID ADQ83815 standard; cDNA; 1363 BP.
DE Human tumor-associated antigenic target (TAT) cDNA sequence #629.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 5.3%; Score 79.4; DB 12; Length 1363;
Best Local Similarity 68.3%; Pred. No. 3.4e-11;
RESULT 188
ID ADR25232 standard; DNA; 1363 BP.
DE Breast cancer prognosis marker #1093.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 5.3%; Score 79.4; DB 13; Length 1363;
Best Local Similarity 68.3%; Pred. No. 3.4e-11;
RESULT 189
ID ABK84756 standard; cDNA; 81800 BP.
DE Human cDNA differentially expressed in granulocytic cells #1327.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 5.3%; Score 79.4; DB 6; Length 81800;
Best Local Similarity 68.3%; Pred. No. 2.6e-10;
RESULT 190
ID AAX89526 standard; cDNA; 1235 BP.
DE Nucleotide sequence of Interferon Responsive Transcript-1.
PN WO9934814-A1.
PD 15-JUL-1999.
PA (UTEM) UNIV TEMPLE.

Query Match 5.1%; Score 76.2; DB 2; Length 1235;
Best Local Similarity 67.1%; Pred. No. 2.5e-10;
RESULT 191
ID ADQ18012 standard; DNA; 325 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 829.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.9%; Score 73.4; DB 12; Length 325;
Best Local Similarity 69.3%; Pred. No. 7.9e-10;
RESULT 192
ID AAH08134 standard; cDNA; 646 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:4969.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.7%; Score 69.2; DB 4; Length 646;
Best Local Similarity 60.4%; Pred. No. 1.7e-08;
RESULT 193
ID AAH18153 standard; cDNA; 1876 BP.
DE Human cDNA sequence SEQ ID NO:18038.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.6%; Score 68.8; DB 4; Length 1876;
Best Local Similarity 59.9%; Pred. No. 3.6e-08;
RESULT 194
ID ABZ11562 standard; cDNA; 1897 BP.
DE Human polynucleotide SEQ ID NO 444.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 4.6%; Score 68.8; DB 6; Length 1897;
Best Local Similarity 59.9%; Pred. No. 3.7e-08;
RESULT 195
ID ADM44080 standard; cDNA; 1897 BP.
DE Novel human arginine-rich protein cDNA #444.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Query Match 4.6%; Score 68.8; DB 12; Length 1897;
Best Local Similarity 59.9%; Pred. No. 3.7e-08;
RESULT 196
ID ACN37848 standard; cDNA; 1898 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA324241, SEQ ID NO:1000.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 4.6%; Score 68.8; DB 13; Length 1898;
Best Local Similarity 59.9%; Pred. No. 3.7e-08;
RESULT 197
ID ABA04457 standard; cDNA; 1923 BP.
DE Human PP3051 protein encoding cDNA SEQ ID NO:19/21.
PN CN13131316-A.
PD 19-SEP-2001.
PA (SHAN-) SHANGHAI INST ONCOLOGY
Query Match 4.6%; Score 68.8; DB 6; Length 1923;
Best Local Similarity 59.9%; Pred. No. 3.7e-08;
RESULT 198
ID ADB47517 standard; cDNA; 1924 BP.
DE Human cDNA upregulated in dendritic cells SEQ ID NO 217.
PN US2003134283-A1.
PD 17-JUL-2003.
PA (PETE/) PETERSON D P.
PA (PEAR/) PEARSON C I.
PA (COCK/) COCKS B G.
Query Match 4.6%; Score 68.8; DB 10; Length 1924;
Best Local Similarity 59.9%; Pred. No. 3.7e-08;
RESULT 199
ID ABA04454 standard; cDNA; 1562 BP.
DE Human PPI187 protein encoding cDNA SEQ ID NO:10/12.
PN CN13131316-A.
PD 19-SEP-2001.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match 4.5%; Score 66.4; DB 6; Length 1562;
Best Local Similarity 62.8%; Pred. No. 1.6e-07;
RESULT 200
ID AAV41920 standard; cDNA; 582 BP.
DE Nucleotide sequence of the cDNA clone AIF-3 (HNGBH45).
PN WO9831800-A2.
PD 23-JUL-1998.
PA (HOMA-) HUMAN GENOME SCI INC.
PA (AUCC-) AUCCLAND UNISERVICES LTD.
Query Match 4.3%; Score 64.2; DB 2; Length 582;
Best Local Similarity 59.7%; Pred. No. 3.9e-07;
RESULT 201
ID ABR43437 standard; cDNA; 717 BP.
DE DNA encoding novel central nervous system protein #17.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 64.2; DB 4; Length 717;
Best Local Similarity 59.7%; Pred. No. 4.3e-07;
RESULT 202
ID AD153824 standard; cDNA; 717 BP.
DE cDNA encoding novel human protein seq id 27.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.3%; Score 64.2; DB 12; Length 717;
Best Local Similarity 59.7%; Pred. No. 4.3e-07;
RESULT 203
ID ADX51980 standard; cDNA; 2277 BP.
DE Human atopic dermatitis/psoriasis-associated cDNA #13.
PN WO2004016785-A1.
PD 26-FEB-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUJENDENO.
Query Match 4.3%; Score 64.2; DB 12; Length 2277;
Best Local Similarity 59.7%; Pred. No. 7.7e-07;
RESULT 204
ID ACN37282 standard; cDNA; 2277 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA323749, SEQ ID NO:62.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 4.3%; Score 64.2; DB 13; Length 2277;
Best Local Similarity 59.7%; Pred. No. 7.7e-07;
RESULT 205
ID ADE54054 standard; cDNA; 2369 BP.
DE Human prostate cancer cDNA #401.
PN US2003190640-A1.
PD 09-OCT-2003.
PA (FARI/) FARIS M.
PA (PEAR/) PEARSON C I.
Query Match 4.3%; Score 64.2; DB 10; Length 2369;
Best Local Similarity 59.7%; Pred. No. 7.9e-07;
RESULT 206
ID ACC79092 standard; cDNA; 2490 BP.
DE Human secreted protein SECP-67 encoding cDNA SEQ ID NO:147.
PN WO2003016506-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.3%; Score 64.2; DB 10; Length 2490;
Best Local Similarity 59.7%; Pred. No. 8.1e-07;
RESULT 207
ID AD130758 standard; cDNA; 1358 BP.
DE Human cDNA #84.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Query Match 4.3%; Score 63.2; DB 11; Length 1358;

Best Local Similarity 59.1%; Pred. No. 1.1e-06;
RESULT 208
ID AAI63901 standard; cDNA; 505 BP.
DE Human polynucleotide seq ID NO 109.
PN WO200155308-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 4.2%; Score 63; DB 4; Length 505;
Best Local Similarity 60.0%; Pred. No. 7.9e-07;
RESULT 209
ID AAS31615 standard; cDNA; 505 BP.
DE cDNA encoding novel human calcium-binding protein #39.
PN WO200155304-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 4.2%; Score 63; DB 4; Length 505;
Best Local Similarity 60.0%; Pred. No. 7.9e-07;
RESULT 210
ID ABR43760 standard; cDNA; 505 BP.
DE DNA encoding novel central nervous system protein #340.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 4.2%; Score 63; DB 4; Length 505;
Best Local Similarity 60.0%; Pred. No. 7.9e-07;
RESULT 211
ID ADI54147 standard; cDNA; 505 BP.
DE cDNA encoding novel human protein seq id 350.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.2%; Score 63; DB 12; Length 505;
Best Local Similarity 60.0%; Pred. No. 7.9e-07;
RESULT 212
ID ADM24452 standard; cDNA; 505 BP.
DE Human PRO polynucleotide #99.
PN US2004014039-A1.
PD 22-JAN-2004.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 4.2%; Score 63; DB 12; Length 505;
Best Local Similarity 60.0%; Pred. No. 7.9e-07;
RESULT 213
ID ABL49896 standard; DNA; 117 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:11.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 4.2%; Score 62.6; DB 6; Length 117;
Best Local Similarity 70.9%; Pred. No. 4.9e-07;
RESULT 214
ID ABL30333 standard; DNA; 1000 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42472.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.1%; Score 60.4; DB 4; Length 1000;
Best Local Similarity 53.4%; Pred. No. 5.9e-06;
RESULT 215
ID ABL49897 standard; DNA; 117 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:12.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 4.0%; Score 59.4; DB 6; Length 117;
Best Local Similarity 69.2%; Pred. No. 3.9e-06;
RESULT 216
ID ABL49898 standard; DNA; 117 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:13.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.

Query Match 3.9%; Score 57.8; DB 6; Length 117;
Best Local Similarity 68.4%; Pred. No. 1.1e-05;
RESULT 217
ID ABL30332 standard; DNA; 10902 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42469.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.8%; Score 56; DB 4; Length 10902;
Best Local Similarity 57.4%; Pred. No. 0.00033;
RESULT 218
ID AAC26771 standard; cDNA; 55 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 30846.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GERS) GENSET.
Query Match 3.7%; Score 54.6; DB 3; Length 55;
Best Local Similarity 98.2%; Pred. No. 5.8e-05;
RESULT 219
ID AAI21783 standard; DNA; 166 BP.
DE Probe #11716 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 220
ID ABA66854 standard; DNA; 186 BP.
DE Human foetal liver single exon nucleic acid probe #15159.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 221
ID AAI47066 standard; DNA; 186 BP.
DE Probe #15752 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 222
ID ABA48939 standard; DNA; 166 BP.
DE Human breast cell single exon nucleic acid probe #7634.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 223
ID ABA33923 standard; DNA; 186 BP.
DE Probe #12389 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 224
ID AAK41013 standard; DNA; 166 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 15570.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 225
ID AAK15290 standard; DNA; 186 BP.
DE Human brain expressed single exon probe SEQ ID NO: 15281.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;

Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 226
ID ABS40605 standard; DNA; 186 BP.
DE Human liver single exon probe, SEQ ID No 15595.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 227
ID AA107468 standard; DNA; 186 BP.
DE Probe #7459 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 5; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 228
ID ABS14985 standard; DNA; 186 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14976.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 6; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 229
ID AA112595 standard; DNA; 500 BP.
DE Probe #2528 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 230
ID ABS43292 standard; DNA; 500 BP.
DE Human foetal liver single exon nucleic acid probe #2597.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 231
ID AA133943 standard; DNA; 500 BP.
DE Probe #2629 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 232
ID ABA43836 standard; DNA; 500 BP.
DE Human breast cell single exon nucleic acid probe #2531.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 233
ID ABA24049 standard; DNA; 500 BP.
DE Probe #2515 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 234
ID AAK8012 standard; DNA; 500 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 2569.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;

RESULT 235
ID AAK02576 standard; DNA; 500 BP.
DE Human brain expressed single exon probe SEQ ID NO: 2567.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 236
ID ABS27607 standard; DNA; 500 BP.
DE Human liver single exon probe, SEQ ID No 2597.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 237
ID AA102500 standard; DNA; 500 BP.
DE Probe #2491 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 5; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 238
ID ABS02484 standard; DNA; 500 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 2475.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 6; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 239
ID AB132566 standard; DNA; 6907 BP.
DE Human immune system associated gene SEQ ID NO: 539.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIDEMIOLOGICS AG.
Query Match 3.6%; Score 54.2; DB 6; Length 6907;
Best Local Similarity 56.4%; Pred. No. 0.00083;
RESULT 240
ID ADCT5907 standard; DNA; 638 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 831.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 3.5%; Score 51.8; DB 10; Length 638;
Best Local Similarity 50.6%; Pred. No. 0.0012;
RESULT 241
ID ADC77192 standard; DNA; 654 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2121.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 3.5%; Score 51.8; DB 10; Length 654;
Best Local Similarity 50.6%; Pred. No. 0.0012;
RESULT 242
ID ADC76478 standard; DNA; 654 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1747.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 3.5%; Score 51.8; DB 10; Length 654;
Best Local Similarity 50.6%; Pred. No. 0.0012;
RESULT 243
ID ADK57002 standard; DNA; 654 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4385.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 3.5%; Score 51.8; DB 10; Length 654;
Best Local Similarity 50.6%; Pred. No. 0.0012;

RESULT 244
ID ADK55204 standard; DNA; 654 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #2587.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
PA (DOMC) DOW AGROSCIENCES LLC.
Query Match 3.5%; Score 51.8; DB 10; Length 654;
Best Local Similarity 50.6%; Pred. No. 0.0012;
RESULT 245
ID ADC76480 standard; DNA; 620 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1749.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
Query Match 3.3%; Score 49.6; DB 10; Length 620;
Best Local Similarity 50.0%; Pred. No. 0.0048;
RESULT 246
ID ADC77196 standard; DNA; 620 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2125.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
Query Match 3.3%; Score 49.6; DB 10; Length 620;
Best Local Similarity 50.0%; Pred. No. 0.0048;
RESULT 247
ID ADK59086 standard; DNA; 620 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #6469.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
PA (DOMC) DOW AGROSCIENCES LLC.
Query Match 3.3%; Score 49.6; DB 10; Length 620;
Best Local Similarity 50.0%; Pred. No. 0.0048;
RESULT 248
ID ADK57006 standard; DNA; 620 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4389.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
PA (DOMC) DOW AGROSCIENCES LLC.
Query Match 3.3%; Score 49.6; DB 10; Length 620;
Best Local Similarity 50.0%; Pred. No. 0.0048;
RESULT 249
ID ADK55190 standard; DNA; 622 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #2573.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
PA (DOMC) DOW AGROSCIENCES LLC.
Query Match 3.3%; Score 49.6; DB 10; Length 622;
Best Local Similarity 50.0%; Pred. No. 0.0048;
RESULT 250
ID ADK58040 standard; DNA; 691 BP.
DE Toxicity-related gene, SEQ ID 3066.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.3%; Score 49.2; DB 10; Length 691;
Best Local Similarity 50.4%; Pred. No. 0.0066;
RESULT 251
ID ADK52516 standard; DNA; 691 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3058.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.3%; Score 49.2; DB 10; Length 691;
Best Local Similarity 50.4%; Pred. No. 0.0066;
RESULT 252
ID ADA71938 standard; DNA; 2000 BP.
PN WO2003000898-A1.
PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.3%; Score 49.2; DB 8; Length 2000;
Best Local Similarity 9.4%; Pred. No. 0.011;
RESULT 253
ID ACA26827 standard; DNA; 2451 BP.
DE Prokaryotic essential gene #8484.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.1%; Score 46.4; DB 8; Length 2451;
Best Local Similarity 46.8%; Pred. No. 0.074;
RESULT 254
ID ADJ42629 standard; cDNA; 768 BP.
DE Plant cDNA #3629.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW) BUDWORTH P.
PA (MUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICE D.
PA (ZHU/) ZHU T.
Query Match 3.1%; Score 46; DB 12; Length 768;
Best Local Similarity 50.9%; Pred. No. 0.054;
RESULT 255
ID AAC01147 standard; cDNA; 452 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 1145.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.1%; Score 45.6; DB 3; Length 452;
Best Local Similarity 51.5%; Pred. No. 0.054;
RESULT 256
ID ADL07540 standard; cDNA; 498 BP.
DE Human His-tagged Tioponin C, TnC, cDNA.
PN CN1412312-A.
PD 23-APR-2003.
PA (CHON-) CHONGQING KANGRWEI PHARM IND CO LTD.
Query Match 3.1%; Score 45.6; DB 12; Length 498;
Best Local Similarity 51.5%; Pred. No. 0.056;
RESULT 257
ID AAC03907 standard; cDNA; 547 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 3905.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.1%; Score 45.6; DB 3; Length 547;
Best Local Similarity 51.5%; Pred. No. 0.059;
RESULT 258
ID ADQ23762 standard; DNA; 1001 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6582.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.1%; Score 45.6; DB 12; Length 1001;
Best Local Similarity 51.5%; Pred. No. 0.08;
RESULT 259
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.1%; Score 45.4; DB 8; Length 2000;
Best Local Similarity 9.9%; Pred. No. 0.13;
RESULT 260
ID ADA58445 standard; cDNA; 303 BP.
DE Maize sucrose synthase EST #89.
PN US2003135870-A1.

PD 17-JUL-2003.
PA (CHET/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 3.0%; Score 45.2; DB 9; Length 303;
Best Local Similarity 54.6%; Pred. No. 0.057;
RESULT 261
ID AD858316 standard; DNA; 1112 BP.
DE Toxicity-related gene, SEQ ID 3342.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.0%; Score 45; DB 10; Length 1112;
Best Local Similarity 49.8%; Pred. No. 0.12;
RESULT 262
ID AB741999 standard; DNA; 1112 BP.
DE Toxicity modelling related rat gene SEQ ID No 1701.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.0%; Score 45; DB 10; Length 1112;
Best Local Similarity 49.8%; Pred. No. 0.12;
RESULT 263
ID ADP72640 standard; DNA; 1112 BP.
DE Renal toxin progression gene marker #1229.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 3.0%; Score 45; DB 12; Length 1112;
Best Local Similarity 49.8%; Pred. No. 0.12;
RESULT 264
ID AAH48729 standard; cDNA; 3372 BP.
DE Human HCN2 cDNA.
PN WO200159153-A2.
PD 16-AUG-2001.
PA (AVET) AVENTIS PHARMA DEUT GMBH.
Query Match 3.0%; Score 44.6; DB 4; Length 3372;
Best Local Similarity 57.6%; Pred. No. 0.28;
RESULT 265
ID AD083419 standard; cDNA; 3372 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #233.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GERTH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.0%; Score 44.6; DB 13; Length 3372;
Best Local Similarity 57.6%; Pred. No. 0.28;
RESULT 266
ID AAH98302 standard; cDNA; 3431 BP.
DE Human EST-derived coding sequence SEQ ID NO: 159.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.0%; Score 44.6; DB 4; Length 3431;
Best Local Similarity 57.6%; Pred. No. 0.28;
RESULT 267
ID AAD29756 standard; DNA; 3459 BP.
DE Human hyperpolarisation-activated cyclic nucleotide-gated channel 2 DNA.
PN WO200202630-A2.
PD 10-JAN-2002.
PA (SMIX) SMITHKLINE BEECHAM PLC.
Query Match 3.0%; Score 44.6; DB 6; Length 3459;
Best Local Similarity 57.6%; Pred. No. 0.28;
RESULT 268
ID ADA9154 standard; DNA; 447 BP.
DE Maize gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.0%; Score 44.4; DB 9; Length 447;
Best Local Similarity 50.5%; Pred. No. 0.12;
RESULT 269

ID ADA49026 standard; DNA; 787 BP.
DE Wheat gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.0%; Score 44.4; DB 9; Length 787;
Best Local Similarity 50.5%; Pred. No. 0.15;
RESULT 270
ID AD111958 standard; DNA; 787 BP.
DE Wheat cDNA modulated by post-transcriptional gene silencing Seqid 594.
PN US200313588-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHANG/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICE D.
Query Match 3.0%; Score 44.4; DB 11; Length 787;
Best Local Similarity 50.5%; Pred. No. 0.15;
RESULT 271
ID ADJ42631 standard; cDNA; 787 BP.
DE Plant cDNA #3631.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICE D.
PA (ZHUT/) ZHU T.
Query Match 3.0%; Score 44.4; DB 12; Length 787;
Best Local Similarity 50.5%; Pred. No. 0.15;
RESULT 272
ID ADJ42636 standard; cDNA; 802 BP.
DE Plant cDNA #3636.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICE D.
PA (ZHUT/) ZHU T.
Query Match 3.0%; Score 44.4; DB 12; Length 802;
Best Local Similarity 50.5%; Pred. No. 0.15;
RESULT 273
ID ADJ42639 standard; cDNA; 841 BP.
DE Plant cDNA #3639.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.

PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
PA (ZHUT/) ZHU T.
Query Match 3.0%; Score 44; DB 13; Length 841;
Best Local Similarity 50.5%; Pred. No. 0.16;
RESULT 274
ID AAC40960 standard; DNA; 490 BP.
DE Zee mays DNA fragment SEQ ID NO: 30145.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 3.0%; Score 44; DB 3; Length 490;
Best Local Similarity 50.0%; Pred. No. 0.16;
RESULT 275
ID AABN83907 standard; DNA; 1251 BP.
DE Calcium sensor G85 encoding sequence.
PN EP1209167-A1.
PD 29-MAY-2002.
PA (OKAZ-) OKAZAKI NAT RES INST.
Query Match 3.0%; Score 44; DB 6; Length 1251;
Best Local Similarity 49.2%; Pred. No. 0.25;
RESULT 276
ID ADJ67515 standard; DNA; 1527 BP.
DE Human ovarian specific gene SEQ ID NO:229.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 3.0%; Score 44; DB 12; Length 1527;
Best Local Similarity 58.3%; Pred. No. 0.27;
RESULT 277
ID ADJ67300 standard; DNA; 1527 BP.
DE Human ovarian specific gene SEQ ID NO:14.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 3.0%; Score 44; DB 12; Length 1527;
Best Local Similarity 58.3%; Pred. No. 0.27;
RESULT 278
ID ABR63767 standard; cDNA; 2175 BP.
DE Human cDNA differentially expressed in granulocytic cells #338.
PN WO20028999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.0%; Score 44; DB 6; Length 2175;
Best Local Similarity 49.2%; Pred. No. 0.33;
RESULT 279
ID ABR64770 standard; DNA; 2190 BP.
DE Human calmodulin 2 gene.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 3.0%; Score 44; DB 10; Length 2190;
Best Local Similarity 49.2%; Pred. No. 0.33;
RESULT 280
ID ABD21000 standard; DNA; 2190 BP.
DE Human calmodulin 2 DNA.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 3.0%; Score 44; DB 11; Length 2190;
Best Local Similarity 49.2%; Pred. No. 0.33;
RESULT 281
ID ADN60285 standard; cDNA; 2190 BP.
DE Human calmodulin 2 encoding cDNA.
PN WO2004039955-A2.
PD 13-MAY-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match 3.0%; Score 44; DB 13; Length 2190;
Best Local Similarity 49.2%; Pred. No. 0.33;
RESULT 282
ID AAS44450 standard; cDNA; 2247 BP.
DE cDNA encoding novel human secretory protein, Seq ID No 31.

PN WO200166689-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.0%; Score 44; DB 5; Length 2247;
Best Local Similarity 49.2%; Pred. No. 0.33;
RESULT 283
ID ADQ84750 standard; cDNA; 2363 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1564.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH-) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.0%; Score 44; DB 12; Length 2363;
Best Local Similarity 49.2%; Pred. No. 0.34;
RESULT 284
ID ADQ86930 standard; cDNA; 2363 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3805.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH-) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.0%; Score 44; DB 13; Length 2363;
Best Local Similarity 49.2%; Pred. No. 0.34;
RESULT 285
ID ADA58674 standard; cDNA; 255 BP.
DE Maize sucrose synthase EST #318.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.9%; Score 43.8; DB 9; Length 255;
Best Local Similarity 54.4%; Pred. No. 0.13;
RESULT 286
ID ABR63305 standard; DNA; 1161 BP.
DE Breast cancer related gene sequence SEQ ID NO:1642.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.9%; Score 43.6; DB 6; Length 1161;
Best Local Similarity 52.8%; Pred. No. 0.31;
RESULT 287
ID AAX90997 standard; DNA; 1173 BP.
DE Human centrin-2 gene (Hcen-2).
PN WO9951186-A2.
PD 14-OCT-1999.
PA (MILL-) MILLENNIUM PHARM INC.
PA (REGC-) UNIV CALIFORNIA.
Query Match 2.9%; Score 43.6; DB 2; Length 1173;
Best Local Similarity 52.8%; Pred. No. 0.31;
RESULT 288
ID AAX90998 standard; DNA; 6710 BP.
DE Human centrin-2 genomic sequence (Hcen-2).
PN WO9951186-A2.
PD 14-OCT-1999.
PA (MILL-) MILLENNIUM PHARM INC.
PA (REGC-) UNIV CALIFORNIA.
Query Match 2.9%; Score 43.6; DB 2; Length 6710;
Best Local Similarity 52.8%; Pred. No. 0.74;
RESULT 289
ID ADT66612 standard; cDNA; 1084 BP.
DE Rat calmodulin cDNA.
PN WO2004070383-A2.
PD 19-AUG-2004.
PA (CHEP-) GRUENTHAL GMBH.
Query Match 2.9%; Score 43.4; DB 13; Length 1084;
Best Local Similarity 49.3%; Pred. No. 0.34;
RESULT 290
ID AAC55847 standard; DNA; 2466 BP.
DE Mitomycin biosynthetic gene cluster related alpha amy1ase orf20.
PN WO200053737-A2.

PD 14-SEP-2000.
 PA (MINU) UNIV MINNESOTA.
 PA (SHER) SHERMAN D H.
 PA (MAOY) MAO Y.
 PA (VARO) VAROGLU M.
 PA (HEMW) HE M.
 PA (SHEL) SHELTON P C.
 Query Match 2.9%; Score 43.4; DB 3; Length 2466;
 Best Local Similarity 52.5%; Pred. No. 0.51;
 RESULT 291
 ID ADE10328 standard; DNA; 2466 BP.
 DE S. lavendulae gene for orf20.
 PN US2003134398-A1.
 PD 17-JUL-2003.
 PA (SHER) SHERMAN D H.
 PA (MAOY) MAO Y.
 PA (VARO) VAROGLU M.
 PA (HEMW) HE M.
 PA (SHEL) SHELTON P.
 Query Match 2.9%; Score 43.4; DB 10; Length 2466;
 Best Local Similarity 52.5%; Pred. No. 0.51;
 RESULT 292
 ID AAC5841 standard; DNA; 18034 BP.
 DE Complete Mitomycin ORF 11-22 nucleotide sequence.
 PN WO200053737-A2.
 PD 14-SEP-2000.
 PA (MINU) UNIV MINNESOTA.
 PA (SHER) SHERMAN D H.
 PA (MAOY) MAO Y.
 PA (VARO) VAROGLU M.
 PA (HEMW) HE M.
 PA (SHEL) SHELTON P C.
 Query Match 2.9%; Score 43.4; DB 3; Length 18034;
 Best Local Similarity 52.5%; Pred. No. 1.4;
 RESULT 293
 ID ADE10260 standard; DNA; 18034 BP.
 DE S. lavendulae mitomycin C gene cluster for ORFs 11-22.
 PN US2003134398-A1.
 PD 17-JUL-2003.
 PA (SHER) SHERMAN D H.
 PA (MAOY) MAO Y.
 PA (VARO) VAROGLU M.
 PA (HEMW) HE M.
 PA (SHEL) SHELTON P.
 Query Match 2.9%; Score 43.4; DB 10; Length 18034;
 Best Local Similarity 52.5%; Pred. No. 1.4;
 RESULT 294
 ID ADA58464 standard; cDNA; 294 BP.
 DE Maize sucrose synthase EST #108.
 PN US2003135870-A1.
 PD 17-JUL-2003.
 PA (CHEI) CHEIKH N.
 PA (FISH) FISHER D K.
 PA (LIUJ) LIU J.
 Query Match 2.9%; Score 43.2; DB 9; Length 294;
 Best Local Similarity 54.9%; Pred. No. 0.2;
 RESULT 295
 ID ABA63905 standard; cDNA; 447 BP.
 DE Rat calmodulin encoding sequence.
 PN EPI209167-A1.
 PD 29-MAY-2002.
 PA (OKAZ) OKAZAKI NAT RES INST.
 Query Match 2.9%; Score 43.2; DB 6; Length 447;
 Best Local Similarity 50.5%; Pred. No. 0.25;
 RESULT 296
 ID ADO21558 standard; DNA; 450 BP.
 DE Calmodulin mutant y99f/y138f-encoding DNA, SEQ ID NO:5.
 PN WO2004046179-A1.
 PD 03-JUN-2004.
 PA (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
 Query Match 2.9%; Score 43.2; DB 12; Length 450;
 Best Local Similarity 50.5%; Pred. No. 0.25;
 RESULT 297

ID ADO21554 standard; DNA; 450 BP.
 DE Calmodulin mutant y99f-encoding DNA, SEQ ID NO:1.
 PN WO2004046179-A1.
 PD 03-JUN-2004.
 PA (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
 Query Match 2.9%; Score 43.2; DB 12; Length 450;
 Best Local Similarity 50.5%; Pred. No. 0.25;
 RESULT 298
 ID ADO21556 standard; DNA; 450 BP.
 DE Calmodulin mutant y138f-encoding DNA, SEQ ID NO:3.
 PN WO2004046179-A1.
 PD 03-JUN-2004.
 PA (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
 Query Match 2.9%; Score 43.2; DB 12; Length 450;
 Best Local Similarity 50.5%; Pred. No. 0.25;
 RESULT 299
 ID AAC03838 standard; cDNA; 564 BP.
 DE Human secreted protein 5' EST, SEQ ID NO: 3836.
 PN EPI033401-A2.
 PD 06-SEP-2000.
 PA (GERS) GENSET.
 Query Match 2.9%; Score 43.2; DB 3; Length 564;
 Best Local Similarity 49.1%; Pred. No. 0.28;
 RESULT 300
 ID ADF60791 standard; DNA; 1182 BP.
 DE BCC DNA #SEQ ID 13.
 PN WO2003076466-A1.
 PD 18-SEP-2003.
 PA (NEUR) NEUROGENEX CO LTD.
 Query Match 2.9%; Score 43.2; DB 10; Length 1182;
 Best Local Similarity 50.5%; Pred. No. 0.4;
 RESULT 301
 ID AAD45852 standard; cDNA; 2908 BP.
 DE Corn sucrose synthase (Sue1) cDNA.
 PN WO200267662-A1.
 PD 06-SEP-2002.
 PA (PION) PIONEER HI-BRED INT INC.
 Query Match 2.9%; Score 43.2; DB 6; Length 2908;
 Best Local Similarity 54.4%; Pred. No. 0.63;
 RESULT 302
 ID ADA58522 standard; cDNA; 285 BP.
 DE Maize sucrose synthase EST #166.
 PN US2003135870-A1.
 PD 17-JUL-2003.
 PA (CHEI) CHEIKH N.
 PA (FISH) FISHER D K.
 PA (LIUJ) LIU J.
 Query Match 2.9%; Score 43; DB 9; Length 285;
 Best Local Similarity 54.8%; Pred. No. 0.23;
 RESULT 303
 ID AAA31581 standard; DNA; 378 BP.
 DE Plant microsatellite marker #542.
 PN WO9967421-A1.
 PD 29-DEC-1999.
 PA (GENE) GENESIS RES & DEV CORP LTD.
 PA (FLET) FLETCHER CHALLENGE FOREST LTD.
 Query Match 2.9%; Score 43; DB 3; Length 378;
 Best Local Similarity 48.9%; Pred. No. 0.26;
 RESULT 304
 ID AAA31434 standard; DNA; 450 BP.
 DE Plant microsatellite marker #395.
 PN WO9967421-A1.
 PD 29-DEC-1999.
 PA (GENE) GENESIS RES & DEV CORP LTD.
 PA (FLET) FLETCHER CHALLENGE FOREST LTD.
 Query Match 2.9%; Score 43; DB 3; Length 450;
 Best Local Similarity 48.9%; Pred. No. 0.26;
 RESULT 305
 ID AAA31901 standard; DNA; 495 BP.
 DE Plant microsatellite marker #862.
 PN WO9967421-A1.
 PD 29-DEC-1999.
 PA (GENE) GENESIS RES & DEV CORP LTD.

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PA (FLEET-) FLETCHER CHALLENGE FOREST LTD.
Query Match 2.9%; Score 43; DB 3; Length 495;
Best Local Similarity 48.9%; Pred. No. 0.3;
RESULT 306
ID AD42635 standard; cDNA; 820 BP.
DE Plant cDNA #3635.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUN/) MOUNGAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
Query Match 2.9%; Score 42.8; DB 12; Length 820;
Best Local Similarity 50.0%; Pred. No. 0.44;
RESULT 307
ID ADA58468 standard; cDNA; 306 BP.
DE Maize sucrose synthase EST #112.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.9%; Score 42.6; DB 9; Length 306;
Best Local Similarity 54.9%; Pred. No. 0.3;
RESULT 308
ID ADA58455 standard; cDNA; 313 BP.
DE Maize sucrose synthase EST #99.
PN US200135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.9%; Score 42.6; DB 9; Length 313;
Best Local Similarity 54.9%; Pred. No. 0.31;
RESULT 309
ID ADC7180 standard; DNA; 624 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2109.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
Query Match 2.9%; Score 42.6; DB 10; Length 624;
Best Local Similarity 50.7%; Pred. No. 0.43;
RESULT 310
ID ADC75909 standard; DNA; 624 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 833.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
Query Match 2.9%; Score 42.6; DB 10; Length 624;
Best Local Similarity 50.7%; Pred. No. 0.43;
RESULT 311
ID ADS59089 standard; DNA; 624 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #6472.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
Query Match 2.9%; Score 42.6; DB 10; Length 624;
Best Local Similarity 50.7%; Pred. No. 0.43;
RESULT 312
ID ADS6990 standard; DNA; 624 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4373.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
PA (DOMC) DOW AGROSCIENCES LLC.
Query Match 2.8%; Score 41.8; DB 10; Length 695;
Best Local Similarity 48.2%; Pred. No. 0.76;
RESULT 317
ID ADS6997 standard; DNA; 695 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4380.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
Query Match 2.8%; Score 41.8; DB 10; Length 695;
Best Local Similarity 48.2%; Pred. No. 0.76;
RESULT 318
ID ADS59090 standard; DNA; 695 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #6473.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
Query Match 2.8%; Score 41.8; DB 10; Length 695;
Best Local Similarity 48.2%; Pred. No. 0.76;
RESULT 319
ID ABI99274 standard; cDNA; 1361 BP.
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:111.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UNVI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 2.8%; Score 41.8; DB 6; Length 1361;
Best Local Similarity 48.9%; Pred. No. 1.1;
RESULT 320
ID ADR66614 standard; cDNA; 1361 BP.
DE Murine calmodulin cDNA.
PN WO2004070383-A2.
PD 19-AUG-2004.
PA (CHEF) GRUENENTHAL GMBH.
Query Match 2.8%; Score 41.8; DB 13; Length 1361;
Best Local Similarity 48.9%; Pred. No. 1.1;
RESULT 321
ID AAH74541 standard; cDNA; 905 BP.
DE Nucleotide sequence of a chitobiosidase polypeptide.
PN WO200146387-A1.
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PD 28-JUN-2001.
PA (CORR) CORNELL RES FOUND INC.
Query Match 2.8%; Score 41.4; DB 4; Length 905;
Best Local Similarity 52.6%; Pred. No. 1.1;
RESULT 322
ID AD449171 standard; DNA; 447 BP.
DE Maize gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.8%; Score 41.2; DB 9; Length 447;
Best Local Similarity 51.1%; Pred. No. 0.9;
RESULT 323
ID ADJ12052 standard; DNA; 447 BP.
DE Maize cDNA modulated by post-transcriptional gene silencing SeqID 688.
PN US200313588-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
Query Match 2.8%; Score 41.2; DB 11; Length 447;
Best Local Similarity 51.1%; Pred. No. 0.9;
RESULT 324
ID ADJ42640 standard; cDNA; 727 BP.
DE Plant cDNA #3640.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDM/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
PA (ZHUT/) ZHU T.
Query Match 2.8%; Score 41.2; DB 12; Length 727;
Best Local Similarity 51.1%; Pred. No. 1.1;
RESULT 325
ID ADQ97220 standard; DNA; 52640 BP.
DE Mouse cancer associated sequence MD08-015, SEQ ID 196.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.8%; Score 41.2; DB 12; Length 52640;
Best Local Similarity 57.9%; Pred. No. 9.7;
RESULT 326
ID ADC76479 standard; DNA; 521 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1748.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match 2.8%; Score 41; DB 10; Length 521;
Best Local Similarity 48.5%; Pred. No. 1.1;
RESULT 327
ID ADC77193 standard; DNA; 521 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2122.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match 2.8%; Score 41; DB 10; Length 521;
Best Local Similarity 48.5%; Pred. No. 1.1;

RESULT 328
ID ADK57003 standard; DNA; 521 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4386.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
PA (DOMC) DOM AGROSCIENCES LLC.
Query Match 2.8%; Score 41; DB 10; Length 521;
Best Local Similarity 48.5%; Pred. No. 1.1;
RESULT 329
ID ADK55199 standard; DNA; 521 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #2582.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
PA (DOMC) DOM AGROSCIENCES LLC.
Query Match 2.8%; Score 41; DB 10; Length 521;
Best Local Similarity 48.5%; Pred. No. 1.1;
RESULT 330
ID ABZ51912 standard; cDNA; 936 BP.
DE Aspergillus oryzae polynucleotide SEQ ID NO 1025.
PN WO200279476-A1.
PD 10-OCT-2002.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (NARE-) NAT RES INST BREWING.
PA (NORO) NAT FOOD RES INST MIN AGRIC.
Query Match 2.8%; Score 41; DB 8; Length 936;
Best Local Similarity 49.3%; Pred. No. 1.5;
RESULT 331
ID AAC43155 standard; DNA; 975 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38229.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 2.8%; Score 41; DB 3; Length 975;
Best Local Similarity 48.9%; Pred. No. 1.5;
RESULT 332
ID ABZ14388 standard; DNA; 975 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2193.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.8%; Score 41; DB 6; Length 975;
Best Local Similarity 48.9%; Pred. No. 1.5;
RESULT 333
ID ABZ42072 standard; cDNA; 975 BP.
DE Arabidopsis thaliana gene #56 modulated by PRGS.
PN WO200281695-A2.
PD 17-OCT-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (FRIE-) FRIEDRICH KIESCHER INST.
Query Match 2.8%; Score 41; DB 8; Length 975;
Best Local Similarity 48.9%; Pred. No. 1.5;
RESULT 334
ID ADA68266 standard; DNA; 975 BP.
DE Arabidopsis thaliana gene, SEQ ID 847.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.8%; Score 41; DB 8; Length 975;
Best Local Similarity 48.9%; Pred. No. 1.5;
RESULT 335
ID AAF14569 standard; cDNA; 1129 BP.
DE Aspergillus oryzae EST SEQ ID NO:7092.
PN WO200056762-A2.
PD 28-SEP-2000.
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
Query Match 2.8%; Score 41; DB 3; Length 1129;
Best Local Similarity 49.3%; Pred. No. 1.6;
RESULT 336
ID ADJ67514 standard; DNA; 1457 BP.
DE Human ovarian specific gene SEQ ID NO:228.

PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 2.7%; Score 40.8; DB 12; Length 1457;
Best Local Similarity 56.8%; Pred. No. 2.1;
RESULT 337
ID AD067299 standard; DNA; 1457 BP.
DE Human ovarian specific gene SEQ ID NO:13.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 2.7%; Score 40.8; DB 12; Length 1457;
Best Local Similarity 56.8%; Pred. No. 2.1;
RESULT 338
ID AAQ04331 standard; CDNA; 447 BP.
DE Recombinant calmodulin gene.
PN JP02092286-A.
PD 03-APR-1990.
PA (KIRI) KIRIN BREWERY KK.
Query Match 2.7%; Score 40.6; DB 2; Length 447;
Best Local Similarity 49.8%; Pred. No. 1.3;
RESULT 339
ID AAQ04334 standard; DNA; 504 BP.
DE Plasmid pOCAL7 cong. gene for calmodulin.
PN JP02092286-A.
PD 03-APR-1990.
PA (KIRI) KIRIN BREWERY KK.
Query Match 2.7%; Score 40.6; DB 2; Length 504;
Best Local Similarity 49.8%; Pred. No. 1.4;
RESULT 340
ID AD064131 standard; CDNA; 560 BP.
DE Cotton cDNA sequence, SEQ ID 4912.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA) KOVALIC D K.
PA (ZHOV) ZHOV Y.
PA (CHOV) CAO Y.
Query Match 2.7%; Score 40.6; DB 13; Length 560;
Best Local Similarity 49.3%; Pred. No. 1.5;
RESULT 341
ID AD041936 standard; CDNA; 724 BP.
DE Plant cDNA #2936.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW) BUDWORTH P.
PA (MOUG) MOUGHAMER T.
PA (BRIG) BRIGGS S P.
PA (COOP) COOPER B.
PA (GLAZ) GLAZEBROOK J.
PA (GOFF) GOFF S A.
PA (KATA) KATAGIRI F.
PA (KEEP) KEEPS J.
PA (PROV) PROVART N.
PA (RICK) RICKES D.
PA (ZHUT) ZHU T.
Query Match 2.7%; Score 40.6; DB 12; Length 724;
Best Local Similarity 49.3%; Pred. No. 1.7;
RESULT 342
ID ABD33266 standard; DNA; 166407 BP.
DE Murine cancer-associated (CA) gene MD07-046.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 40.6; DB 13; Length 166407;
Best Local Similarity 52.0%; Pred. No. 25;
RESULT 343
ID ABN74463 standard; CDNA; 974 BP.
DE Bovine embryonic germ (EG) cell cDNA EST #514.
PN WO200194550-A2.
PD 13-DEC-2001.
PA (INFI-) INFIGEN INC.
Query Match 2.7%; Score 40.4; DB 6; Length 974;
Best Local Similarity 41.2%; Pred. No. 2.2;

RESULT 344
ID ABN74464 standard; CDNA; 974 BP.
DE Bovine embryonic germ (EG) cell cDNA EST #515.
PN WO200194550-A2.
PD 13-DEC-2001.
PA (INFI-) INFIGEN INC.
Query Match 2.7%; Score 40.4; DB 6; Length 974;
Best Local Similarity 41.2%; Pred. No. 2.2;
RESULT 345
ID ADM02510 standard; CDNA; 2240 BP.
DE Human cDNA of the invention SEQ ID NO:1195.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 40.4; DB 11; Length 2240;
Best Local Similarity 63.3%; Pred. No. 3.4;
RESULT 346
ID ADQ63828 standard; CDNA; 2284 BP.
DE Novel human cDNA sequence #989.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 40.4; DB 12; Length 2284;
Best Local Similarity 63.3%; Pred. No. 3.4;
RESULT 347
ID AAQ04332 standard; DNA; 654 BP.
DE Plasmid pRCM1 and gene for construction of calmodulin expression vector.
PN JP02092286-A.
PD 03-APR-1990.
PA (KIRI) KIRIN BREWERY KK.
Query Match 2.7%; Score 40.2; DB 2; Length 654;
Best Local Similarity 48.5%; Pred. No. 2.1;
RESULT 348
ID ABK63445 standard; CDNA; 654 BP.
DE Rat Sequence differentially expressed in response to a hepatotoxin #1352.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 40.2; DB 6; Length 654;
Best Local Similarity 48.5%; Pred. No. 2.1;
RESULT 349
ID ACA43874 standard; DNA; 2394 BP.
DE Prokaryotic essential gene #25531.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.7%; Score 40.2; DB 8; Length 2394;
Best Local Similarity 47.8%; Pred. No. 4;
RESULT 350
ID ADQ22652 standard; DNA; 3446 BP.
DE Human bofe c18ne barcoma-upregulated DNA - SEQ ID 5472.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 40.2; DB 12; Length 3446;
Best Local Similarity 54.4%; Pred. No. 4.7;
RESULT 351
ID ADB58685 standard; DNA; 3513 BP.
DE Toxicity-related gene, SEQ ID 3711.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 40.2; DB 10; Length 3513;
Best Local Similarity 48.5%; Pred. No. 4.8;
RESULT 352
ID ADB53373 standard; DNA; 3513 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3915.
PN WO2003065893-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 40.2; DB 10; Length 3513;
Best Local Similarity 48.5%; Pred. No. 4.8;
RESULT 353

ID ABR42260 standard; DNA; 3513 BP.
DE Toxicity modelling related rat gene SEQ ID No 1962.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 40.2; DB 10; Length 3513;
Best Local Similarity 48.5%; Pred. No. 4.8;
RESULT 354
ID ADP72764 standard; DNA; 3513 BP.
DE Renal toxin progression gene marker #1353.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 40.2; DB 12; Length 3513;
Best Local Similarity 48.5%; Pred. No. 4.8;
RESULT 355
ID ABR16482 standard; DNA; 693 BP.
DE Human intracellular signalling protein coding sequence - SEQ ID No 35.
PN WO2002101008-A2.
PD 19-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.7%; Score 40; DB 10; Length 693;
Best Local Similarity 47.3%; Pred. No. 2.4;
RESULT 356
ID ABR55208 standard; CDNA; 1278 BP.
DE Calcium sensitive circularly permuted EYFP (CPEYFP), #1, CDNA.
PN EP138982-A1.
PD 11-SEP-2002.
PA (RIKE) RIKEN KK.
Query Match 2.7%; Score 40; DB 6; Length 1278;
Best Local Similarity 46.4%; Pred. No. 3.3;
RESULT 357
ID ABA16487 standard; DNA; 6058 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8818.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 40; DB 5; Length 6058;
Best Local Similarity 53.1%; Pred. No. 7.1;
RESULT 358
ID ADA58565 standard; CDNA; 289 BP.
DE Maize sucrose synthase EST #209.
PN US2003135870-A1.
PD 17-JUN-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.7%; Score 39.8; DB 9; Length 289;
Best Local Similarity 57.7%; Pred. No. 1.8;
RESULT 359
ID ADA58555 standard; CDNA; 329 BP.
DE Maize sucrose synthase EST #199.
PN US2003135870-A1.
PD 17-JUN-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.7%; Score 39.8; DB 9; Length 329;
Best Local Similarity 53.5%; Pred. No. 1.9;
RESULT 360
ID AAA1443 standard; DNA; 350 BP.
DE Plant microsatellite marker #404.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FOREST LTD.
Query Match 2.7%; Score 39.8; DB 3; Length 350;
Best Local Similarity 48.1%; Pred. No. 2;
RESULT 361
ID ADC77194 standard; DNA; 631 BP.
DE DNA homologous to phytopathogen resistance-related CDNA - SEQ ID 2123.
PN WO2003020905-A2.
PD 13-MAR-2003.

PA (DOWC) DOW CHEM CO.
Query Match 2.7%; Score 39.8; DB 10; Length 631;
Best Local Similarity 50.3%; Pred. No. 2.6;
RESULT 362
ID ADK59087 standard; DNA; 631 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #6470.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 2.7%; Score 39.8; DB 10; Length 631;
Best Local Similarity 50.3%; Pred. No. 2.6;
RESULT 363
ID ADK57004 standard; DNA; 631 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4387.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 2.7%; Score 39.8; DB 10; Length 631;
Best Local Similarity 50.3%; Pred. No. 2.6;
RESULT 364
ID AAC10892 standard; CDNA; 681 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 14967.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GSEST) GENSET.
Query Match 2.7%; Score 39.8; DB 3; Length 681;
Best Local Similarity 49.8%; Pred. No. 2.7;
RESULT 365
ID ADA68724 standard; DNA; 798 BP.
DE Rice gene, SEQ ID 2047.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.7%; Score 39.8; DB 8; Length 798;
Best Local Similarity 50.3%; Pred. No. 3;
RESULT 366
ID ADB58320 standard; DNA; 1139 BP.
DE Toxicity-related gene, SEQ ID 3346.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 39.8; DB 10; Length 1139;
Best Local Similarity 48.9%; Pred. No. 3.5;
RESULT 367
ID ADB52875 standard; DNA; 1139 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3417.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 39.8; DB 10; Length 1139;
Best Local Similarity 48.9%; Pred. No. 3.5;
RESULT 368
ID ABR142002 standard; DNA; 1139 BP.
DE Toxicity modelling related rat gene SEQ ID No 1704.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 39.8; DB 10; Length 1139;
Best Local Similarity 48.9%; Pred. No. 3.5;
RESULT 369
ID ADA69683 standard; DNA; 1248 BP.
DE Rice gene, SEQ ID 3006.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.7%; Score 39.8; DB 8; Length 1248;
Best Local Similarity 50.3%; Pred. No. 3.7;
RESULT 370
ID ADS55071 standard; CDNA; 1890 BP.
DE Bacterial polynucleotide #7058.
PN US2003233675-A1.

PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 2.7%; Score 39.8; DB 13; Length 1890;
RESULT 371
ID ADS49559 standard; cDNA; 1929 BP.
DE Bacterial polynucleotide #4302.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 2.7%; Score 39.8; DB 13; Length 1929;
RESULT 372
ID AB199819 standard; cDNA; 6512 BP.
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:932.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match
Best Local Similarity 2.7%; Score 39.8; DB 6; Length 6512;
RESULT 373
ID AA80188 standard; DNA; 462 BP.
DE DNA encoding bioynthetic multifunctional protein.
PN WO8809344-A.
PD 01-DEC-1988.
PA (CREA-) CREATIVE BIOMOLECULES INC.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 1; Length 462;
RESULT 374
ID ADJ42634 standard; cDNA; 541 BP.
DE Plant cDNA #3634.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 12; Length 541;
RESULT 375
ID ADA48926 standard; DNA; 709 BP.
DE Wheat gene conferring disease resistance in plants.
PN WO00300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 9; Length 709;
RESULT 376
ID ADJ41937 standard; cDNA; 709 BP.
DE Plant cDNA #2937.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.

PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 12; Length 709;
RESULT 377
ID AB120145 standard; DNA; 739 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11908.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 4; Length 739;
RESULT 378
ID AB14119 standard; cDNA; 995 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 36839.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 4; Length 995;
RESULT 379
ID AD46441 standard; DNA; 1011 BP.
DE Barley caltractin-like protein coding sequence SEQ ID NO: 7.
PN WO2004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 13; Length 1011;
RESULT 380
ID AB120141 standard; DNA; 1049 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11896.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 4; Length 1049;
RESULT 381
ID ADA69549 standard; DNA; 1434 BP.
DE Rice gene, SEQ ID 2872.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 8; Length 1434;
RESULT 382
ID ABN80332 standard; DNA; 3001 BP.
DE Human chemically modified disease associated gene SEQ ID NO 349.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 6; Length 3001;
RESULT 383
ID ABR28440 standard; DNA; 6120 BP.
DE DNA transcripction associated complementary genomic DNA #157.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 6; Length 6120;
RESULT 384
ID ABN80303 standard; DNA; 6120 BP.
DE Human chemically modified disease associated gene SEQ ID NO 320.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 6; Length 6120;
RESULT 385
ID ADQ97180 standard; DNA; 118063 BP.

DE Mouse cancer associated sequence MD08-011, SEQ ID 156.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 39.6; DB 12; Length 118063;
Best Local Similarity 50.5%; Pred. No. 40;
RESULT 386
ID AD035602 standard; DNA; 1125 BP.
DE Novel mouse gene sequence #275.
PN WO2004046310-A2.
PD 03-JUN-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.7%; Score 39.4; DB 12; Length 1125;
Best Local Similarity 50.3%; Pred. No. 4.5;
RESULT 387
ID AB195566 standard; cDNA; 3396 BP.
DE Mouse ischemic condition related cDNA sequence SEQ ID NO:569.
PN WO20018188-A2.
PD 22-NOV-2001.
PA (UWVI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 2.7%; Score 39.4; DB 6; Length 3396;
Best Local Similarity 45.8%; Pred. No. 7.9;
RESULT 388
ID ADC85485 standard; DNA; 20448 BP.
DE Mouse Calm2 genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 39.4; DB 10; Length 20448;
Best Local Similarity 48.4%; Pred. No. 19;
RESULT 389
ID ADA03005 standard; DNA; 20450 BP.
DE Mouse Calm2 carcinoma associated gene, SEQ ID NO:1523.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 39.4; DB 9; Length 20450;
Best Local Similarity 48.4%; Pred. No. 19;
RESULT 390
ID ADB72743 standard; DNA; 20450 BP.
DE Mouse Calm2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 39.4; DB 10; Length 20450;
Best Local Similarity 48.4%; Pred. No. 19;
RESULT 391
ID ADM74600 standard; DNA; 20450 BP.
DE Murine carcinoma associated (CA) nucleic acid #136.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 2.7%; Score 39.4; DB 12; Length 20450;
Best Local Similarity 48.4%; Pred. No. 19;
RESULT 392
ID AAC50296 standard; DNA; 514 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 64306.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (UWVI-) UNIV MIAMI.
Query Match 2.6%; Score 39.2; DB 3; Length 514;
Best Local Similarity 55.0%; Pred. No. 3.5;
RESULT 393
ID ADA70926 standard; DNA; 1146 BP.
DE Rice gene, SEQ ID 4249.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.6%; Score 39.2; DB 8; Length 1146;
Best Local Similarity 50.0%; Pred. No. 5.2;
RESULT 394
ID AD040264 standard; cDNA; 1308 BP.
DE Plant cDNA #1264.

PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDMORTH P.
PA (MOUTG/) MOUTHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KEEP/) KEEPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICK D.
PA (ZHUT/) ZHU T.
Query Match 2.6%; Score 39.2; DB 12; Length 1308;
Best Local Similarity 44.0%; Pred. No. 5.6;
RESULT 395
ID ACN44588 standard; DNA; 33454 BP.
DE Mouse genomic sequence mcG22056.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 39.2; DB 11; Length 33454;
Best Local Similarity 64.1%; Pred. No. 28;
RESULT 396
ID AAK82012 standard; DNA; 49561 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36824.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 39.2; DB 4; Length 49561;
Best Local Similarity 53.2%; Pred. No. 34;
RESULT 397
ID ACH16715 standard; cDNA; 402 BP.
DE Human adult heart cDNA #1029.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.6%; Score 39; DB 9; Length 402;
Best Local Similarity 51.4%; Pred. No. 3.5;
RESULT 398
ID ACH18454 standard; cDNA; 451 BP.
DE Human adult heart cDNA #2768.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.6%; Score 39; DB 9; Length 451;
Best Local Similarity 51.4%; Pred. No. 3.7;
RESULT 399
ID AAV04232 standard; cDNA; 495 BP.
DE Human cardiac troponin C cDNA.
PN WO9739132-A1.
PD 23-OCT-1997.
PA (UWVI-) UNIV MIAMI.
Query Match 2.6%; Score 39; DB 2; Length 495;
Best Local Similarity 51.4%; Pred. No. 3.9;
RESULT 400
ID ADT02425 standard; cDNA; 744 BP.
DE cDNA encoding Troponin I N-term-troponin C.
PN US6475785-B1.
PD 05-NOV-2002.
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
Query Match 2.6%; Score 39; DB 5; Length 744;
Best Local Similarity 51.4%; Pred. No. 4.8;
RESULT 401
ID ADT02427 standard; cDNA; 795 BP.

DE cDNA encoding Troponin I N-term-linker-troponin C.
PN US6475785-B1.
PD 05-NOV-2002.
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
Query Match 2.6%; Score 39; DB 5; Length 795;
Best Local Similarity 51.4%; Pred. No. 4.9;
RESULT 402
ID AC103848 standard; cDNA; 844 BP.
DE Human cDNA differentially expressed in lung cancer #53.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASE/) LASEK A W.
Query Match 2.6%; Score 39; DB 9; Length 844;
Best Local Similarity 51.4%; Pred. No. 5.1;
RESULT 403
ID ADE77154 standard; cDNA; 846 BP.
DE Human cDNA differentially expressed in a liver disorder #237.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Query Match 2.6%; Score 39; DB 12; Length 846;
Best Local Similarity 51.4%; Pred. No. 5.1;
RESULT 404
ID ADG14210 standard; cDNA; 1116 BP.
DE Human cDNA encoding troponin I.
PN US2003176655-A1.
PD 18-SEP-2003.
PA (SHIO/) SHI O.
PA (SONG/) SONG Q.
Query Match 2.6%; Score 39; DB 10; Length 1116;
Best Local Similarity 51.4%; Pred. No. 5.8;
RESULT 405
ID AAV04225 standard; cDNA; 1119 BP.
DE DNA encoding cardiac troponin I/cardiac troponin C fusion.
PN WO97393132-A1.
PD 23-OCT-1997.
PA (UMI-) UNIV MIAMI.
Query Match 2.6%; Score 39; DB 2; Length 1119;
Best Local Similarity 51.4%; Pred. No. 5.9;
RESULT 406
ID ADE77155 standard; cDNA; 1158 BP.
DE Human cDNA differentially expressed in a liver disorder #238.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Query Match 2.6%; Score 39; DB 12; Length 1158;
Best Local Similarity 51.4%; Pred. No. 6;
RESULT 407
ID AAX78382 standard; DNA; 1173 BP.
DE Human cardiac troponin I and troponin C DNA.
PN WO99311235-A1.
PD 24-JUN-1999.
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
Query Match 2.6%; Score 39; DB 2; Length 1173;
Best Local Similarity 51.4%; Pred. No. 6;
RESULT 408
ID ADG14205 standard; cDNA; 1173 BP.
DE Human cDNA encoding troponin I-troponin C fusion protein.
PN US2003176655-A1.
PD 18-SEP-2003.
PA (SHIO/) SHI O.
PA (SONG/) SONG Q.
Query Match 2.6%; Score 39; DB 10; Length 1173;
Best Local Similarity 51.4%; Pred. No. 6;
RESULT 409
ID ADO23279 standard; DNA; 1225 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6099.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.6%; Score 39; DB 12; Length 1225;
Best Local Similarity 54.5%; Pred. No. 6.1;
RESULT 410

ID ABX62996 standard; cDNA; 1248 BP.
DE Human activated T cell cDNA #112.
PN US2002137077-A1.
PD 26-SEP-2002.
PA (HOPK/) HOPKINS C M.
PA (PETE/) PETERSON D P.
PA (COCK/) COCKS B G.
PA (HAWK/) HAWKINS P R.
Query Match 2.6%; Score 39; DB 8; Length 1248;
Best Local Similarity 51.4%; Pred. No. 6.2;
RESULT 411
ID ABS55209 standard; cDNA; 1284 BP.
DE Calcium sensitive circularly permuted EYFP (CPEYFP), #2, cDNA.
PN EP1238982-A1.
PD 11-SEP-2002.
PA (RIKE/) RIKEN KK.
Query Match 2.6%; Score 39; DB 6; Length 1284;
Best Local Similarity 48.8%; Pred. No. 6.3;
RESULT 412
ID AAV58275 standard; cDNA; 1929 BP.
DE Fluorescent calmodulin-based calcium indicator cameleon-2 cDNA.
PN WO9840477-A1.
PD 17-SEP-1998.
PA (RBGC) UNIV CALIFORNIA.
Query Match 2.6%; Score 39; DB 2; Length 1929;
Best Local Similarity 48.8%; Pred. No. 7.7;
RESULT 413
ID AAV58277 standard; cDNA; 1929 BP.
DE Fluorescent calmodulin-based calcium indicator cameleon-3 cDNA.
PN WO9840477-A1.
PD 17-SEP-1998.
PA (RBGC) UNIV CALIFORNIA.
Query Match 2.6%; Score 39; DB 2; Length 1929;
Best Local Similarity 48.8%; Pred. No. 7.7;
RESULT 414
ID AAV58276 standard; cDNA; 1958 BP.
DE Fluorescent calmodulin-based calcium indicator cameleon-2nu cDNA.
PN WO9840477-A1.
PD 17-SEP-1998.
PA (RBGC) UNIV CALIFORNIA.
Query Match 2.6%; Score 39; DB 2; Length 1958;
Best Local Similarity 48.8%; Pred. No. 7.7;
RESULT 415
ID AAV58278 standard; cDNA; 1971 BP.
DE Fluorescent calmodulin-based calcium indicator cameleon-3er cDNA.
PN WO9840477-A1.
PD 17-SEP-1998.
PA (RBGC) UNIV CALIFORNIA.
Query Match 2.6%; Score 39; DB 2; Length 1971;
Best Local Similarity 48.8%; Pred. No. 7.8;
RESULT 416
ID AB132789 standard; DNA; 6171 BP.
DE Human immune system associated gene SEQ ID NO: 762.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 2.6%; Score 39; DB 6; Length 6171;
Best Local Similarity 55.6%; Pred. No. 14;
RESULT 417
ID ADE74816 standard; DNA; 137560 BP.
DE Parapoxvirus ovls genome DNA sequence Seg1.
Query Match 2.6%; Score 39; DB 12; Length 137560;
Best Local Similarity 50.3%; Pred. No. 64;
RESULT 418
ID AAA31857 standard; DNA; 278 BP.
DE Plant microsatellite marker #818.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FOREST LTD.
Query Match 2.6%; Score 38.9; DB 3; Length 278;
Best Local Similarity 47.9%; Pred. No. 3.3;
RESULT 419

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ID ABR42401 standard; DNA; 1008 BP.
DE Toxicity modelling related rat gene SEQ ID No 2103.
PN WO200295000-A2.
RESULT 421
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 2.6%; Score 38.8; DB 10; Length 1008;
PD 28-NOV-2002.
DE Renal cell carcinoma differentially expressed gene #35.
PN WO2004048933-A2.
RESULT 420
ID ADP72800 standard; DNA; 1008 BP.
DE Renal toxin progression gene marker #1389.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 2.6%; Score 38.8; DB 12; Length 1008;
PD 03-JAN-2003.
DE Rice gene, SEQ ID 3104.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 2.6%; Score 38.8; DB 8; Length 1650;
RESULT 422
ID ACH89551 standard; DNA; 455 BP.
DE Human genome derived single exon probe #22746.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match
Best Local Similarity 2.6%; Score 38.6; DB 12; Length 455;
RESULT 423
ID ADD3310 standard; DNA; 500 BP.
DE Mouse mitochondrial DNA sequence SEQ ID NO:1081.
PN WO2003020220-A2.
PD 13-MAR-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 2.6%; Score 38.6; DB 10; Length 500;
RESULT 424
ID AAF93577 standard; cDNA; 773 BP.
DE Lung carcinoma cDNA encoding SRT protein SEQ ID 398.
PN WO200107611-A2.
PD 01-FEB-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 38.6; DB 5; Length 773;
RESULT 425
ID AD63193 standard; DNA; 1275 BP.
DE Human zygote arrest 1 (Zarl) DNA sequence #2.
PN WO2003091400-A2.
PD 06-NOV-2003.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (AMHP) WYETH.
Query Match
Best Local Similarity 2.6%; Score 38.6; DB 10; Length 1275;
RESULT 426
ID ADW99174 standard; DNA; 1293 BP.
DE Bacterial source DNA encoding a protease SegID 57.
PN WO2004033668-A2.
PD 22-APR-2004.
PA (DIVE-) DIVERSA CORP.
Query Match
Best Local Similarity 2.6%; Score 38.6; DB 12; Length 1293;
RESULT 427
ID ADA10931 standard; cDNA; 2107 BP.
DE Human cDNA differentially expressed in colon cancer #34.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Query Match
Best Local Similarity 2.6%; Score 38.6; DB 9; Length 2107;
RESULT 428
ID ADP13299 standard; DNA; 2110 BP.
DE Renal cell carcinoma differentially expressed gene #35.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
Query Match
Best Local Similarity 2.6%; Score 38.6; DB 12; Length 2110;
RESULT 429
ID ADR25985 standard; DNA; 2110 BP.
DE Breast cancer prognosis marker #1846.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match
Best Local Similarity 2.6%; Score 38.6; DB 13; Length 2110;
RESULT 430
ID ADP28533 standard; cDNA; 2885 BP.
DE Human scavenger receptor-like cDNA - SED ID 443.
PN WO2003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.6%; Score 38.6; DB 10; Length 2885;
RESULT 431
ID ADS09939 standard; DNA; 2885 BP.
DE Human therapeutic DNA - SEQ ID 176.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NIVE-) NIVELO INC.
Query Match
Best Local Similarity 2.6%; Score 38.6; DB 13; Length 2885;
RESULT 432
ID ABR70004 standard; cDNA; 2945 BP.
DE cDNA encoding human Pro peptide #44.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 38.6; DB 6; Length 2945;
RESULT 433
ID ADA01355 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 38.6; DB 9; Length 2945;
RESULT 434
ID ADA43784 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 38.6; DB 9; Length 2945;
RESULT 435
ID ADA43552 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 38.6; DB 9; Length 2945;
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RESULT 436
ID ADA01227 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 437
ID ADA01111 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 438
ID ADA43668 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 439
ID ADA06930 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 440
ID ADA08418 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 cDNA.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 441
ID ADB99711 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide SEQ ID 87.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 442
ID ADB86994 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 443
ID ADB66149 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 444
ID ADB99827 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide SEQ ID 87.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 445

ID ADB99482 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 cDNA.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 446
ID ADB66033 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 447
ID ADC23431 standard; cDNA; 2945 BP.
DE Human cDNA clone (SeqID 87) encoding the transmembrane PRO protein.
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 448
ID ADC26124 standard; cDNA; 2945 BP.
DE Human PRO28700 cDNA.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 449
ID ADE04951 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 450
ID ADS11257 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 451
ID ADD8188 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 452
ID ADD95483 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 453
ID ADE06413 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 454
ID ADE38188 standard; cDNA; 2945 BP.

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DE Human PRO polynucleotide #44.
PD US2003119120-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 455
ID ADP88304 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PD US2003073189-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 456
ID ADP90885 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PD US2003073188-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 457
ID ADP9440 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PD US2003078401-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 458
ID ADG06533 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PD US2003077742-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 459
ID ADG05484 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PD US2003077741-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 460
ID ADG82485 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PD US2003077744-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 461
ID ADEB1738 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PD US2003104560-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 462
ID ADEB1854 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PD US2003104561-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 463
ID ADEB37712 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PD US2003104564-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 464
ID ADEB37596 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PD US2003104565-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 465
ID ADP95367 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PD US2003138901-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 466
ID ADEB38067 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PD US2003104566-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 467
ID ADEB76156 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PD US2003124665-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 468
ID ADEB39479 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PD US2003119117-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 469
ID ADEB04283 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PD US200309364-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 470
ID ADEB39880 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PD US2003138896-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 471
ID ADEB19745 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PD US2003138903-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 58.1%; Pred. No. 12; Length 2945;
RESULT 472
ID ADEB77323 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PD US2003124666-A1.
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PD 03-JUL-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 473
ID ADE65431 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 474
ID ADE76040 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 475
ID ADE37951 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 476
ID ADE64561 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 477
ID ADE38896 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 478
ID ADE51970 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/cranmembrane polypeptide PRO28700.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 479
ID ADE91001 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/cranmembrane polypeptide PRO28700.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 480
ID ADE38780 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 481
ID ADE37480 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/cranmembrane polypeptide PRO28700.
PN US2003104563-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 482
ID ADE06297 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 483
ID ADE90156 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/cranmembrane polypeptide PRO28700.
PN US2003138804-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 484
ID ADE38664 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 485
ID ADE39595 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 486
ID ADE89200 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 487
ID ADE88667 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 488
ID ADE19861 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 489
ID ADE77439 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/cranmembrane polypeptide PRO28700.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 490
ID ADE65315 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 491
ID ADH39363 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 492
ID ADH38548 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 493
ID ADG11101 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 494
ID ADG10985 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 495
ID ADH31513 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 496
ID ADH38761 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 497
ID ADH29396 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 498
ID ADH23699 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 499
ID ADH27029 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;

Best Local Similarity 58.1%; Pred. No. 12;
RESULT 500
ID ADH38297 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 cDNA.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 501
ID ADH26913 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 502
ID ADH38181 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 cDNA.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 503
ID ADH38877 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 504
ID ADH23815 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 505
ID ADH40190 standard; cDNA; 2945 BP.
DE Human PRO28700 cDNA.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 506
ID ADH40075 standard; cDNA; 2945 BP.
DE Human PRO28700 cDNA.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 507
ID ADH31397 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 508
ID ADH29275 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;

RESULT 509
ID ADH49490 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 CDNA.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 510
ID ADH51954 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 CDNA.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 511
ID ADH49809 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 CDNA.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 512
ID ADH52410 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 CDNA.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 513
ID ADH52526 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 CDNA.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 514
ID ADH58523 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 CDNA.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 515
ID ADH51638 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 CDNA.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 516
ID ADH58399 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 CDNA.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 517
ID ADH13596 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 CDNA.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 518

ID ADK00852 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 519
ID ADI08593 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 520
ID ADM12925 standard; cDNA; 2945 BP.
DE PRO28700 encoding sequence.
PN WO2004024077-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 521
ID ADN05760 standard; cDNA; 2945 BP.
DE Antiporiatic cDNA sequence #1111.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 522
ID ADS82045 standard; DNA; 3608 BP.
DE Human cancer-associated protein coding sequence #3.
PN WO2004035789-A1.
PD 29-APR-2004.
PA (GLDS) IG LIFE SCI LTD.
Query Match 2.6%; Score 38.6; DB 13; Length 3608;
Best Local Similarity 58.1%; Pred. No. 14;
RESULT 523
ID ADJ63204 standard; DNA; 6002 BP.
DE Human zygote arrest 1 (Zarl) DNA sequence #3.
PN WO2003091400-A2.
PD 06-NOV-2003.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (AMHP) WYETH.
Query Match 2.6%; Score 38.6; DB 10; Length 6002;
Best Local Similarity 54.6%; Pred. No. 17;
RESULT 524
ID ACN45200 standard; DNA; 95982 BP.
DE Mouse genomic sequence MCG9440.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 38.6; DB 11; Length 95982;
Best Local Similarity 53.7%; Pred. No. 69;
RESULT 525
ID AAC23266 standard; cDNA; 214 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 27341.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 2.6%; Score 38.4; DB 3; Length 214;
Best Local Similarity 54.5%; Pred. No. 3.8;
RESULT 526
ID ADA58703 standard; cDNA; 233 BP.
DE Maize sucrose synthase EST #347.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIRG N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.6%; Score 38.4; DB 9; Length 233;

Best Local Similarity 52.5%; Pred. No. 3.9;
RESULT 527
ID ADA58629 standard; cDNA; 257 BP.
DE Maize sucrose synthase EST #273.
PN US2003135870-A1.
PD 17-JUL-2003
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LITU/) LIT J.
Query Match 2.6%; Score 38.4; DB 9; Length 257;
Best Local Similarity 53.3%; Pred. No. 4.1;
RESULT 528
ID ADA58619 standard; cDNA; 268 BP.
DE Maize sucrose synthase EST #263.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LITU/) LIT J.
Query Match 2.6%; Score 38.4; DB 9; Length 268;
Best Local Similarity 52.5%; Pred. No. 4.2;
RESULT 529
ID ADA58535 standard; cDNA; 274 BP.
DE Maize sucrose synthase EST #179.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LITU/) LIT J.
Query Match 2.6%; Score 38.4; DB 9; Length 274;
Best Local Similarity 52.5%; Pred. No. 4.3;
RESULT 530
ID ADA58492 standard; cDNA; 286 BP.
DE Maize sucrose synthase EST #136.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LITU/) LIT J.
Query Match 2.6%; Score 38.4; DB 9; Length 286;
Best Local Similarity 52.5%; Pred. No. 4.4;
RESULT 531
ID ADA58422 standard; cDNA; 306 BP.
DE Maize sucrose synthase EST #66.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LITU/) LIT J.
Query Match 2.6%; Score 38.4; DB 9; Length 306;
Best Local Similarity 52.5%; Pred. No. 4.5;
RESULT 532
ID ADA58410 standard; cDNA; 316 BP.
DE Maize sucrose synthase EST #54.
PN US2003135870-A1.
PD 17-JUL-2003
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LITU/) LIT J.
Query Match 2.6%; Score 38.4; DB 9; Length 316;
Best Local Similarity 52.5%; Pred. No. 4.6;
RESULT 533
ID ADA58904 standard; cDNA; 360 BP.
DE Maize sucrose synthase EST #548.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LITU/) LIT J.
Query Match 2.6%; Score 38.4; DB 9; Length 360;
Best Local Similarity 52.5%; Pred. No. 4.9;
RESULT 534
ID ADA5895 standard; cDNA; 383 BP.

DE Maize sucrose synthase EST #539.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LITU/) LIT J.
Query Match 2.6%; Score 38.4; DB 9; Length 383;
Best Local Similarity 52.5%; Pred. No. 5.1;
RESULT 535
ID AD041964 standard; cDNA; 392 BP.
DE Plant cDNA #2964.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDMORTH P.
PA (MOUTG/) MOUTCHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOF/) GOF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICE D.
PA (ZHUT/) ZHU T.
Query Match 2.6%; Score 38.4; DB 12; Length 392;
Best Local Similarity 44.8%; Pred. No. 5.1;
RESULT 536
ID ADA58909 standard; cDNA; 413 BP.
DE Maize sucrose synthase EST #553.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LITU/) LIT J.
Query Match 2.6%; Score 38.4; DB 9; Length 413;
Best Local Similarity 52.5%; Pred. No. 5.2;
RESULT 537
ID ADA58875 standard; cDNA; 425 BP.
DE Maize sucrose synthase EST #519.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LITU/) LIT J.
Query Match 2.6%; Score 38.4; DB 9; Length 425;
Best Local Similarity 52.5%; Pred. No. 5.3;
RESULT 538
ID ADA5893 standard; cDNA; 433 BP.
DE Maize sucrose synthase EST #537.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LITU/) LIT J.
Query Match 2.6%; Score 38.4; DB 9; Length 433;
Best Local Similarity 52.5%; Pred. No. 5.4;
RESULT 539
ID ABN95419 standard; DNA; 442 BP.
DE Gene #1917 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.6%; Score 38.4; DB 6; Length 442;
Best Local Similarity 52.9%; Pred. No. 5.4;
RESULT 540
ID ADA03007 standard; cDNA; 450 BP.
DE Mouse Calm2 carcinoma associated coding sequence, SEQ ID NO.1525.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 38.4; DB 9; Length 450;
Best Local Similarity 49.0%; Pred. No. 5.5;
RESULT 541

ID ADB72745 standard; cDNA; 450 BP.
DE Mouse Calm2 cDNA.
FN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 38.4; DB 10; Length 450;
Best Local Similarity 49.0%; Pred. No. 5.5;
RESULT 542
ID ADC85487 standard; DNA; 450 BP.
DE Mouse Calm2 coding sequence.
FN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 38.4; DB 10; Length 450;
Best Local Similarity 49.0%; Pred. No. 5.5;
RESULT 543
ID ADM74602 standard; DNA; 450 BP.
DE Murine carcinoma associated (Ca) nucleic acid #138.
FN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 2.6%; Score 38.4; DB 12; Length 450;
Best Local Similarity 49.0%; Pred. No. 5.5;
RESULT 544
ID ADA58866 standard; cDNA; 469 BP.
DE Maize sucrose synthase EST #510.
FN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.6%; Score 38.4; DB 9; Length 469;
Best Local Similarity 52.5%; Pred. No. 5.6;
RESULT 545
ID ADA58877 standard; cDNA; 512 BP.
DE Maize sucrose synthase EST #521.
FN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.6%; Score 38.4; DB 9; Length 512;
Best Local Similarity 52.5%; Pred. No. 5.8;
RESULT 546
ID ABO55780 standard; cDNA; 591 BP.
DE Human ovarian antigen HOPKG47 cDNA, SEQ ID NO:1660.
FN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 38.4; DB 6; Length 591;
Best Local Similarity 49.3%; Pred. No. 6.3;
RESULT 547
ID ADC77182 standard; DNA; 595 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2111.
FN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match 2.6%; Score 38.4; DB 10; Length 595;
Best Local Similarity 48.6%; Pred. No. 6.3;
RESULT 548
ID ADC75913 standard; DNA; 595 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 837.
FN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match 2.6%; Score 38.4; DB 10; Length 595;
Best Local Similarity 48.6%; Pred. No. 6.3;
RESULT 549
ID ADK56992 standard; DNA; 595 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4375.
FN WO2003020936-A1.
PD 13-MAR-2003.

PA (DOMC) DOM CHEM CO.
PA (DOMC) DOM AGROSCIENCES LLC.
Query Match 2.6%; Score 38.4; DB 10; Length 595;
Best Local Similarity 48.6%; Pred. No. 6.3;
RESULT 550
ID ADK55191 standard; DNA; 595 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #2574.
FN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
PA (DOMC) DOM AGROSCIENCES LLC.
Query Match 2.6%; Score 38.4; DB 10; Length 595;
Best Local Similarity 48.6%; Pred. No. 6.3;
RESULT 551
ID AAA27845 standard; cDNA; 916 BP.
DE Soybean calmodulin-5 cDNA.
FN EP1018553-A1.
PD 12-JUL-2000.
PA (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
Query Match 2.6%; Score 38.4; DB 3; Length 916;
Best Local Similarity 47.8%; Pred. No. 7.8;
RESULT 552
ID ABA16489 standard; DNA; 3375 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8820.
FN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 38.4; DB 5; Length 3375;
Best Local Similarity 52.5%; Pred. No. 15;
RESULT 553
ID ADC10129 standard; DNA; 5053 BP.
DE Human NOVX polypeptide coding sequence SEQ ID NO: 149.
FN WO2003000842-A2.
PD 03-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.6%; Score 38.4; DB 10; Length 5053;
Best Local Similarity 44.3%; Pred. No. 18;
RESULT 554
ID ABA16488 standard; DNA; 6072 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8819.
FN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 38.4; DB 5; Length 6072;
Best Local Similarity 52.5%; Pred. No. 20;
RESULT 555
ID ACN45034 standard; DNA; 99588 BP.
DE Human genomic sequence hCG1640838.
FN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 38.4; DB 11; Length 99588;
Best Local Similarity 56.2%; Pred. No. 80;
RESULT 556
ID ACN44740 standard; DNA; 101241 BP.
DE Mouse genomic sequence mCG3043.
FN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 38.4; DB 11; Length 101241;
Best Local Similarity 42.1%; Pred. No. 81;
RESULT 557
ID ADA58523 standard; cDNA; 281 BP.
DE Maize sucrose synthase EST #167.
FN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.6%; Score 38.2; DB 9; Length 281;
Best Local Similarity 56.9%; Pred. No. 4.9;
RESULT 558
ID ADA58496 standard; cDNA; 288 BP.

DE Maize sucrose synthase EST #140.
PN US200335870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 9; Length 288;
56.9%; Pred. No. 5;
RESULT 559
ID ADA58458 standard; cDNA; 307 BP.
DE Maize sucrose synthase EST #102.
PN US200335870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 9; Length 307;
56.9%; Pred. No. 5.1;
RESULT 560
ID AAC41022 standard; DNA; 388 BP.
DE Zea mays DNA fragment SEQ ID NO: 30368.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 3; Length 388;
47.3%; Pred. No. 5.8;
RESULT 561
ID ACH87297 standard; DNA; 603 BP.
DE Human genome derived single exon probe #20492.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENR/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 12; Length 603;
49.8%; Pred. No. 7.2;
RESULT 562
ID ADBQ7673 standard; DNA; 747 BP.
DE Novel coding sequence (useful for identifying genetic disorders) #739.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 10; Length 747;
49.8%; Pred. No. 8;
RESULT 563
ID ADJ42633 standard; cDNA; 800 BP.
DE Plant cDNA #3633.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKER D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 12; Length 800;
48.8%; Pred. No. 8.3;
RESULT 564
ID AAO99367 standard; DNA; 1793 BP.
DE S. lividans protease P5-10 gene.
PN WO9517512-A2.
PD 29-JUN-1995.
PA (CANG-) CANGENE CORP.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 2; Length 1793;
48.8%; Pred. No. 12;
RESULT 565
ID ADS49594 standard; cDNA; 2313 BP.
DE Bacterial polynucleotide #4337.
PN US2003333675-A1.

PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 13; Length 2313;
47.0%; Pred. No. 14;
RESULT 566
ID ADS55105 standard; cDNA; 2313 BP.
DE Bacterial polynucleotide #7092.
PN US2003333675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 13; Length 2313;
47.0%; Pred. No. 14;
RESULT 567
ID ACA23764 standard; DNA; 2421 BP.
DE Prokaryotic essential gene #5421.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 8; Length 2421;
47.0%; Pred. No. 14;
RESULT 568
ID ACA25075 standard; DNA; 2421 BP.
DE Prokaryotic essential gene #6732.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 8; Length 2421;
47.0%; Pred. No. 14;
RESULT 569
ID ABV77934 standard; DNA; 3250 BP.
DE Hypoxia-induced protein coding sequence #48.
PN WO200246465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 6; Length 3250;
49.8%; Pred. No. 17;
RESULT 570
ID ADJ44797 standard; cDNA; 3250 BP.
DE Human src biomarker polynucleotide SEQ ID NO:191.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 10; Length 3250;
49.8%; Pred. No. 17;
RESULT 571
ID ADN04316 standard; cDNA; 3250 BP.
DE Antiproliferative cDNA sequence #358.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 12; Length 3250;
49.8%; Pred. No. 17;
RESULT 572
ID ADP24081 standard; cDNA; 3250 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:1259.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 13; Length 3250;
49.8%; Pred. No. 17;
RESULT 573
ID ADK14120 standard; cDNA; 4139 BP.
DE Human autoimmune disorder gene #24.
PN US2003228617-A1.
PD 11-DEC-2003.

PA (UYVA-) UNIV VANDERBILT.
Query Match 2.6%; Score 38.2; DB 12; Length 4139;
Best Local Similarity 49.8%; Pred. No. 19;
RESULT 574
ID AD809821 standard; DNA; 4323 BP.
DE Novel DNA-related contig nucleotide sequence #543.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 38.2; DB 10; Length 4323;
Best Local Similarity 49.8%; Pred. No. 19;
RESULT 575
ID ADP25280 standard; cDNA; 5019 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:2458.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 2.6%; Score 38.2; DB 13; Length 5019;
Best Local Similarity 49.8%; Pred. No. 21;
RESULT 576
ID AAH73300 standard; cDNA; 5552 BP.
DE Human cervical cancer marker nucleic acid 4574.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 38.2; DB 4; Length 5552;
Best Local Similarity 49.8%; Pred. No. 22;
RESULT 577
ID ADU63176 standard; DNA; 7405 BP.
DE Human zygote arrest 1 (Zari) DNA sequence #1.
PN WO2003091400-A2.
PD 06-NOV-2003.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 2.6%; Score 38.2; DB 10; Length 7405;
Best Local Similarity 53.9%; Pred. No. 25;
RESULT 578
ID ACN44936 standard; DNA; 50460 BP.
DE Mouse genomic sequence MCG5738.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 38.2; DB 11; Length 50460;
Best Local Similarity 54.7%; Pred. No. 65;
RESULT 579
ID AAA31969 standard; DNA; 345 BP.
DE Plant microsatellite marker #930.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 2.6%; Score 38; DB 3; Length 345;
Best Local Similarity 49.0%; Pred. No. 6.2;
RESULT 580
ID AAA31680 standard; DNA; 359 BP.
DE Plant microsatellite marker #641.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 2.6%; Score 38; DB 3; Length 359;
Best Local Similarity 49.0%; Pred. No. 6.3;
RESULT 581
ID AAS74660 standard; cDNA; 381 BP.
DE DNA encoding novel human diagnostic protein #10464.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 38; DB 5; Length 381;
Best Local Similarity 56.3%; Pred. No. 6.5;
RESULT 582
ID AAA31454 standard; DNA; 404 BP.
DE Plant microsatellite marker #415.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 2.6%; Score 38; DB 3; Length 404;
Best Local Similarity 49.0%; Pred. No. 6.7;
RESULT 583
ID AAA31708 standard; DNA; 414 BP.
DE Plant microsatellite marker #669.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 2.6%; Score 38; DB 3; Length 414;
Best Local Similarity 49.0%; Pred. No. 6.8;
RESULT 584
ID AB214848 standard; DNA; 450 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2653.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
Query Match 2.6%; Score 38; DB 6; Length 450;
Best Local Similarity 48.6%; Pred. No. 7.1;
RESULT 585
ID ADA68519 standard; DNA; 450 BP.
DE Arabidopsis thaliana gene, SEQ ID 577.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.6%; Score 38; DB 8; Length 450;
Best Local Similarity 48.6%; Pred. No. 7.1;
RESULT 586
ID AAC49319 standard; DNA; 456 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 60710.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.6%; Score 38; DB 3; Length 456;
Best Local Similarity 48.6%; Pred. No. 7.1;
RESULT 587
ID AAC41064 standard; DNA; 501 BP.
DE Zea mays DNA fragment SEQ ID NO: 30519.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.6%; Score 38; DB 3; Length 501;
Best Local Similarity 48.6%; Pred. No. 7.5;
RESULT 588
ID ADC76485 standard; DNA; 560 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1754.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
Query Match 2.6%; Score 38; DB 10; Length 560;
Best Local Similarity 48.6%; Pred. No. 7.9;
RESULT 589
ID ADK55194 standard; DNA; 560 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #2577.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
Query Match 2.6%; Score 38; DB 10; Length 560;
Best Local Similarity 48.6%; Pred. No. 7.9;
RESULT 590
ID ADC77186 standard; DNA; 617 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2115.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
Query Match 2.6%; Score 38; DB 10; Length 617;
Best Local Similarity 48.6%; Pred. No. 8.3;
RESULT 591
ID ADK56996 standard; DNA; 617 BP.

DE Plant DNA sequence which confers altered metabolic characteristic #4379.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
PA (DOMC) DOM AGROSCIENCES LLC.
Query Match 2.6%; Score 38; DB 10; Length 617;
Best Local Similarity 48.6%; Pred. No. 8.3;
RESULT 592
ID AB065708 standard; DNA; 695 BP.
DE Arabidopsis thaliana polynucleotide SEQ ID NO 285.
PN US2002059663-A1.
PD 16-MAY-2002.
PA (GORT/) GORLACH J.
PA (ANYX/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEN A V.
PA (LEDF/) LEDFORD B L.
PA (WOBS/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRICK/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALIE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 2.6%; Score 38; DB 6; Length 695;
Best Local Similarity 48.6%; Pred. No. 8.8;
RESULT 593
ID ABJ32567 standard; DNA; 6907 BP.
DE Human immune system associated gene SEQ ID NO: 540.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 2.6%; Score 38; DB 6; Length 6907;
Best Local Similarity 51.8%; Pred. No. 28;
RESULT 594
ID AAA10594 standard; DNA; 10732 BP.
DE Gene encoding a subunit of cellulose synthase.
PN JP2000060568-A.
PD 29-FEB-2000.
PA (MITU/) MITUNO K.
PA (OUIP) OUI PAPER CO.
Query Match 2.6%; Score 38; DB 3; Length 10732;
Best Local Similarity 13.8%; Pred. No. 34;
RESULT 595
ID ADJ57067 standard; DNA; 13535 BP.
DE Vector plasmid pBS 15.1 hcmv/GFP+not spot for CHO cells.
PN WO2004009823-A1.
PD 29-JAN-2004.
PA (LONZ-) LONZA BIOLOGICS PLC.
Query Match 2.6%; Score 38; DB 12; Length 13535;
Best Local Similarity 56.3%; Pred. No. 38;
RESULT 596
ID ABL68262 standard; DNA; 62944 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6599.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.6%; Score 38; DB 6; Length 62944;
Best Local Similarity 60.8%; Pred. No. 83;
RESULT 597
ID AB166947 standard; DNA; 62944 BP.
DE Lung cancer related gene sequence SEQ ID NO:5284.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.6%; Score 38; DB 6; Length 62944;

Best Local Similarity 60.8%; Pred. No. 83;
RESULT 598
ID ABD32881 standard; DNA; 83943 BP.
DE Mouse cancer-associated genomic DNA MD18-006.
PN WO2004074520-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.6%; Score 38; DB 13; Length 83943;
Best Local Similarity 54.2%; Pred. No. 95;
RESULT 599
ID ABD33157 standard; DNA; 109559 BP.
DE Murine cancer-associated (CA) gene MD07-021.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.6%; Score 38; DB 13; Length 109559;
Best Local Similarity 56.3%; Pred. No. 1.1e+02;
RESULT 600
Query Match 2.6%; Score 38; DB 12; Length 110000;
Best Local Similarity 59.1%; Pred. No. 1.1e+02;
RESULT 601
ID ADA58658 standard; cDNA; 242 BP.
DE Maize sucrose synthase EST #302.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIRI N.
PA (FISH/) FISHER D K.
PA (LITU/) LITU J.
Query Match 2.5%; Score 37.8; DB 9; Length 242;
Best Local Similarity 52.9%; Pred. No. 5.9;
RESULT 602
ID ACH18237 standard; cDNA; 391 BP.
DE Human adult heart cDNA #2551.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.5%; Score 37.8; DB 9; Length 391;
Best Local Similarity 49.3%; Pred. No. 7.5;
RESULT 603
ID ACH24579 standard; cDNA; 449 BP.
DE Human adult ovary cDNA #2959.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.5%; Score 37.8; DB 9; Length 449;
Best Local Similarity 49.3%; Pred. No. 8;
RESULT 604
ID ACH28432 standard; cDNA; 455 BP.
DE Human adult ovary cDNA #6812.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.5%; Score 37.8; DB 9; Length 455;
Best Local Similarity 49.3%; Pred. No. 8.1;
RESULT 605
ID ACH17443 standard; cDNA; 459 BP.
DE Human adult heart cDNA #1757.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.5%; Score 37.8; DB 9; Length 459;
Best Local Similarity 49.3%; Pred. No. 8.1;
RESULT 606
ID ACH16072 standard; cDNA; 465 BP.
DE Human adult heart cDNA #386.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.5%; Score 37.8; DB 9; Length 465;
Best Local Similarity 49.3%; Pred. No. 8.2;
RESULT 607
ID ACH26804 standard; cDNA; 478 BP.
DE Human adult ovary cDNA #5184.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.5%; Score 37.8; DB 9; Length 478;
Best Local Similarity 49.3%; Pred. No. 8.3;
RESULT 608
ID AAH81659 standard; DNA; 557 BP.
DE Human differential transcription-associated cDNA SEQ ID 168.
PN WO200457058-A2.
PD 09-AUG-2001.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 2.5%; Score 37.8; DB 5; Length 557;
Best Local Similarity 49.3%; Pred. No. 8.9;
RESULT 609
ID ACN40763 standard; cDNA; 1116 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326826, SEQ ID NO:5754.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 37.8; DB 13; Length 1116;
Best Local Similarity 49.3%; Pred. No. 13;
RESULT 610
ID ADK70382 standard; cDNA; 1160 BP.
DE Respiratory disease differentially expressed cDNA #118.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 2.5%; Score 37.8; DB 13; Length 1160;
Best Local Similarity 49.3%; Pred. No. 13;
RESULT 611
ID AAS45021 standard; cDNA; 1199 BP.
DE cDNA encoding novel human secretory protein. Seq ID No 102.
PN WO200166889-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.5%; Score 37.8; DB 5; Length 1199;
Best Local Similarity 49.3%; Pred. No. 13;
RESULT 612
ID AA193806 standard; cDNA; 1306 BP.
DE Human polynucleotide SEQ ID NO 13866.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.5%; Score 37.8; DB 4; Length 1306;
Best Local Similarity 49.3%; Pred. No. 14;
RESULT 613
ID AAD56207 standard; cDNA; 1312 BP.
DE Human cDNA differentially expressed in MYCN activated cells Segid 13.
PN US2003119009-A1.

PD 26-JUN-2003.
PA (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PLON/) PLON S E.
PA (SHOH/) SHOHEI J M.
Query Match 2.5%; Score 37.8; DB 10; Length 1312;
Best Local Similarity 49.3%; Pred. No. 14;
RESULT 614
ID ACA26293 standard; DNA; 1404 BP.
DE Prokaryotic essential gene #7950.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.5%; Score 37.8; DB 8; Length 1404;
Best Local Similarity 52.2%; Pred. No. 14;
RESULT 615
ID ADA71195 standard; DNA; 1839 BP.
DE Rice gene, SEQ ID 4518.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 37.8; DB 8; Length 1839;
Best Local Similarity 50.3%; Pred. No. 16;
RESULT 616
ID ACN90405 standard; DNA; 3397 BP.
DE Breast cancer related marker, seq id 11555.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILENNIUM PHARM INC.
Query Match 2.5%; Score 37.8; DB 11; Length 3397;
Best Local Similarity 49.3%; Pred. No. 22;
RESULT 617
ID AAO65476 standard; DNA; 3682 BP.
DE Human beta-3 adrenergic receptor gene.
PN EP600136-A1.
PD 08-JUN-1994.
PA (CNRS) CNRS NAT RECH SCI.
Query Match 2.5%; Score 37.8; DB 2; Length 3682;
Best Local Similarity 52.9%; Pred. No. 23;
RESULT 618
ID ABO8185 standard; cDNA; 4911 BP.
DE Human kinesin motor protein HskIf21b coding sequence.
PN US6426193-B1.
PD 30-JUL-2002.
PA (CYTO-) CYTOKINETICS INC.
Query Match 2.5%; Score 37.8; DB 6; Length 4911;
Best Local Similarity 44.0%; Pred. No. 26;
RESULT 619
ID ABR52651 standard; DNA; 4911 BP.
DE DNA encoding human kinesin motor protein HskIf21b.
PN US6383796-B1.
PD 07-MAY-2002.
PA (CYTO-) CYTOKINETICS INC.
Query Match 2.5%; Score 37.8; DB 6; Length 4911;
Best Local Similarity 44.0%; Pred. No. 26;
RESULT 620
ID ABS7218 standard; DNA; 4911 BP.
DE Human kinesin-like protein, HskIf21b, gene.
PN US6455293-B1.
PD 24-SEP-2002.
PA (CYTO-) CYTOKINETICS INC.
Query Match 2.5%; Score 37.8; DB 10; Length 4911;
Best Local Similarity 44.0%; Pred. No. 26;
RESULT 621
ID ACC47237 standard; cDNA; 5197 BP.
DE Human SCAP encoding cDNA-Incyte Id. 7290157CBL.
PN WO2003008625-A2.
PD 30-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.5%; Score 37.8; DB 8; Length 5197;
Best Local Similarity 44.0%; Pred. No. 27;
RESULT 622
ID ABX11086 standard; DNA; 4299 BP.

DE Human ribosomal RNA (rRNA) gene.
PN US2002160410-A1.
PD 31-OCT-2002.
PA (HADL/) HADLACZKY G.
PA (SZAL/) SZALAY A A.
Query Match 2.5%; Score 37.8; DB 8; Length 42999;
Best Local Similarity 45.3%; Pred. No. 78;
RESULT 623
ID ADA02933 standard; DNA; 96599 BP.
DE Mouse Braf carcinoma associated gene, SEQ ID NO.1451.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 37.8; DB 9; Length 96599;
Best Local Similarity 54.7%; Pred. No. 1.2e+02;
RESULT 624
ID ADB72671 standard; DNA; 96599 BP.
DE Mouse Braf gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 37.8; DB 10; Length 96599;
Best Local Similarity 54.7%; Pred. No. 1.2e+02;
RESULT 625
ID ADC85413 standard; DNA; 96599 BP.
DE Mouse Braf genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 37.8; DB 10; Length 96599;
Best Local Similarity 54.7%; Pred. No. 1.2e+02;
RESULT 626
ID ADM74528 standard; DNA; 96599 BP.
DE Murine carcinoma associated (CA) nucleic acid #100.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 2.5%; Score 37.8; DB 12; Length 96599;
Best Local Similarity 54.7%; Pred. No. 1.2e+02;
RESULT 627
ID ADC77195 standard; DNA; 526 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2124.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC-) DOW CHEM CO.
Query Match 2.5%; Score 37.6; DB 10; Length 526;
Best Local Similarity 47.5%; Pred. No. 9.9;
RESULT 628
ID ADC75911 standard; DNA; 526 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 835.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC-) DOW CHEM CO.
Query Match 2.5%; Score 37.6; DB 10; Length 526;
Best Local Similarity 47.5%; Pred. No. 9.9;
RESULT 629
ID ADS7005 standard; DNA; 526 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4388.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC-) DOW CHEM CO.
Query Match 2.5%; Score 37.6; DB 10; Length 526;
Best Local Similarity 47.5%; Pred. No. 9.9;
RESULT 630
ID ADS5189 standard; DNA; 526 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #2572.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC-) DOW CHEM CO.
Query Match 2.5%; Score 37.6; DB 10; Length 526;
Best Local Similarity 47.5%; Pred. No. 9.9;
RESULT 631
ID ADS5189 standard; DNA; 526 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #2572.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC-) DOW CHEM CO.
Query Match 2.5%; Score 37.6; DB 10; Length 526;
Best Local Similarity 47.5%; Pred. No. 9.9;

Best Local Similarity 47.5%; Pred. No. 9.9;
RESULT 631
ID ACU19198 standard; DNA; 604 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9189.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.6; DB 9; Length 604;
Best Local Similarity 49.0%; Pred. No. 11;
RESULT 632
ID ACU19212 standard; DNA; 708 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9203.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.6; DB 9; Length 708;
Best Local Similarity 49.0%; Pred. No. 11;
RESULT 633
ID ACU19226 standard; DNA; 711 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9217.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.6; DB 9; Length 711;
Best Local Similarity 49.0%; Pred. No. 11;
RESULT 634
ID ADS51517 standard; cDNA; 799 BP.
DE Bacterial polynucleotide #6260.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.5%; Score 37.6; DB 13; Length 799;
Best Local Similarity 47.1%; Pred. No. 12;
RESULT 635
ID ABD06635 standard; DNA; 1344 BP.
DE Pseudomonas aeruginosa polynucleotide #5239.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37.6; DB 11; Length 1344;
Best Local Similarity 51.2%; Pred. No. 16;
RESULT 636
ID ABD06577 standard; DNA; 1794 BP.
DE Pseudomonas aeruginosa polynucleotide #5181.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37.6; DB 11; Length 1794;
Best Local Similarity 51.2%; Pred. No. 18;
RESULT 637
ID ABD06690 standard; DNA; 2547 BP.
DE Pseudomonas aeruginosa polynucleotide #5294.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37.6; DB 11; Length 2547;
Best Local Similarity 51.2%; Pred. No. 22;
RESULT 638
ID ADD00948 standard; cDNA; 4749 BP.
DE Human jagged 2 encoding cDNA SEQ ID NO.3.
PN WO2003077848-A2.
PD 25-SEP-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.5%; Score 37.6; DB 10; Length 4749;
Best Local Similarity 52.6%; Pred. No. 30;
RESULT 639
ID ADH62908 standard; DNA; 4749 BP.
DE Human jagged 2 DNA #1.
PN US2003170636-A1.

PD 11-SEP-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.5%; Score 37.6; DB 10; Length 4749;
Best Local Similarity 52.6%; Pred. No. 30;
RESULT 640
ID ADH57063 standard; DNA; 4749 BP.
DE DNA of a human Jagged 2 RNA sequence Segid 3.
PN US2003207839-A1.
PD 06-NOV-2003.
PA (FREI/) FREIER S. M.
Query Match 2.5%; Score 37.6; DB 10; Length 4749;
Best Local Similarity 52.6%; Pred. No. 30;
RESULT 641
ID ADD00955 standard; cDNA; 4974 BP.
DE Human Jagged 2 encoding cDNA SEQ ID NO:10.
PN WO2003077848-A2.
PD 25-SEP-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.5%; Score 37.6; DB 10; Length 4974;
Best Local Similarity 52.6%; Pred. No. 30;
RESULT 642
ID ADH62915 standard; DNA; 4974 BP.
DE Human Jagged 2 DNA #2.
PN US2003170636-A1.
PD 11-SEP-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.5%; Score 37.6; DB 10; Length 4974;
Best Local Similarity 52.6%; Pred. No. 30;
RESULT 643
ID ADH57070 standard; DNA; 4974 BP.
DE DNA of a human Jagged 2 RNA sequence Segid 10.
PN US2003207839-A1.
PD 06-NOV-2003.
PA (FREI/) FREIER S. M.
Query Match 2.5%; Score 37.6; DB 10; Length 4974;
Best Local Similarity 52.6%; Pred. No. 30;
RESULT 644
ID ADN03615 standard; cDNA; 5077 BP.
DE Antipeptidic cDNA sequence #5.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GEITH) GENENTECH INC.
Query Match 2.5%; Score 37.6; DB 12; Length 5077;
Best Local Similarity 52.6%; Pred. No. 31;
RESULT 645
ID ADR83400 standard; DNA; 5077 BP.
DE Human Jagged 2 DNA, target gene of miRNA.
PN WO2004076622-A2.
PD 10-SEP-2004.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 2.5%; Score 37.6; DB 13; Length 5077;
Best Local Similarity 52.6%; Pred. No. 31;
RESULT 646
ID ADR73469 standard; DNA; 5077 BP.
DE Human Jagged 2, JAG2, gene.
PN WO2004076682-A2.
PD 10-SEP-2004.
PA (SURR-) SURROMED INC.
Query Match 2.5%; Score 37.6; DB 13; Length 5077;
Best Local Similarity 52.6%; Pred. No. 31;
RESULT 647
ID ABD32670 standard; DNA; 111331 BP.
DE Mouse cancer-associated genomic DNA MD17-083.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 37.6; DB 13; Length 111331;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 648
ID ABD32610 standard; DNA; 115780 BP.
DE Mouse cancer-associated genomic DNA MD12-017.
PN WO2004074320-A2.
PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 37.6; DB 13; Length 115780;
Best Local Similarity 46.2%; Pred. No. 1.4e+02;
RESULT 649
ID ADD50650 standard; DNA; 175590 BP.
DE BAC sequence #1 containing hCHT DNA.
PN US2003114399-A1.
PD 19-JUN-2003.
PA (BLAK/) BLAKELY R D.
PA (APPA/) APPASUNDARAM S.
PA (FERG/) FERGUSON S.
Query Match 2.5%; Score 37.6; DB 10; Length 175590;
Best Local Similarity 51.8%; Pred. No. 1.8e+02;
RESULT 650
ID ACN44514 standard; DNA; 256493 BP.
DE Human genomic sequence hCG17361.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 37.6; DB 11; Length 256493;
Best Local Similarity 46.0%; Pred. No. 2.1e+02;
RESULT 651
ID ADH00876 standard; DNA; 327 BP.
DE Kidney disease-associated gene-related mouse DNA sequence Segid2005.
PN WO2003091427-A1.
PD 06-NOV-2003.
PA (KANSAI) KANSAI TECHNOLOGY LICENSING ORG CO LTD.
Query Match 2.5%; Score 37.4; DB 12; Length 327;
Best Local Similarity 58.6%; Pred. No. 8.9;
RESULT 652
ID ADB59059 standard; DNA; 511 BP.
DE Toxicity-related gene, SEQ ID 4085.
PN WO2003064524-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.5%; Score 37.4; DB 10; Length 511;
Best Local Similarity 47.0%; Pred. No. 11;
RESULT 653
ID ADB53812 standard; DNA; 511 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4354.
PN WO2003065593-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.5%; Score 37.4; DB 10; Length 511;
Best Local Similarity 47.0%; Pred. No. 11;
RESULT 654
ID ADB68842 standard; DNA; 536 BP.
DE Minority luxI consensus sequence DNA 14.
PN WO2003057802-A2.
PD 17-JUL-2003.
PA (FRANU) FRADUNHOFER USA INC.
Query Match 2.5%; Score 37.4; DB 10; Length 536;
Best Local Similarity 13.4%; Pred. No. 11;
RESULT 655
ID ACU19217 standard; DNA; 559 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9208.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 559;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 656
ID ACU19219 standard; DNA; 593 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9210.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 593;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 657
ID ACU19199 standard; DNA; 593 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9190.
PN WO2003057877-A1.

PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 593;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 658
ID ACL19225 standard; DNA; 607 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9216.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 607;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 659
ID ACL19201 standard; DNA; 608 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9192.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 608;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 660
ID ACL19204 standard; DNA; 621 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9195.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 621;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 661
ID ACL19206 standard; DNA; 623 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9197.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 623;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 662
ID ACL19208 standard; DNA; 629 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9199.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 629;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 663
ID ACL19205 standard; DNA; 633 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9196.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 633;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 664
ID ACL19221 standard; DNA; 664 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9212.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 664;
Best Local Similarity 49.2%; Pred. No. 13;
RESULT 665
ID ACL19213 standard; DNA; 669 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9204.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 669;
Best Local Similarity 49.2%; Pred. No. 13;
RESULT 666
ID ACL19216 standard; DNA; 670 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9207.
PN WO2003057877-A1.
PD 17-JUL-2003.

PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 670;
Best Local Similarity 49.2%; Pred. No. 13;
RESULT 667
ID ACL19220 standard; DNA; 696 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9211.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 696;
Best Local Similarity 49.2%; Pred. No. 13;
RESULT 668
ID ACL19223 standard; DNA; 710 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9214.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 710;
Best Local Similarity 49.2%; Pred. No. 13;
RESULT 669
ID ADP29084 standard; DNA; 1044 BP.
DE Human secreted protein encoding sequence SEQ ID #1082.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.5%; Score 37.4; DB 12; Length 1044;
Best Local Similarity 47.6%; Pred. No. 16;
RESULT 670
ID ADJ39564 standard; cDNA; 1930 BP.
DE Plant cDNA #564.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUNG/) MOUNGHER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOF/) GOF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKS D.
PA (ZHU/) ZHU T.
Query Match 2.5%; Score 37.4; DB 12; Length 1930;
Best Local Similarity 53.8%; Pred. No. 21;
RESULT 671
ID ABX72264 standard; cDNA; 2209 BP.
DE Human NOVX polynucleotide #95.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.5%; Score 37.4; DB 8; Length 2209;
Best Local Similarity 47.6%; Pred. No. 23;
RESULT 672
ID AAD34007 standard; cDNA; 2258 BP.
DE Human HIPHUM 0000029 protein encoding cDNA.
PN GB2365432-A.
PD 20-FEB-2002.
PA (GLAX) GLAXO GROUP LTD.
Query Match 2.5%; Score 37.4; DB 6; Length 2258;
Best Local Similarity 47.6%; Pred. No. 23;
RESULT 673
ID ADG63696 standard; cDNA; 2336 BP.
DE Novel human cDNA sequence #857.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) REAS ASSOC BIOTECHNOLOGY.
Query Match 2.5%; Score 37.4; DB 12; Length 2336;
Best Local Similarity 53.8%; Pred. No. 24;
RESULT 674
ID ACF79238 standard; cDNA; 2388 BP.
DE Human neurotransmitter transporter variant polynucleotide.
PN WO2003059947-A1.

PD 24-JUL-2003.
PA (FARB) BAYER AG.
Query Match 2.5%; Score 37.4; DB 10; Length 2388;
Best Local Similarity 47.6%; Pred. No. 24;
RESULT 675
ID AC679237 standard; cDNA; 2432 BP.
DE Human neurotensin transporter polynucleotide.
PN WO2003059947-A1.
PD 24-JUL-2003.
PA (FARB) BAYER AG.
Query Match 2.5%; Score 37.4; DB 10; Length 2432;
Best Local Similarity 47.6%; Pred. No. 24;
RESULT 676
ID AAT09866 standard; cDNA; 2486 BP.
DE Human neurotensin transporter protein cDNA.
PN WO9531539-A1.
PD 23-NOV-1995.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 37.4; DB 2; Length 2486;
Best Local Similarity 47.6%; Pred. No. 24;
RESULT 677
ID ACC43635 standard; DNA; 2490 BP.
DE Nucleotide sequence of the human F-box polypeptide FBW3B.
PN FR2828208-A1.
PD 07-FEB-2003.
PA (CYTO-) CYTOMICS SYSTEMS SA.
Query Match 2.5%; Score 37.4; DB 8; Length 2490;
Best Local Similarity 58.6%; Pred. No. 24;
RESULT 678
ID ADG97161 standard; DNA; 107432 BP.
DE Mouse cancer associated sequence MD08-009, SEQ ID 137.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 37.4; DB 12; Length 107432;
Best Local Similarity 55.9%; Pred. No. 1.6e+02;
RESULT 679
ID AA184688 standard; cDNA; 439 BP.
DE Human polynucleotide SEQ ID NO 4748.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.5%; Score 37.2; DB 4; Length 439;
Best Local Similarity 50.3%; Pred. No. 12;
RESULT 680
ID AAC56719 standard; DNA; 476 BP.
DE Eucalyptus grandis transcription factor DNA sequence #590.
PN WO2000053724-A2.
PD 14-SEP-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 2.5%; Score 37.2; DB 3; Length 476;
Best Local Similarity 49.0%; Pred. No. 12;
RESULT 681
ID ABD17057 standard; DNA; 864 BP.
DE Pseudomonas aeruginosa polynucleotide #15661.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37.2; DB 11; Length 864;
Best Local Similarity 44.7%; Pred. No. 16;
RESULT 682
ID ABD17123 standard; DNA; 1428 BP.
DE Pseudomonas aeruginosa polynucleotide #15727.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37.2; DB 11; Length 1428;
Best Local Similarity 44.7%; Pred. No. 21;
RESULT 683
ID ABK92063 standard; DNA; 1782 BP.
DE DNA encoding novel transmembrane segment 2-like protein #4.
PN WO200229058-A2.

PD 11-APR-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.5%; Score 37.2; DB 6; Length 1782;
Best Local Similarity 54.3%; Pred. No. 23;
RESULT 684
ID ADG47785 standard; DNA; 1881 BP.
DE Human NOV45D gene SEQ ID NO:147.
PN WO2003076642-A2.
PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.5%; Score 37.2; DB 10; Length 1881;
Best Local Similarity 54.3%; Pred. No. 24;
RESULT 685
ID ADH41902 standard; DNA; 1881 BP.
DE Novel human nucleic acid NOV36f.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.5%; Score 37.2; DB 12; Length 1881;
Best Local Similarity 54.3%; Pred. No. 24;
RESULT 686
ID ADU79055 standard; DNA; 1881 BP.
DE Human NOVX protein NOV45D gene sequence.
PN US2004014053-A1.
PD 22-JAN-2004.
PA (ZERR-) ZERRHISEN B D.
PA (PAT/) PATTRAJAN M.
PA (KEKU/) KEKUDA R.
PA (MILL/) MILLER C E.
PA (RIEG/) RIEGER D K.
PA (PENNA/) PENNA C E A.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (BERG/) BERGHS C.
PA (ZHON/) ZHONG M.
PA (CASW/) CASMAN S J.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDIG F L.
PA (PADI/) PADIGARU M.
PA (SMIT/) SMITHSON G.
PA (JIMW/) JI W.
PA (GORM/) GORMAN L.
PA (VERN/) VERNET C A M.
PA (LEIT/) LEITE M W.
PA (GROX/) GUO X S.
PA (ANDE/) ANDERSON D W.
PA (SPYT/) SPYTEK K A.
PA (GERL/) GERLACH V.
PA (BURG/) BURGESS C E.
PA (KHRA/) KHRAMTSOV N V.
PA (ORTT/) ORT T.
PA (ELLE/) ELLERMAN K.
PA (RAST/) RASTELLI L.
PA (AGEE/) AGE M L.
PA (CHAU/) CHAUDHURI A.
PA (CHAN/) CHANT J S.
PA (DIEP/) DIPIPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A J.
PA (GANG/) GANGOLLI E A.
PA (GIOT/) GIOT L.
PA (OOIC/) OOI C E.
PA (ROTH/) ROTHENBERG M E.
PA (SPAD/) SPADERNA S K.
PA (HJAL/) HJALT T.
PA (LIUX/) LIU X.
PA (TAUP/) TAUPIER R J.
PA (CATY/) CATTERTON E.
PA (SHEN/) SHENDY S G.
Query Match 2.5%; Score 37.2; DB 12; Length 1881;
Best Local Similarity 54.3%; Pred. No. 24;
RESULT 687
ID ABD17019 standard; DNA; 2679 BP.

DE Pseudomonas aeruginosa polynucleotide #15623.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37.2; DB 11; Length 2679;
Best Local Similarity 44.7%; Pred. No. 29;
RESULT 688
ID AAF32508 standard; cDNA; 5068 BP.
DE Human male enhanced antigen-2 (MEA-2) nucleotide sequence SEQ ID NO.1.
PN JP2000316580-A.
PD 21-NOV-2000.
PA (ITOH-) ITO HAM KK.
Query Match 2.5%; Score 37.2; DB 5; Length 5068;
Best Local Similarity 48.2%; Pred. No. 39;
RESULT 689
ID AAL37335 standard; DNA; 7791 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3700.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMAN-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 37.2; DB 4; Length 7791;
Best Local Similarity 51.2%; Pred. No. 49;
RESULT 690
ID ABX60323 standard; cDNA; 7791 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2667.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.5%; Score 37.2; DB 8; Length 7791;
Best Local Similarity 51.2%; Pred. No. 49;
RESULT 691
ID ADJ31073 standard; DNA; 7791 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3700.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 37.2; DB 12; Length 7791;
Best Local Similarity 51.2%; Pred. No. 49;
RESULT 692
ID ABD33078 standard; DNA; 21457 BP.
DE Murine cancer-associated (CA) gene MD07-003.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 37.2; DB 13; Length 21457;
Best Local Similarity 56.6%; Pred. No. 81;
RESULT 693
ID ACC60906 standard; DNA; 43064 BP.
DE Human CYP1A2 gene SEQ ID NO:76.
PN WO2003014387-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 37.2; DB 8; Length 43064;
Best Local Similarity 50.6%; Pred. No. 1.1e+02;
RESULT 694
ID AAL51405 standard; DNA; 80959 BP.
DE Human secreted protein gene sequence. SEQ ID NO 3.
Query Match 2.5%; Score 37.2; DB 8; Length 80959;
Best Local Similarity 48.6%; Pred. No. 1.6e+02;
RESULT 695
ID ACN45182 standard; DNA; 261817 BP.
DE Human genomic sequence hCG14925.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 37.2; DB 11; Length 261817;
Best Local Similarity 53.4%; Pred. No. 2.8e+02;
RESULT 696
ID ADA58478 standard; cDNA; 289 BP.
DE Maize sucrose synthase EST #122.
PN US2003135870-A1.

PD 17-JUL-2003.
PA (CHRI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIUV/) LIU J.
Query Match 2.5%; Score 37; DB 9; Length 289;
Best Local Similarity 53.0%; Pred. No. 11;
RESULT 697
ID ABD09208 standard; DNA; 429 BP.
DE Pseudomonas aeruginosa polynucleotide #7812.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37; DB 11; Length 429;
Best Local Similarity 45.6%; Pred. No. 13;
RESULT 698
ID ACL19215 standard; DNA; 439 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9206.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37; DB 9; Length 439;
Best Local Similarity 48.7%; Pred. No. 13;
RESULT 699
ID AAC43517 standard; DNA; 549 BP.
DE Zea mays DNA fragment SEQ ID NO: 39522.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.5%; Score 37; DB 3; Length 549;
Best Local Similarity 54.9%; Pred. No. 15;
RESULT 700
ID ADR38458 standard; DNA; 1002 BP.
DE Streptomyces sp KNR269 aldehyde oxidase beta subunit DNA Seq 5.
PN WO2004072281-A1.
PD 26-AUG-2004.
PA (KANF/) KANEKA CORP.
Query Match 2.5%; Score 37; DB 13; Length 1002;
Best Local Similarity 48.0%; Pred. No. 20;
RESULT 701
ID ABX65499 standard; DNA; 1024 BP.
DE Helicobacter pylori selected interacting domain (SID) DNA #98.
PN WO200286501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP) INST PASTEUR.
Query Match 2.5%; Score 37; DB 6; Length 1024;
Best Local Similarity 56.0%; Pred. No. 20;
RESULT 702
ID ACA23920 standard; DNA; 1092 BP.
DE Prokaryotic essential gene #5577.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.5%; Score 37; DB 8; Length 1092;
Best Local Similarity 53.9%; Pred. No. 21;
RESULT 703
ID ABD08997 standard; DNA; 1434 BP.
DE Pseudomonas aeruginosa polynucleotide #7601.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37; DB 11; Length 1434;
Best Local Similarity 45.6%; Pred. No. 24;
RESULT 704
ID ABD09346 standard; DNA; 1626 BP.
DE Pseudomonas aeruginosa polynucleotide #7950.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37; DB 11; Length 1626;
Best Local Similarity 45.6%; Pred. No. 25;
RESULT 705
ID AAF85145 standard; DNA; 1800 BP.
DE Nucleotide sequence of the relaxase vlrD2.

PN WO200130810-A2.
PD 03-MAY-2001.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 2.5%; Score 37; DB 4; Length 1800;
Best Local Similarity 56.0%; Pred. No. 27;
RESULT 706
ID AAF85146 standard; DNA; 1800 BP.
DE Nucleotide sequence of the relaxase vlrD2.
PN WO200130810-A2.
PD 03-MAY-2001.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 2.5%; Score 37; DB 4; Length 1800;
Best Local Similarity 56.0%; Pred. No. 27;
RESULT 707
ID AAX14387 standard; DNA; 1934 BP.
DE H. pylori GHPD 504 gene.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 37; DB 2; Length 1934;
Best Local Similarity 56.0%; Pred. No. 28;
RESULT 708
ID ABD08927 standard; DNA; 2169 BP.
DE Pseudomonas aeruginosa polynucleotide #7531.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37; DB 11; Length 2169;
Best Local Similarity 45.6%; Pred. No. 29;
RESULT 709
ID ABV74815 standard; DNA; 3644 BP.
DE Human scavenger receptor class A protein ADSE coding sequence #2.
PN WO200264770-A1.
PD 22-AUG-2002.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 2.5%; Score 37; DB 8; Length 3644;
Best Local Similarity 57.3%; Pred. No. 38;
RESULT 710
ID ADD08990 standard; DNA; 44442 BP.
DE Human pancreatic genomic DNA SEQ ID NO:15.
PN WO2003085377-A2.
PD 16-OCT-2003.
PA (AMHP) WYETH.
Query Match 2.5%; Score 37; DB 10; Length 44442;
Best Local Similarity 62.4%; Pred. No. 1.3e+02;
RESULT 711
ID ADM80676 standard; DNA; 46374 BP.
DE Human USH3A gene genomic sequence SegID5.
PN WO2003097685-A1.
PD 27-NOV-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 2.5%; Score 37; DB 12; Length 46374;
Best Local Similarity 49.7%; Pred. No. 1.4e+02;
RESULT 712
ID ABS52847 standard; DNA; 90541 BP.
DE Human SR protein-specific kinase 2, SRPK2, genomic DNA.
PN US2002094560-A1.
PD 18-JUL-2002.
PA (ABUT/) ABU-THREIDER J.
PA (GONG/) GONG F.
PA (KETC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 2.5%; Score 37; DB 6; Length 90541;
Best Local Similarity 52.2%; Pred. No. 1.9e+02;
RESULT 713
ID ADJ37690 standard; DNA; 90541 BP.
DE Human kinase genomic DNA.
PN US2003175927-A1.
PD 18-SEP-2003.
PA (APPL-) APPLERA CORP.
Query Match 2.5%; Score 37; DB 10; Length 90541;

Best Local Similarity 52.2%; Pred. No. 1.9e+02;
RESULT 714
ID ADJ31219 standard; DNA; 90541 BP.
DE Human SRPK2 kinase protein alternative splice form genomic DNA.
PN US2004157297-A1.
PD 12-AUG-2004.
PA (APPL-) APPLERA CORP.
Query Match 2.5%; Score 37; DB 13; Length 90541;
Best Local Similarity 52.2%; Pred. No. 1.9e+02;
RESULT 715
ID AAH88704 standard; DNA; 160755 BP.
DE Human DNA sequence SEQ ID 544.
PN WO200151659-A2.
PD 19-JUL-2001.
PA (GRST) GENSET.
Query Match 2.5%; Score 37; DB 4; Length 160755;
Best Local Similarity 39.7%; Pred. No. 2.5e+02;
RESULT 716
ID ADA58682 standard; cDNA; 262 BP.
DE Maize sucrose synthase EST #326.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHRI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.5%; Score 36.8; DB 9; Length 262;
Best Local Similarity 51.9%; Pred. No. 12;
RESULT 717
ID AAC36202 standard; DNA; 508 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 12916.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.5%; Score 36.8; DB 3; Length 508;
Best Local Similarity 54.4%; Pred. No. 16;
RESULT 718
ID ACH78156 standard; DNA; 518 BP.
DE Human genome derived single exon probe #11351.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 2.5%; Score 36.8; DB 12; Length 518;
Best Local Similarity 50.6%; Pred. No. 16;
RESULT 719
ID ACH78575 standard; DNA; 518 BP.
DE Human genome derived single exon probe #11770.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 2.5%; Score 36.8; DB 12; Length 518;
Best Local Similarity 50.6%; Pred. No. 16;
RESULT 720
ID ABG6069 standard; DNA; 636 BP.
DE Arabidopsis thaliana polynucleotide SEQ ID NO 646.
PN US2002059663-A1.
PD 16-MAY-2002.
PA (GORT/) GORTLACH J.
PA (ANYV/) AN Y.
PA (HAMT/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYV/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.

PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALIE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 2.5%; Score 36.8; DB 6; Length 636;
Best Local Similarity 49.0%; Pred. No. 18;
RESULT 721
ID ABD03162 standard; DNA; 873 BP.
DE Pseudomonas aeruginosa polynucleotide #1766.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 36.8; DB 11; Length 873;
Best Local Similarity 54.4%; Pred. No. 21;
RESULT 722
ID ABD03306 standard; DNA; 2169 BP.
DE Pseudomonas aeruginosa polynucleotide #1910.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 36.8; DB 11; Length 2169;
Best Local Similarity 54.4%; Pred. No. 33;
RESULT 723
ID AAF02218 standard; DNA; 2796 BP.
DE Melon ethylene receptor gene promoter-related sequence.
PN JP2001037484-A.
PD 13-FEB-2001.
PA (IBAR-) IBARAKI PREFECTURE.
Query Match 2.5%; Score 36.8; DB 5; Length 2796;
Best Local Similarity 49.5%; Pred. No. 38;
RESULT 724
ID ABD03441 standard; DNA; 2946 BP.
DE Pseudomonas aeruginosa polynucleotide #2045.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 36.8; DB 11; Length 2946;
Best Local Similarity 54.4%; Pred. No. 39;
RESULT 725
ID AB106732 standard; cDNA; 4298 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 14678.
PN WO20011042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 2.5%; Score 36.8; DB 4; Length 4298;
Best Local Similarity 49.6%; Pred. No. 47;
RESULT 726
ID AAX84332 standard; DNA; 5059 BP.
DE Stealth virus nucleic acid clone, SEQ ID NO: 24.
Query Match 2.5%; Score 36.8; DB 2; Length 5059;
Best Local Similarity 19.2%; Pred. No. 51;
RESULT 727
ID AAQ79728 standard; DNA; 6100 BP.
DE Human U5/3 tumour suppressor gene (genomic sequence).
PN US5315000-A.
PD 24-MAY-1994.
PA (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.
Query Match 2.5%; Score 36.8; DB 2; Length 6100;
Best Local Similarity 55.5%; Pred. No. 56;
RESULT 728
ID AAT62440 standard; DNA; 6100 BP.
DE Human U5/3 growth factor genomic sequence.
PN US5606029-A.
PD 25-FEB-1997.
PA (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.
Query Match 2.5%; Score 36.8; DB 2; Length 6100;
Best Local Similarity 55.5%; Pred. No. 56;
RESULT 729
ID ABL68609 standard; DNA; 9980 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6946.
PN WO200194629-A2.
PD 13-DEC-2001.

PA (AVAL-) AVALON PHARM.
Query Match 2.5%; Score 36.8; DB 6; Length 9980;
Best Local Similarity 55.5%; Pred. No. 71;
RESULT 730
ID ABN96855 standard; DNA; 9980 BP.
DE Gene #3353 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.5%; Score 36.8; DB 6; Length 9980;
Best Local Similarity 55.5%; Pred. No. 71;
RESULT 731
ID AA229063 standard; DNA; 35828 BP.
DE Murine TGF-beta binding protein (BBER) genomic MluI-AvII DNA fragment.
PN WO200032773-A1.
PD 08-JUN-2000.
PA (DARW-) DARWIN DISCOVERY LTD.
Query Match 2.5%; Score 36.8; DB 3; Length 35828;
Best Local Similarity 69.4%; Pred. No. 1.4e+02;
RESULT 732
ID AAD50739 standard; DNA; 64467 BP.
DE Human kinase gene.
Query Match 2.5%; Score 36.8; DB 8; Length 64467;
Best Local Similarity 56.7%; Pred. No. 1.8e+02;
RESULT 733
ID ACH00100 standard; DNA; 64467 BP.
DE Human kinase protein genomic DNA.
Query Match 2.5%; Score 36.8; DB 9; Length 64467;
Best Local Similarity 56.7%; Pred. No. 1.8e+02;
RESULT 734
ID ADD15783 standard; DNA; 64467 BP.
DE Human MEK kinase subfamily kinase genomic DNA.
PN US6582946-B1.
PD 24-JUN-2003.
PA (APPL-) APPLERA CORP.
Query Match 2.5%; Score 36.8; DB 10; Length 64467;
Best Local Similarity 56.7%; Pred. No. 1.8e+02;
RESULT 735
ID ADP45591 standard; DNA; 92500 BP.
DE Human intercellular adhesion molecule ICAM-1/ICAM-4/ICAM-5 cDNA.
Query Match 2.5%; Score 36.8; DB 12; Length 92500;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
RESULT 736
ID ADF13110 standard; DNA; 118067 BP.
DE Hypermethylation site in human breast cancer Cpg island locus HBC-37.
PN US2003129602-A1.
PD 10-JUN-2003.
PA (HUAN/) HUANG T H.
Query Match 2.5%; Score 36.8; DB 12; Length 118067;
Best Local Similarity 55.5%; Pred. No. 2.4e+02;
RESULT 737
ID AD137256 standard; DNA; 118067 BP.
DE Hypermethylation in cancer (HBC) locus-37.
PN US6605432-B1.
PD 12-AUG-2003.
PA (UMOR-) UNIV MISSOURI.
Query Match 2.5%; Score 36.8; DB 12; Length 118067;
Best Local Similarity 55.5%; Pred. No. 2.4e+02;
RESULT 738
ID ABR83562 standard; cDNA; 139904 BP.
DE Human cDNA differentially expressed in granulocytic cells #133.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.5%; Score 36.8; DB 6; Length 139904;
Best Local Similarity 58.0%; Pred. No. 2.7e+02;
RESULT 739
ID ACA64924 standard; DNA; 201239 BP.
DE Human PLZF DNA corresponding to AF060568.
PN DE10127572-A1.
PD 05-DEC-2002.
PA (PATR-) PATHOARRAY GMBH.
Query Match 2.5%; Score 36.8; DB 8; Length 201239;

Best Local Similarity 48.1%; Pred. No. 3.2e+02;
RESULT 740
ID ADA58461 standard; cDNA; 295 BP.
DE Maize sucrose synthase EST #105.
PN US2003135870-A1.
PD 17-JUN-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.5%; Score 36.6; DB 9; Length 295;
Best Local Similarity 56.1%; Pred. No. 14;
RESULT 741
ID ADA58383 standard; cDNA; 340 BP.
DE Maize sucrose synthase EST #27.
PN US2003135870-A1.
PD 17-JUN-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.5%; Score 36.6; DB 9; Length 340;
Best Local Similarity 58.9%; Pred. No. 15;
RESULT 742
ID ABX52791 standard; cDNA; 438 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2720.
PN US2002137160-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAN/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.5%; Score 36.6; DB 8; Length 438;
Best Local Similarity 46.9%; Pred. No. 17;
RESULT 743
ID ADA48906 standard; DNA; 689 BP.
DE Wheat gene conferring disease resistance in plants.
PN WO200300905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.6; DB 9; Length 689;
Best Local Similarity 49.7%; Pred. No. 22;
RESULT 744
ID ADC08648 standard; DNA; 689 BP.
DE Wheat DNA sequence Seq ID953 related to grain filling.
PN WO200300905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.6; DB 10; Length 689;
Best Local Similarity 49.7%; Pred. No. 22;
RESULT 745
ID ADJ41713 standard; cDNA; 689 BP.
DE Plant cDNA #2713.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KEPP/) KEPPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHU/) ZHU T.
Query Match 2.5%; Score 36.6; DB 12; Length 689;
Best Local Similarity 49.7%; Pred. No. 22;
RESULT 746
ID AAH74539 standard; cDNA; 905 BP.
DE Nucleotide sequence of a chitobiosidase polypeptide.
PN WO200146387-A1.
PD 28-JUN-2001.
PA (CORR) CORNELL RES FOUND INC.
Query Match 2.5%; Score 36.6; DB 4; Length 905;
Best Local Similarity 49.7%; Pred. No. 22;
RESULT 747
ID ADA69391 standard; DNA; 1182 BP.
DE Rice gene, SEQ ID 2714.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.6; DB 8; Length 1182;
Best Local Similarity 49.7%; Pred. No. 28;
RESULT 748
ID ADA47947 standard; DNA; 1182 BP.
DE Rice gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.6; DB 9; Length 1182;
Best Local Similarity 49.7%; Pred. No. 28;
RESULT 749
ID ADC07965 standard; DNA; 1182 BP.
DE Rice DNA sequence Seq ID231 related to grain filling.
PN WO2003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.6; DB 10; Length 1182;
Best Local Similarity 49.7%; Pred. No. 28;
RESULT 750
ID ADJ39882 standard; cDNA; 1182 BP.
DE Plant cDNA #882.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KEPP/) KEPPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHU/) ZHU T.
Query Match 2.5%; Score 36.6; DB 12; Length 1182;
Best Local Similarity 49.7%; Pred. No. 28;
RESULT 751
ID AA206824 standard; DNA; 1294 BP.
DE Streptomyces albidoflavus chitobiosidase DNA.
PN WO9942594-A1.
PD 26-AUG-1999.
PA (CORR) CORNELL RES FOUND INC.
Query Match 2.5%; Score 36.6; DB 2; Length 1294;
Best Local Similarity 50.9%; Pred. No. 29;
RESULT 752
ID AAH74537 standard; DNA; 1294 BP.
DE Nucleotide sequence of a chitobiosidase polypeptide.
PN WO200146387-A1.
PD 28-JUN-2001.
PA (CORR) CORNELL RES FOUND INC.
Query Match 2.5%; Score 36.6; DB 4; Length 1294;
Best Local Similarity 50.9%; Pred. No. 29;
RESULT 753
ID ADQ25850 standard; DNA; 4145 BP.
DE Rat G-protein coupled receptor 88 coding sequence.
PN WO2004054617-A1.
PD 01-JUL-2004.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 2.5%; Score 36.6; DB 12; Length 4145;
Best Local Similarity 51.5%; Pred. No. 53;
RESULT 754
ID AAH41184 standard; DNA; 4164 BP.
DE Rat G-protein-coupled receptor, strg, coding sequence.
PN WO200136634-A1.
PD 25-MAY-2001.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

Query Match 2.5%; Score 36.6; DB 5; Length 4164;
Best Local Similarity 51.5%; Pred. No. 53;
RESULT 755
ID ADE59567 standard; DNA; 5761 BP.
DE Human gene XM_038377, SEQ ID NO 5463.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 2.5%; Score 36.6; DB 10; Length 5761;
Best Local Similarity 57.0%; Pred. No. 62;
RESULT 756
ID ADE59563 standard; DNA; 5761 BP.
DE Human gene XM_038377, SEQ ID NO 5459.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 2.5%; Score 36.6; DB 10; Length 5761;
Best Local Similarity 57.0%; Pred. No. 62;
RESULT 757
ID ACN44528 standard; DNA; 49806 BP.
DE Mouse genomic sequence mCG20647.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 36.6; DB 11; Length 49806;
Best Local Similarity 57.4%; Pred. No. 1.8e+02;
RESULT 758
ID AD570697 standard; cDNA; 272 BP.
DE Corn seedling-derived polynucleotide (cpds), SEQ ID 5713.
PN US200337110-A9.
PD 25-DEC-2003.
PA (INCY-) INCYTE PHARM INC.
Query Match 2.5%; Score 36.4; DB 7; Length 272;
Best Local Similarity 58.1%; Pred. No. 15;
RESULT 759
ID ADP29106 standard; DNA; 279 BP.
DE Human secreted protein encoding sequence SEQ ID #1104.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.5%; Score 36.4; DB 12; Length 279;
Best Local Similarity 48.9%; Pred. No. 16;
RESULT 760
ID ADA49220 standard; DNA; 399 BP.
DE Maize gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.4; DB 9; Length 399;
Best Local Similarity 52.7%; Pred. No. 19;
RESULT 761
ID ACL19211 standard; DNA; 409 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9202.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UNIV-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 36.4; DB 9; Length 409;
Best Local Similarity 46.7%; Pred. No. 19;
RESULT 762
ID ACL19207 standard; DNA; 418 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9198.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UNIV-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 36.4; DB 9; Length 418;
Best Local Similarity 48.1%; Pred. No. 19;
RESULT 763
ID ADA69502 standard; DNA; 450 BP.
DE Rice gene, SEQ ID 2825.
PN WO200300898-A1.
PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.4; DB 8; Length 450;
Best Local Similarity 48.1%; Pred. No. 20;
RESULT 764
ID ADA48603 standard; DNA; 450 BP.
DE Rice gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.4; DB 9; Length 450;
Best Local Similarity 48.1%; Pred. No. 20;
RESULT 765
ID ADJ44943 standard; cDNA; 450 BP.
DE Plant cDNA #5943.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MUG/) MUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICE D.
PA (ZHUT/) ZHU T.
Query Match 2.5%; Score 36.4; DB 12; Length 450;
Best Local Similarity 48.1%; Pred. No. 20;
RESULT 766
ID ABV59448 standard; cDNA; 456 BP.
DE Human prostate expression marker cDNA 59439.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.5%; Score 36.4; DB 5; Length 456;
Best Local Similarity 55.6%; Pred. No. 20;
RESULT 767
ID ACH22587 standard; cDNA; 486 BP.
DE Human adult ovary cDNA #967.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STRAC/) STRACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.5%; Score 36.4; DB 9; Length 486;
Best Local Similarity 49.5%; Pred. No. 21;
RESULT 768
ID ADA69813 standard; DNA; 516 BP.
DE Rice gene, SEQ ID 3136.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.4; DB 8; Length 516;
Best Local Similarity 48.5%; Pred. No. 21;
RESULT 769
ID ACL19210 standard; DNA; 517 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9201.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UNIV-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 36.4; DB 9; Length 517;
Best Local Similarity 46.7%; Pred. No. 21;
RESULT 770
ID ADA4885 standard; DNA; 600 BP.
DE Banana gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.4; DB 9; Length 600;
Best Local Similarity 48.1%; Pred. No. 23;

RESULT 771
ID ADJ42628 standard; cDNA; 606 BP.
DE Plant cDNA #3628.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKER D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 12; Length 606;
56.8%; Pred. No. 23;
RESULT 772
ID ADJ6477 standard; DNA; 647 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1746.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 10; Length 647;
48.1%; Pred. No. 24;
RESULT 773
ID ADK59088 standard; DNA; 647 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #6471.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
PA (DOMC) DOM AGROSCIENCES LLC.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 10; Length 647;
48.1%; Pred. No. 24;
RESULT 774
ID ADJ42638 standard; cDNA; 662 BP.
DE Plant cDNA #3638.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKER D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 12; Length 662;
48.1%; Pred. No. 24;
RESULT 775
ID ADJ6482 standard; DNA; 784 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 839.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 10; Length 784;
48.1%; Pred. No. 25;
RESULT 776
ID ADJ6482 standard; DNA; 784 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1751.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 10; Length 784;
48.1%; Pred. No. 26;
RESULT 777
ID ADJ7183 standard; DNA; 784 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2112.
PN WO2003020905-A2.

PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 10; Length 784;
48.1%; Pred. No. 26;
RESULT 778
ID ADK56993 standard; DNA; 784 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4376.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
PA (DOMC) DOM AGROSCIENCES LLC.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 10; Length 784;
48.1%; Pred. No. 26;
RESULT 779
ID ADK59091 standard; DNA; 784 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #6474.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
PA (DOMC) DOM AGROSCIENCES LLC.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 10; Length 784;
48.1%; Pred. No. 26;
RESULT 780
ID ADJ42632 standard; cDNA; 868 BP.
DE Plant cDNA #3632.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKER D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 12; Length 868;
48.1%; Pred. No. 27;
RESULT 781
ID AAS80397 standard; cDNA; 1203 BP.
DE DNA encoding novel human diagnostic protein #16201.
PN WO2001075067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 5; Length 1203;
51.9%; Pred. No. 32;
RESULT 782
ID ABL67798 standard; DNA; 1306 BP.
DE Oesophagus cancer related gene sequence SEQ ID NO:6135.
PN WO2001094629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 6; Length 1306;
48.1%; Pred. No. 34;
RESULT 783
ID ABL65422 standard; DNA; 1306 BP.
DE Lung cancer related gene sequence SEQ ID NO:3759.
PN WO2001094629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 6; Length 1306;
48.1%; Pred. No. 34;
RESULT 784
ID ABL65524 standard; DNA; 1306 BP.
DE Lung cancer related gene sequence SEQ ID NO:4661.
PN WO2001094629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 6; Length 1306;
48.1%; Pred. No. 34;
RESULT 785

ID ADN04465 standard; cDNA; 1367 BP.
DE Antipsoriatic cDNA sequence #434.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 36.4; DB 12; Length 1367;
Best Local Similarity 48.1%; Pred. No. 34;
RESULT 786
ID ADE47781 standard; DNA; 1710 BP.
DE Human NOV45b gene SEQ ID NO:143.
PN WO2003076642-A2.
PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.5%; Score 36.4; DB 10; Length 1710;
Best Local Similarity 58.2%; Pred. No. 38;
RESULT 787
ID ADH41898 standard; DNA; 1710 BP.
DE Novel human nucleic acid NOV36d.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.5%; Score 36.4; DB 12; Length 1710;
Best Local Similarity 58.2%; Pred. No. 38;
RESULT 788
ID ADV79051 standard; DNA; 1710 BP.
DE Human NOVX protein NOV45b gene sequence.
PN US2004014053-A1.
PD 22-JAN-2004.
PA (ZERRH) ZERRHUSEN B. D.
PA (PATT) PATTURAJAN M.
PA (KESK) KESKUDA R.
PA (MILL) MILLER C. E.
PA (RIEG) RIEGER D. K.
PA (PENA) PENNA C E A.
PA (SHIM) SHIMKETS R. A.
PA (LILL) LI L.
PA (BERG) BERGHS C.
PA (ZHON) ZHONG M.
PA (CASM) CASMAN S. J.
PA (VOSS) VOSS E. Z.
PA (BOLD) BOLDOG F. L.
PA (PADI) PADIGARU M.
PA (SMIT) SMITHSON G.
PA (JIMW) JI W.
PA (GORN) GORMAN L.
PA (VERN) VERNET C. A. M.
PA (LEIT) LEITE M. W.
PA (GROX) GRO X. S.
PA (ANDE) ANDERSON D. W.
PA (SPYT) SPYTEK K. A.
PA (GERL) GERLACH V.
PA (BURG) BURGESS C. E.
PA (KHRA) KHRAMTSOV N. V.
PA (ORTT) ORT T.
PA (ELLE) ELLERMAN K.
PA (RAST) RASTELLI L.
PA (AGEE) AGE E. M. L.
PA (CHAU) CHAUDHURI A.
PA (CHAN) CHANT J. S.
PA (DIP) DIPPO V. A.
PA (EDIN) EDINGER S. R.
PA (ERSE) EISEN A. J.
PA (GANG) GANGOLLI E. A.
PA (GIOT) GIOT L.
PA (OOIC) OOI C. E.
PA (ROTH) ROTHENBERG M. E.
PA (SPAD) SPADERNA S. K.
PA (HTAL) HTALT T.
PA (LITX) LIT X.
PA (TAUP) TAUPLER R. J.
PA (CAT) CATERTON E.
PA (SHEN) SHENOY S. G.
Query Match 2.5%; Score 36.4; DB 12; Length 1710;

Best Local Similarity 58.2%; Pred. No. 38;
RESULT 789
ID ABLE7803 standard; DNA; 2746 BP.
DE Oesophagus cancer related gene sequence SEQ ID NO:6140.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL) AVALON PHARM.
Query Match 2.5%; Score 36.4; DB 6; Length 2746;
Best Local Similarity 48.1%; Pred. No. 49;
RESULT 790
ID ADM67108 standard; DNA; 2947 BP.
DE Murine adipocyte specific DNA SeqID 243.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HNGE) HNGENE INC.
Query Match 2.5%; Score 36.4; DB 12; Length 2947;
Best Local Similarity 49.5%; Pred. No. 50;
RESULT 791
ID ABS78681 standard; DNA; 5877 BP.
DE Kitasatospora sp. DNA encoding PKSE.
PN CA2387401-A1.
PD 04-SEP-2002.
PA (ECOP) ECOPHA BIOSCIENCES INC.
Query Match 2.5%; Score 36.4; DB 6; Length 5877;
Best Local Similarity 50.0%; Pred. No. 71;
RESULT 792
ID AAS42021 standard; DNA; 32121 BP.
DE Genomic sequence #337 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 36.4; DB 4; Length 32121;
Best Local Similarity 50.6%; Pred. No. 1.7e+02;
RESULT 793
ID AAS35076 standard; DNA; 32121 BP.
DE DNA #26 encoding human neoplastic disease associated polypeptide.
PN WO200155163-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 36.4; DB 4; Length 32121;
Best Local Similarity 50.6%; Pred. No. 1.7e+02;
RESULT 794
ID ADC46518 standard; DNA; 32121 BP.
DE Human neoplastic disease-associated gene 55 DNA #1.
PN US2003082758-A1.
PD 01-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 36.4; DB 10; Length 32121;
Best Local Similarity 50.6%; Pred. No. 1.7e+02;
RESULT 795
ID ACN44094 standard; DNA; 35236 BP.
DE Human genomic sequence hCG23314.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 36.4; DB 11; Length 35236;
Best Local Similarity 54.7%; Pred. No. 1.7e+02;
RESULT 796
ID AAK79963 standard; DNA; 57144 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34775.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 36.4; DB 4; Length 57144;
Best Local Similarity 50.6%; Pred. No. 2.2e+02;
RESULT 797
ID ACN44608 standard; DNA; 90043 BP.
DE Mouse genomic sequence mCG22175.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 36.4; DB 11; Length 90043;
Best Local Similarity 55.6%; Pred. No. 2.8e+02;

RESULT 798
ID ABD33254 standard; DNA; 97415 BP.
DE Murine cancer-associated (CA) gene MD07-043.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 36.4; DB 13; Length 97415;
Best Local Similarity 48.5%; Pred. No. 2.9e+02;
RESULT 799
ID AAD16230 standard; DNA; 107820 BP.
DE Human ATP-binding cassette transporter ABC6 (MRP6) complementary gene.
Query Match 2.5%; Score 36.4; DB 4; Length 107820;
Best Local Similarity 53.5%; Pred. No. 3e+02;
RESULT 800
ID ABD33489 standard; DNA; 151858 BP.
DE Murine cancer-associated (CA) gene MD07-095.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 36.4; DB 13; Length 151858;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
RESULT 801
ID ACF62733 standard; DNA; 172984 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:661.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 172984;
Best Local Similarity 53.5%; Pred. No. 3.8e+02;
RESULT 802
ID ADB20848 standard; DNA; 172984 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:661.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 172984;
Best Local Similarity 53.5%; Pred. No. 3.8e+02;
RESULT 803
ID ADB87937 standard; DNA; 172984 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:661.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 172984;
Best Local Similarity 53.5%; Pred. No. 3.8e+02;
RESULT 804
ID ADB96920 standard; DNA; 172984 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:661.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 172984;
Best Local Similarity 53.5%; Pred. No. 3.8e+02;
RESULT 805
ID ADB92111 standard; DNA; 172984 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:661.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 172984;
Best Local Similarity 53.5%; Pred. No. 3.8e+02;
RESULT 806
ID ACF62750 standard; DNA; 186591 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:682.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 186591;
Best Local Similarity 53.5%; Pred. No. 3.9e+02;
RESULT 807
ID ADB20869 standard; DNA; 186591 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:682.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 186591;
Best Local Similarity 53.5%; Pred. No. 3.9e+02;
RESULT 808
ID ADB87958 standard; DNA; 186591 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:682.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 186591;
Best Local Similarity 53.5%; Pred. No. 3.9e+02;
RESULT 809
ID ADB96941 standard; DNA; 186591 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:682.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 186591;
Best Local Similarity 53.5%; Pred. No. 3.9e+02;
RESULT 810
ID ADB92132 standard; DNA; 186591 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:682.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 186591;
Best Local Similarity 53.5%; Pred. No. 3.9e+02;
RESULT 811
ID ACF62735 standard; DNA; 208648 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:663.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 812
ID ACF62740 standard; DNA; 208648 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:668.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 813
ID ADB20850 standard; DNA; 208648 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:663.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 814
ID ADB20855 standard; DNA; 208648 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:668.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 815
ID ADB87944 standard; DNA; 208648 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:668.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 816
ID ADB87939 standard; DNA; 208648 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:663.
PN WO2003013536-A2.
PD 20-FEB-2003.

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 817
ID ADB96922 standard; DNA; 208648 BP.
DE Human MDRI related DNA sequence SEQ ID NO:663.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 818
ID ADB96927 standard; DNA; 208648 BP.
DE Human MDRI related DNA sequence SEQ ID NO:668.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 819
ID ADB92113 standard; DNA; 208648 BP.
DE Human MDRI related DNA sequence SEQ ID NO:663.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 820
ID ADB92118 standard; DNA; 208648 BP.
DE Human MDRI related DNA sequence SEQ ID NO:668.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 821
ID ADA58486 standard; cDNA; 294 BP.
DE Maize sucrose synthase EST #130.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LITU/) LITU J.
Query Match 2.4%; Score 36.2; DB 9; Length 294;
Best Local Similarity 59.0%; Pred. No. 18;
RESULT 822
ID AA182080 standard; cDNA; 433 BP.
DE Human polynucleotide SEQ ID NO 2140.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 36.2; DB 4; Length 433;
Best Local Similarity 54.0%; Pred. No. 22;
RESULT 823
ID ABS73398 standard; DNA; 1086 BP.
DE DNA encoding human GPCR HP1948 mutant 1128F.
PN WO200268600-A2.
PD 06-SEP-2002.
PA (AREN-) ARENA PHARM INC.
Query Match 2.4%; Score 36.2; DB 6; Length 1086;
Best Local Similarity 54.0%; Pred. No. 35;
RESULT 824
ID AAX87371 standard; cDNA; 1120 BP.
DE Human myosin light chain cDNA.
PN WO9936531-A1.
PD 22-JUL-1999.
PA (ZENEC) ZENECA LTD.
Query Match 2.4%; Score 36.2; DB 2; Length 1120;
Best Local Similarity 48.8%; Pred. No. 35;
RESULT 825
ID AAD07361 standard; DNA; 1120 BP.
DE Human DNA encoding myosin light chain protein (marker 12).
PN WO200136674-A2.

PD 25-MAY-2001.
PA (ASTR) ASTRAZENECA AB.
PA (ASTR) ASTRAZENECA UK LTD.
Query Match 2.4%; Score 36.2; DB 4; Length 1120;
Best Local Similarity 48.8%; Pred. No. 35;
RESULT 826
ID ABL62349 standard; DNA; 1120 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:686.
PN WO200194639-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.4%; Score 36.2; DB 6; Length 1120;
Best Local Similarity 48.8%; Pred. No. 35;
RESULT 827
ID ABL69454 standard; DNA; 1120 BP.
DE Prostate cancer related gene sequence SEQ ID NO:7791.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.4%; Score 36.2; DB 6; Length 1120;
Best Local Similarity 48.8%; Pred. No. 35;
RESULT 828
ID ADN03695 standard; cDNA; 1120 BP.
DE Antipsoriatic cDNA sequence #45.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 36.2; DB 12; Length 1120;
Best Local Similarity 48.8%; Pred. No. 35;
RESULT 829
ID ADM33386 standard; cDNA; 1120 BP.
DE Human PRO1267 encoding cDNA SEQ ID NO:3.
PN WO2004028447-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 36.2; DB 12; Length 1120;
Best Local Similarity 48.8%; Pred. No. 35;
RESULT 830
ID ADP13398 standard; DNA; 1120 BP.
DE Renal cell carcinoma differentially expressed gene #134.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
Query Match 2.4%; Score 36.2; DB 12; Length 1120;
Best Local Similarity 48.8%; Pred. No. 35;
RESULT 831
ID ADQ22648 standard; DNA; 1303 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5468.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.4%; Score 36.2; DB 12; Length 1303;
Best Local Similarity 45.9%; Pred. No. 38;
RESULT 832
ID ADL62786 standard; DNA; 1941 BP.
DE Human ovarian cancer DNA marker #20998.
PN WO2001170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.4%; Score 36.2; DB 5; Length 1941;
Best Local Similarity 46.9%; Pred. No. 47;
RESULT 833
ID ABD16767 standard; DNA; 1989 BP.
DE Pseudomonas aeruginosa polynucleotide #15371.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 2.4%; Score 36.2; DB 11; Length 1989;
Best Local Similarity 48.3%; Pred. No. 47;
RESULT 834
ID ADA52522 standard; cDNA; 2044 BP.
DE Human coding sequence, SEQ ID 90.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.4%; Score 36.2; DB 10; Length 2044;
Best Local Similarity 55.0%; Pred. No. 48;
RESULT 835
ID ABD16858 standard; DNA; 2058 BP.
DE Pseudomonas aeruginosa polynucleotide #15462.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 36.2; DB 11; Length 2058;
Best Local Similarity 48.3%; Pred. No. 48;
RESULT 836
ID ACA51409 standard; DNA; 2355 BP.
DE Prokaryotic essential gene #33066.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.4%; Score 36.2; DB 8; Length 2355;
Best Local Similarity 46.9%; Pred. No. 51;
RESULT 837
ID ABD16799 standard; DNA; 2637 BP.
DE Pseudomonas aeruginosa polynucleotide #15403.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 36.2; DB 11; Length 2637;
Best Local Similarity 48.3%; Pred. No. 54;
RESULT 838
ID AAA8444 standard; DNA; 2893 BP.
DE Human deamin gene 5' flanking region, including the promoter region.
PN EP99278-A1.
PD 10-MAY-2000.
PA (UTPA-) UNIV PARIS VII.
Query Match 2.4%; Score 36.2; DB 3; Length 2893;
Best Local Similarity 52.3%; Pred. No. 57;
RESULT 839
ID ABT16471 standard; DNA; 3270 BP.
DE Human intracellular signalling protein coding sequence - SEQ ID No 24.
PN WO2002101008-A2.
PD 19-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 36.2; DB 10; Length 3270;
Best Local Similarity 59.0%; Pred. No. 60;
RESULT 840
ID AAD49464 standard; cDNA; 5230 BP.
DE Human vesicle-associated protein-8 (VAP)-8 cDNA.
PN WO000286061-A2.
PD 31-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 36.2; DB 10; Length 5230;
Best Local Similarity 50.3%; Pred. No. 76;
RESULT 841
ID ADL13006 standard; cDNA; 5467 BP.
DE Human steroid-induced C3a liver cell cDNA #735.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.4%; Score 36.2; DB 12; Length 5467;
Best Local Similarity 50.3%; Pred. No. 78;
RESULT 842
ID AA055145 standard; DNA; 9515 BP.
DE Pseudomonas aeruginosa probe P2-2.
PN WO9401583-A1.
PD 20-JAN-1994.
PA (FUSO) FUSO PHARM IND LTD.

Query Match 2.4%; Score 36.2; DB 2; Length 9515;
Best Local Similarity 44.5%; Pred. No. 1e+02;
RESULT 843
ID AB277356 standard; DNA; 9515 BP.
DE Nucleotide sequence designated PS-2.
PN WO2002101037-A1.
PD 19-DEC-2002.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 2.4%; Score 36.2; DB 8; Length 9515;
Best Local Similarity 44.5%; Pred. No. 1e+02;
RESULT 844
ID AAL51844 standard; DNA; 9515 BP.
DE Pseudomonas aeruginosa microbe identification-related DNA sequence.
PN WO200299133-A1.
PD 12-DEC-2002.
PA (FUSO) FUSO PHARM IND LTD.
PA (OHNO/) OHNO T.
Query Match 2.4%; Score 36.2; DB 10; Length 9515;
Best Local Similarity 44.5%; Pred. No. 1e+02;
RESULT 845
ID AAD40350 standard; DNA; 11771 BP.
DE Bovine DGAT1 gene.
Query Match 2.4%; Score 36.2; DB 6; Length 11771;
Best Local Similarity 50.9%; Pred. No. 1.1e+02;
RESULT 846
ID AB277045 standard; DNA; 14117 BP.
DE Bovine DGAT gene SEQ ID NO:3.
PN WO2003004630-A2.
PD 16-JAN-2003.
PA (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUCHTER.
Query Match 2.4%; Score 36.2; DB 10; Length 14117;
Best Local Similarity 50.9%; Pred. No. 1.2e+02;
RESULT 847
ID AB277044 standard; DNA; 14117 BP.
DE Bovine DGAT gene SEQ ID NO:1.
PN WO2003004630-A2.
PD 16-JAN-2003.
PA (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUCHTER.
Query Match 2.4%; Score 36.2; DB 10; Length 14117;
Best Local Similarity 50.9%; Pred. No. 1.2e+02;
RESULT 848
ID AAT68715 standard; DNA; 15872 BP.
DE Streptomyces venezuelae polyketide synthase vep ORF1.
PN WO9722711-A1.
PD 26-JUN-1997.
PA (MINU) UNIV MINNESOTA.
Query Match 2.4%; Score 36.2; DB 2; Length 15872;
Best Local Similarity 52.3%; Pred. No. 1.3e+02;
RESULT 849
ID AAZ87283 standard; DNA; 15872 BP.
DE S. venezuelae vep ORF 1, SEQ ID NO:1.
PN WO200000620-A2.
PD 06-JAN-2000.
PA (MINU) UNIV MINNESOTA.
Query Match 2.4%; Score 36.2; DB 3; Length 15872;
Best Local Similarity 52.3%; Pred. No. 1.3e+02;
RESULT 850
ID ADI91929 standard; DNA; 15872 BP.
DE Streptomyces venezuelae vep ORF1 coding sequence.
PN US2003194784-A1.
PD 16-OCT-2003.
PA (SHER/) SHERMAN D H.
PA (LITU/) LITU H.
PA (XUEY/) XUE Y.
PA (ZHAO/) ZHAO L.
Query Match 2.4%; Score 36.2; DB 12; Length 15872;
Best Local Similarity 52.3%; Pred. No. 1.3e+02;
RESULT 851
ID ACN44556 standard; DNA; 22262 BP.
DE Mouse genomic sequence mCG21411.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 2.4%; Score 36.2; DB 11; Length 2262;
Best Local Similarity 54.0%; Pred. No. 1.6e+02;
RESULT 852
ID AAT93095 standard; cDNA; 24379 BP.
DE Streptomyces firenolicin gene cluster.
PN EP806480-A2.
PD 12-NOV-1997.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 2.4%; Score 36.2; DB 2; Length 24379;
Best Local Similarity 55.0%; Pred. No. 1.6e+02;
RESULT 853
ID AAV25925 standard; cDNA; 24379 BP.
DE Streptomyces roseofulvus firenolicin gene cluster.
PN JP10094395-A.
PD 14-APR-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 2.4%; Score 36.2; DB 2; Length 24379;
Best Local Similarity 55.0%; Pred. No. 1.6e+02;
RESULT 854
ID ABD33195 standard; DNA; 27485 BP.
DE Human cancer-associated (CA) gene HD07-029.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 36.2; DB 13; Length 27485;
Best Local Similarity 51.7%; Pred. No. 1.7e+02;
RESULT 855
ID AAT80413 standard; DNA; 43280 BP.
DE Ty lactone synthase gene cluster.
PN EP791655-A2.
PD 27-AUG-1997.
PA (ELIT) LITILY & CO BLI.
Query Match 2.4%; Score 36.2; DB 2; Length 43280;
Best Local Similarity 52.3%; Pred. No. 2.2e+02;
RESULT 856
ID ADR28249 standard; DNA; 59999 BP.
DE Human low density lipoprotein (LDL) receptor gene sequence SegID1.
PN WO2004067740-A1.
PD 12-AUG-2004.
PA (EPAR-) EPARMS SA.
Query Match 2.4%; Score 36.2; DB 13; Length 59999;
Best Local Similarity 55.0%; Pred. No. 2.6e+02;
RESULT 857
ID ABD33301 standard; DNA; 89829 BP.
DE Murine cancer-associated (CA) gene MD07-054.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 36.2; DB 13; Length 89829;
Best Local Similarity 60.8%; Pred. No. 3.1e+02;
RESULT 858
Query Match 2.4%; Score 36.2; DB 13; Length 110000;
Best Local Similarity 56.2%; Pred. No. 3.5e+02;
RESULT 859
ID ADG97107 standard; DNA; 121124 BP.
DE Mouse cancer associated sequence MD08-002, SEQ ID 83.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 36.2; DB 13; Length 121124;
Best Local Similarity 56.2%; Pred. No. 3.6e+02;
RESULT 860
ID ABD32868 standard; DNA; 238417 BP.
DE Human cancer-associated genomic DNA HD17-053.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 36.2; DB 13; Length 238417;
Best Local Similarity 48.3%; Pred. No. 5e+02;
RESULT 861
ID ADQ19085 standard; DNA; 452 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1904.
PN WO2004048938-A2.

PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.4%; Score 36; DB 12; Length 452;
Best Local Similarity 55.5%; Pred. No. 26;
RESULT 862
ID AAC41067 standard; DNA; 489 BP.
DE Zea mays DNA fragment SEQ ID NO: 30530.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.4%; Score 36; DB 3; Length 489;
Best Local Similarity 46.7%; Pred. No. 27;
RESULT 863
ID AAC40977 standard; DNA; 507 BP.
DE Zea mays DNA fragment SEQ ID NO: 30205.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.4%; Score 36; DB 3; Length 507;
Best Local Similarity 46.7%; Pred. No. 27;
RESULT 864
ID ADA4888 standard; DNA; 766 BP.
DE Banana gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 36; DB 9; Length 766;
Best Local Similarity 46.7%; Pred. No. 33;
RESULT 865
ID ABD11412 standard; DNA; 894 BP.
DE Pseudomonas aeruginosa polynucleotide #10016.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 36; DB 11; Length 894;
Best Local Similarity 49.2%; Pred. No. 36;
RESULT 866
ID ABD02947 standard; DNA; 1512 BP.
DE Pseudomonas aeruginosa polynucleotide #1551.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 36; DB 11; Length 1512;
Best Local Similarity 46.4%; Pred. No. 47;
RESULT 867
ID ABD03012 standard; DNA; 1677 BP.
DE Pseudomonas aeruginosa polynucleotide #1616.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 36; DB 11; Length 1677;
Best Local Similarity 46.4%; Pred. No. 49;
RESULT 868
ID ADP4458 standard; cDNA; 2235 BP.
DE Bacterial polynucleotide #19309.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.4%; Score 36; DB 13; Length 2235;
Best Local Similarity 52.7%; Pred. No. 57;
RESULT 869
ID ACA42098 standard; DNA; 3099 BP.
DE Prokaryotic essential gene #33755.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.4%; Score 36; DB 8; Length 3099;
Best Local Similarity 50.6%; Pred. No. 67;
RESULT 870
ID AAP16277 standard; cDNA; 3779 BP.
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:712.

PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 2.4%; Score 36; DB 3; Length 3779;
Best Local Similarity 51.3%; Pred. No. 74;
RESULT 871
ID AAV63754 standard; cDNA; 4315 BP.
DE Human JAGGED2 cDNA.
PN WO9858958-A2.
PD 30-DEC-1998.
PA (UNIW) UNIV WASHINGTON.
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
Query Match 2.4%; Score 36; DB 2; Length 4315;
Best Local Similarity 51.9%; Pred. No. 79;
RESULT 872
ID AD085357 standard; cDNA; 5079 BP.
DE Human tumor-associated antigenic target (TAT) cDNA sequence #2171.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.4%; Score 36; DB 12; Length 5079;
Best Local Similarity 51.9%; Pred. No. 85;
RESULT 873
ID AAL36491 standard; DNA; 15362 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2856.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.4%; Score 36; DB 4; Length 15362;
Best Local Similarity 49.0%; Pred. No. 1.5e+02;
RESULT 874
ID ABX59479 standard; cDNA; 15362 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1823.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.4%; Score 36; DB 8; Length 15362;
Best Local Similarity 49.0%; Pred. No. 1.5e+02;
RESULT 875
ID ADJ30229 standard; DNA; 15362 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2856.
PN US200400948-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.4%; Score 36; DB 12; Length 15362;
Best Local Similarity 49.0%; Pred. No. 1.5e+02;
RESULT 876
ID AAG99655 standard; DNA; 19303 BP.
DE Human membrane spanning 4-domain family, subfamily A genomic sequence.
PN WO200262946-A2.
PD 15-AUG-2002.
PA (UYDU-) UNIV DUKE.
Query Match 2.4%; Score 36; DB 6; Length 19303;
Best Local Similarity 43.0%; Pred. No. 1.7e+02;
RESULT 877
ID ADD00956 standard; DNA; 28000 BP.
DE Human jagged 2 encoding DNA SEQ ID NO:11.
PN WO200307848-A2.
PD 25-SEP-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.4%; Score 36; DB 10; Length 28000;
Best Local Similarity 51.9%; Pred. No. 2e+02;
RESULT 878
ID ADH62916 standard; DNA; 28000 BP.
DE Human jagged 2 gene.
PN US2003170636-A1.
PD 11-SEP-2003.
PA (ISIS-) ISIS PHARM INC.

Query Match 2.4%; Score 36; DB 10; Length 28000;
Best Local Similarity 51.9%; Pred. No. 2e+02;
RESULT 879
ID ADH57071 standard; DNA; 28000 BP.
DE Genomic human jagged 2 DNA sequence SeqID 11.
PN US200307839-A1.
PD 06-NOV-2003.
PA (FREIR/) FREIER S M.
Query Match 2.4%; Score 36; DB 10; Length 28000;
Best Local Similarity 51.9%; Pred. No. 2e+02;
RESULT 880
ID ACN44596 standard; DNA; 69090 BP.
DE Mouse genomic sequence mCG2215.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 36; DB 11; Length 69090;
Best Local Similarity 58.3%; Pred. No. 3.1e+02;
RESULT 881
ID ADL13931 standard; DNA; 180385 BP.
DE Osteoarthritis-associated polymorphic nucleotide #463.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 36; DB 10; Length 180385;
Best Local Similarity 48.1%; Pred. No. 5e+02;
RESULT 882
ID ACN44124 standard; DNA; 189158 BP.
DE Mouse genomic sequence mCG14749.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 36; DB 11; Length 189158;
Best Local Similarity 48.1%; Pred. No. 5.1e+02;
RESULT 883
ID ACN45150 standard; DNA; 217409 BP.
DE Human genomic sequence hCG34092.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 36; DB 11; Length 217409;
Best Local Similarity 48.5%; Pred. No. 5.5e+02;
RESULT 884
ID ACH44435 standard; cDNA; 469 BP.
DE Human foetal brain cDNA #5160.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.4%; Score 35.8; DB 9; Length 469;
Best Local Similarity 61.1%; Pred. No. 30;
RESULT 885
ID ADJ11721 standard; DNA; 561 BP.
DE Rice cDNA modulated by post-transcriptional gene silencing SeqID 357.
PN US200313588-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KEEP/) KEEPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICHKE D.
Query Match 2.4%; Score 35.8; DB 11; Length 561;
Best Local Similarity 47.9%; Pred. No. 32;

RESULT 886
ID ADA70499 standard; DNA; 564 BP.
DE Rice gene SEQ ID 3822.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 35.8; DB 8; Length 564;
Best Local Similarity 47.9%; Pred. No. 33;
RESULT 887
ID ADA8727 standard; DNA; 564 BP.
DE Rice gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 35.8; DB 9; Length 564;
Best Local Similarity 47.9%; Pred. No. 33;
RESULT 888
ID AD11367 standard; DNA; 564 BP.
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 3.
PN US200335888-A1.
PD 17-JUL-2003.
PA (ZHUT) ZHU T.
PA (WANG) WANG X.
PA (CHANG) CHANG H.
PA (BRIG) BRIGGS S P.
PA (COOP) COOPER B.
PA (GLAZ) GLAZEBROOK J.
PA (GOLF) GOLF S A.
PA (KATA) KATAGIRI F.
PA (KREP) KREPS J.
PA (MOUG) MOUGHAMER T.
PA (PROV) PROVANT N.
PA (RICK) RICE D.
Query Match 2.4%; Score 35.8; DB 11; Length 564;
Best Local Similarity 47.9%; Pred. No. 33;
RESULT 889
ID ADB5962 standard; DNA; 648 BP.
DE Toxicity related gene, SEQ ID 4088.
PN WO200306462-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.4%; Score 35.8; DB 10; Length 648;
Best Local Similarity 46.6%; Pred. No. 35;
RESULT 890
ID ADB53815 standard; DNA; 648 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4357.
PN WO200306593-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.4%; Score 35.8; DB 10; Length 648;
Best Local Similarity 46.6%; Pred. No. 35;
RESULT 891
ID ABT2404 standard; DNA; 648 BP.
DE Toxicity modelling related rat gene SEQ ID NO 2106.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.4%; Score 35.8; DB 10; Length 648;
Best Local Similarity 46.6%; Pred. No. 35;
RESULT 892
ID AA29365 standard; DNA; 774 BP.
DE Sequence encoding F-box protein FBP-15.
PN WO200012679-A1.
PD 09-MAR-2000.
PA (UNIV) UNIV NEW YORK STATE.
Query Match 2.4%; Score 35.8; DB 3; Length 774;
Best Local Similarity 51.7%; Pred. No. 38;
RESULT 893
ID AA141056 standard; cDNA; 774 BP.
DE cDNA of Human F-box protein FBPL5 SEQ ID NO 39.
PN WO20025665-A2.
PD 18-JUL-2002.
PA (UNIV) UNIV NEW YORK STATE.

Query Match 2.4%; Score 35.8; DB 6; Length 774;
Best Local Similarity 51.7%; Pred. No. 38;
RESULT 894
ID ABD08278 standard; DNA; 783 BP.
DE Pseudomonas aeruginosa polynucleotide #6882.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 35.8; DB 11; Length 783;
Best Local Similarity 55.1%; Pred. No. 38;
RESULT 895
ID AAS87609 standard; cDNA; 1074 BP.
DE DNA encoding novel human diagnostic protein #23413.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35.8; DB 5; Length 1074;
Best Local Similarity 51.6%; Pred. No. 45;
RESULT 896
ID AAI58521 standard; cDNA; 1457 BP.
DE Human polynucleotide SEQ ID NO 724.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35.8; DB 4; Length 1457;
Best Local Similarity 51.7%; Pred. No. 52;
RESULT 897
ID ADQ98738 standard; cDNA; 1457 BP.
DE DNA encoding human GPCR-like protein seqid 408.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35.8; DB 5; Length 1457;
Best Local Similarity 51.7%; Pred. No. 52;
RESULT 898
ID ADB48498 standard; cDNA; 1457 BP.
DE Novel human cDNA SEQ ID NO 408.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU) ZHOU P.
PA (TANG) TANG Y T.
PA (LIUC) LIU C.
PA (ASUN) ASUNDI V.
PA (DRMA) DRMANAC R T.
Query Match 2.4%; Score 35.8; DB 9; Length 1457;
Best Local Similarity 51.7%; Pred. No. 52;
RESULT 899
ID ADM01372 standard; cDNA; 2281 BP.
DE Human cDNA of the invention SEQ ID NO:57.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) REAS ASSOC BIOTECHNOLOGY.
Query Match 2.4%; Score 35.8; DB 11; Length 2281;
Best Local Similarity 56.3%; Pred. No. 65;
RESULT 900
ID ADM6961 standard; cDNA; 2394 BP.
DE Human protein encoding cDNA SEQ ID NO:54.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 2.4%; Score 35.8; DB 12; Length 2394;
Best Local Similarity 57.7%; Pred. No. 67;
RESULT 901
ID ADM6960 standard; cDNA; 2490 BP.
DE Human protein encoding cDNA SEQ ID NO:53.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 2.4%; Score 35.8; DB 12; Length 2490;
Best Local Similarity 57.7%; Pred. No. 68;
RESULT 902
ID ADH76501 standard; DNA; 2572 BP.
DE 727 amino acid human neurotransmitter transporter protein encoding DNA.

PN US2003219774-A1.
PD 27-NOV-2003.
PA (SHAR/) SHARMA R.
PA (RAMA/) RAMANATHAN C S.
PA (WEST/) WESTPHAL R.
PA (FEDER/) FEDER J N.
PA (LEBEL/) LEE L M.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 12; Length 2572;
47.2%; Pred. No. 69;
RESULT 903
ID ADU11615 standard; DNA; 2874 BP.
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 251.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KEEP/) KEEPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 11; Length 2874;
47.9%; Pred. No. 73;
RESULT 904
ID ABX71181 standard; cDNA; 3168 BP.
DE Novel human cDNA sequence #406.
PN WO200281731-A2.
PD 17-OCT-2002.
PA (HYSE-) HYSEQ INC.
PA (GOOD/) GOODRICH R W.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 8; Length 3168;
47.2%; Pred. No. 77;
RESULT 905
ID AAS72201 standard; cDNA; 3599 BP.
DE DNA encoding novel human diagnostic protein #8005.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 5; Length 3599;
50.3%; Pred. No. 82;
RESULT 906
ID ADS10356 standard; DNA; 3662 BP.
DE Human therapeutic DNA - SEQ ID 593.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 13; Length 3662;
53.1%; Pred. No. 83;
RESULT 907
ID ACNA40359 standard; cDNA; 3686 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326477, SEQ ID NO:5089.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 13; Length 3686;
50.3%; Pred. No. 83;
RESULT 908
ID ADR25659 standard; DNA; 4080 BP.
DE Breast cancer prognosis marker #1520.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 13; Length 4080;
51.6%; Pred. No. 87;
RESULT 909
ID AAD36022 standard; DNA; 43950 BP.
DE Human kinase genomic DNA.

Query Match
Best Local Similarity 2.4%; Score 35.8; DB 6; Length 43950;
51.6%; Pred. No. 2.8e+02;
RESULT 910
ID ABD33339 standard; DNA; 62658 BP.
DE Human cancer-associated (CA) gene HD07-061.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 13; Length 62658;
51.6%; Pred. No. 3.4e+02;
RESULT 911
ID ADD97640 standard; DNA; 79731 BP.
DE Mouse cancer associated sequence MD10-020, SEQ ID 617.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 12; Length 79731;
57.1%; Pred. No. 3.8e+02;
RESULT 912
ID AAA78038 standard; cDNA; 174 BP.
DE cDNA encoding human colon tumour polypeptide, SEQ ID NO:325.
PN WO200037643-A2.
PD 29-JUN-2000.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 3; Length 174;
51.2%; Pred. No. 21;
RESULT 913
ID AAA78081 standard; cDNA; 174 BP.
DE cDNA encoding human colon tumour polypeptide, SEQ ID NO:368.
PN WO200037643-A2.
PD 29-JUN-2000.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 3; Length 174;
51.2%; Pred. No. 21;
RESULT 914
ID AA128776 standard; cDNA; 174 BP.
DE Colon tumour related determined cDNA sequence for clone 25886.
PN WO200149716-A2.
PD 12-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 174;
51.2%; Pred. No. 21;
RESULT 915
ID AA128819 standard; cDNA; 174 BP.
DE Colon tumour related determined cDNA sequence for clone 25934.
PN WO200149716-A2.
PD 12-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 174;
51.2%; Pred. No. 21;
RESULT 916
ID AB333005 standard; cDNA; 174 BP.
DE Human colon tumour cDNA clone 25934 SEQ ID NO:368.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 8; Length 174;
51.2%; Pred. No. 21;
RESULT 917
ID AB32962 standard; cDNA; 174 BP.
DE Human colon tumour cDNA clone 25886 SEQ ID NO:325.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 8; Length 174;
51.2%; Pred. No. 21;
RESULT 918
ID AD567663 standard; cDNA; 242 BP.
DE Corn seedling-derived polynucleotide (cpds), SEQ ID 2699.
PN US200337110-A9.
PD 25-DEC-2003.
PA (INCY-) INCYTE PHARM INC.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 7; Length 242;

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|---|-------|--------------------------------|
| Best Local Similarity | 62.2% | Pred. No. 24; |
| RESULT 919 | | |
| ID ADA58416 standard; cDNA; 309 BP. | | |
| DE Maize sucrose synthase EST #60. | | |
| PN US2003135870-A1. | | |
| PD 17-JUL-2003. | | |
| PA (CHEI/) CHEIKH N. | | |
| PA (FISH/) FISHER D K. | | |
| PA (LIU/) LIU J. | | |
| Query Match | 2.4% | Score 35.6; DB 9; Length 309; |
| Best Local Similarity | 58.5% | Pred. No. 27; |
| RESULT 920 | | |
| ID AC119214 standard; DNA; 410 BP. | | |
| DE DNA clone originating in barley containing SNP encoding sequence #9205. | | |
| PN WO200305787-A1. | | |
| PD 17-JUL-2003. | | |
| PA (UYNI-) UNIV JAPAN OKAYAMA. | | |
| Query Match | 2.4% | Score 35.6; DB 9; Length 410; |
| Best Local Similarity | 47.7% | Pred. No. 32; |
| RESULT 921 | | |
| ID ACN51862 standard; cDNA; 458 BP. | | |
| DE Cotton androecium tissue EST Clone ID: L1B3828-009-Q1-N6-B6, SEQ:6663. | | |
| PN US2004123340-A1. | | |
| PD 24-JUN-2004. | | |
| PA (DEIK/) DEIKMAN J. | | |
| PA (FENG/) FENG P C.C. | | |
| PA (FINC/) FINCHER K L. | | |
| PA (ZIEG/) ZIEGLER T E. | | |
| Query Match | 2.4% | Score 35.6; DB 13; Length 458; |
| Best Local Similarity | 52.7% | Pred. No. 33; |
| RESULT 922 | | |
| ID ACH45185 standard; cDNA; 504 BP. | | |
| DE Human foetal brain cDNA #5910. | | |
| PN US2003073623-A1. | | |
| PD 17-APR-2003. | | |
| PA (DRMA/) DRMANAC R T. | | |
| PA (LABA/) LABAT I. | | |
| PA (STAC/) STACHE-CRAIN B. | | |
| PA (DICK/) DICKSON M C. | | |
| PA (JONE/) JONES L W. | | |
| Query Match | 2.4% | Score 35.6; DB 9; Length 504; |
| Best Local Similarity | 58.5% | Pred. No. 35; |
| RESULT 923 | | |
| ID AAS65914 standard; cDNA; 558 BP. | | |
| DE DNA encoding novel human diagnostic protein #1718. | | |
| PN WO2001175067-A2. | | |
| PD 11-OCT-2001. | | |
| PA (HYSE-) HYSEQ INC. | | |
| Query Match | 2.4% | Score 35.6; DB 5; Length 558; |
| Best Local Similarity | 51.2% | Pred. No. 37; |
| RESULT 924 | | |
| ID AA123315 standard; DNA; 575 BP. | | |
| DE Probe #13248 for gene expression analysis in human cervical cell sample. | | |
| PN WO200157278-A2. | | |
| PD 09-AUG-2001. | | |
| PA (MOLE-) MOLECULAR DYNAMICS INC. | | |
| Query Match | 2.4% | Score 35.6; DB 4; Length 575; |
| Best Local Similarity | 45.9% | Pred. No. 37; |
| RESULT 925 | | |
| ID ABA68422 standard; DNA; 575 BP. | | |
| DE Human foetal liver single exon nucleic acid probe #16727. | | |
| PN WO200157277-A2. | | |
| PD 09-AUG-2001. | | |
| PA (MOLE-) MOLECULAR DYNAMICS INC. | | |
| Query Match | 2.4% | Score 35.6; DB 4; Length 575; |
| Best Local Similarity | 45.9% | Pred. No. 37; |
| RESULT 926 | | |
| ID AA148636 standard; DNA; 575 BP. | | |
| DE Probe #17122 used to measure gene expression in human placenta sample. | | |
| PN WO200157272-A2. | | |
| PD 09-AUG-2001. | | |
| PA (MOLE-) MOLECULAR DYNAMICS INC. | | |
| Query Match | 2.4% | Score 35.6; DB 4; Length 575; |
| Best Local Similarity | 45.9% | Pred. No. 37; |
| RESULT 927 | | |
| ID AA148636 standard; DNA; 575 BP. | | |
| DE Probe #17122 used to measure gene expression in human placenta sample. | | |
| PN WO200157272-A2. | | |
| PD 09-AUG-2001. | | |
| PA (MOLE-) MOLECULAR DYNAMICS INC. | | |
| Query Match | 2.4% | Score 35.6; DB 4; Length 575; |
| Best Local Similarity | 45.9% | Pred. No. 37; |

| | | |
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| Best Local Similarity | 45.9%; | Pred. No. 37; |
| RESULT 927 | | |
| ID | ABA50472 standard; DNA; 575 BP. | |
| DE | Human breast cell single exon nucleic acid probe #9167. | |
| PN | WO200157271-A2. | |
| PD | 09-AUG-2001. | |
| PA | (MOLE-) MOLECULAR DYNAMICS INC. | |
| Query Match | 2.4%; | Score 35.6; DB 4; Length 575; |
| Best Local Similarity | 45.9%; | Pred. No. 37; |
| RESULT 928 | | |
| ID | ABA35413 standard; DNA; 575 BP. | |
| DE | Probe #13679 for gene expression analysis in human heart cell sample. | |
| PN | WO200157271-A2. | |
| PD | 09-AUG-2001. | |
| PA | (MOLE-) MOLECULAR DYNAMICS INC. | |
| Query Match | 2.4%; | Score 35.6; DB 4; Length 575; |
| Best Local Similarity | 45.9%; | Pred. No. 37; |
| RESULT 929 | | |
| ID | AAK42567 standard; DNA; 575 BP. | |
| DE | Human bone marrow expressed single exon probe SEQ ID NO: 17124. | |
| PN | WO200157271-A2. | |
| PD | 09-AUG-2001. | |
| PA | (MOLE-) MOLECULAR DYNAMICS INC. | |
| Query Match | 2.4%; | Score 35.6; DB 4; Length 575; |
| Best Local Similarity | 45.9%; | Pred. No. 37; |
| RESULT 930 | | |
| ID | AAK16793 standard; DNA; 575 BP. | |
| DE | Human brain expressed single exon probe SEQ ID NO: 16784. | |
| PN | WO200157271-A2. | |
| PD | 09-AUG-2001. | |
| PA | (MOLE-) MOLECULAR DYNAMICS INC. | |
| Query Match | 2.4%; | Score 35.6; DB 4; Length 575; |
| Best Local Similarity | 45.9%; | Pred. No. 37; |
| RESULT 931 | | |
| ID | ABS42178 standard; DNA; 575 BP. | |
| DE | Human liver single exon probe, SEQ ID NO 17168. | |
| PN | WO200157273-A2. | |
| PD | 09-AUG-2001. | |
| PA | (MOLE-) MOLECULAR DYNAMICS INC. | |
| Query Match | 2.4%; | Score 35.6; DB 4; Length 575; |
| Best Local Similarity | 45.9%; | Pred. No. 37; |
| RESULT 932 | | |
| ID | AAI08956 standard; DNA; 575 BP. | |
| DE | Probe #8947 used to measure gene expression in human breast sample. | |
| PN | WO200157270-A2. | |
| PD | 09-AUG-2001. | |
| PA | (MOLE-) MOLECULAR DYNAMICS INC. | |
| Query Match | 2.4%; | Score 35.6; DB 5; Length 575; |
| Best Local Similarity | 45.9%; | Pred. No. 37; |
| RESULT 933 | | |
| ID | ABS116615 standard; DNA; 575 BP. | |
| DE | Human genome-derived single exon probe ORF from lung SEQ ID NO 16606. | |
| PN | WO200186003-A2. | |
| PD | 15-NOV-2001. | |
| PA | (MOLE-) MOLECULAR DYNAMICS INC. | |
| Query Match | 2.4%; | Score 35.6; DB 6; Length 575; |
| Best Local Similarity | 45.9%; | Pred. No. 37; |
| RESULT 934 | | |
| ID | ABQ19226 standard; DNA; 687 BP. | |
| DE | Oligonucleotide for detecting cytosine methylation SEQ ID NO 5817. | |
| PN | WO200218632-A2. | |
| PD | 07-MAR-2002. | |
| PA | (EPIC-) EPICENOMICS AG. | |
| Query Match | 2.4%; | Score 35.6; DB 6; Length 687; |
| Best Local Similarity | 53.7%; | Pred. No. 41; |
| RESULT 935 | | |
| ID | ABQ19227 standard; DNA; 687 BP. | |
| DE | Oligonucleotide for detecting cytosine methylation SEQ ID NO 5818. | |
| PN | WO200218632-A2. | |
| PD | 07-MAR-2002. | |
| PA | (EPIC-) EPICENOMICS AG. | |
| Query Match | 2.4%; | Score 35.6; DB 6; Length 687; |
| Best Local Similarity | 53.7%; | Pred. No. 41; |

RESULT 936
ID ADR46437 standard; DNA; 719 BP.
DE A thaliana caltrectin-like protein coding sequence SEQ ID NO: 3.
PN WO2004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SONGENE GMBH & CO KGAA.
Query Match 2.4%; Score 35.6; DB 13; Length 719;
Best Local Similarity 47.3%; Pred. No. 42;
RESULT 937
ID ADT42681 standard; cDNA; 747 BP.
DE Bacterial polynucleotide #17432.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.4%; Score 35.6; DB 13; Length 747;
Best Local Similarity 55.7%; Pred. No. 43;
RESULT 938
ID AAC35370 standard; DNA; 760 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 9944.
PN EP1033405-A2.
PD 06-SEP-2000.
PA
Query Match 2.4%; Score 35.6; DB 3; Length 760;
Best Local Similarity 57.0%; Pred. No. 43;
RESULT 939
ID AA160307 standard; cDNA; 1627 BP.
DE Human polynucleotide SEQ ID NO 4296.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSEQ-) HYSEQ INC.
Query Match 2.4%; Score 35.6; DB 4; Length 1627;
Best Local Similarity 52.0%; Pred. No. 63;
RESULT 940
ID AAH15073 standard; cDNA; 1790 BP.
DE Human cDNA sequence SEQ ID NO.13081.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.4%; Score 35.6; DB 4; Length 1790;
Best Local Similarity 47.0%; Pred. No. 66;
RESULT 941
ID AAT14105 standard; DNA; 1969 BP.
DE Probe #4038 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.4%; Score 35.6; DB 4; Length 1969;
Best Local Similarity 45.9%; Pred. No. 69;
RESULT 942
ID ABA55830 standard; DNA; 1969 BP.
DE Human foetal liver single exon nucleic acid probe #4135.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.4%; Score 35.6; DB 4; Length 1969;
Best Local Similarity 45.9%; Pred. No. 69;
RESULT 943
ID AA135486 standard; DNA; 1969 BP.
DE Probe #4172 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.4%; Score 35.6; DB 4; Length 1969;
Best Local Similarity 45.9%; Pred. No. 69;
RESULT 944
ID ABA45341 standard; DNA; 1969 BP.
DE Human breast cell single exon nucleic acid probe #4036.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 2.4%; Score 35.6; DB 4; Length 1969;
Best Local Similarity 45.9%; Pred. No. 69;
RESULT 945
ID ABA25506 standard; DNA; 1969 BP.
DE Probe #3972 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.4%; Score 35.6; DB 4; Length 1969;
Best Local Similarity 45.9%; Pred. No. 69;
RESULT 946
ID AAK29533 standard; DNA; 1969 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 4090.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.4%; Score 35.6; DB 4; Length 1969;
Best Local Similarity 45.9%; Pred. No. 69;
RESULT 947
ID AAK04048 standard; DNA; 1969 BP.
DE Human brain expressed single exon probe SEQ ID NO: 4039.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.4%; Score 35.6; DB 4; Length 1969;
Best Local Similarity 45.9%; Pred. No. 69;
RESULT 948
ID ABS29157 standard; DNA; 1969 BP.
DE Human liver single exon probe, SEQ ID NO 4147.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.4%; Score 35.6; DB 4; Length 1969;
Best Local Similarity 45.9%; Pred. No. 69;
RESULT 949
ID AA103958 standard; DNA; 1969 BP.
DE Probe #3949 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.4%; Score 35.6; DB 5; Length 1969;
Best Local Similarity 45.9%; Pred. No. 69;
RESULT 950
ID ABS04084 standard; DNA; 1969 BP.
DE Human genome-derived single exon probe from lung SEQ ID NO 4075.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.4%; Score 35.6; DB 6; Length 1969;
Best Local Similarity 45.9%; Pred. No. 69;
RESULT 951
ID AAF59600 standard; cDNA; 2035 BP.
DE Human cell cycle and proliferation protein CCYPR-11 cDNA, SEQ ID NO:65.
PN WO200107471-A2.
PD 01-FEB-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 35.6; DB 4; Length 2035;
Best Local Similarity 47.0%; Pred. No. 70;
RESULT 952
ID ADE47789 standard; DNA; 2066 BP.
DE Human NOV45F gene SEQ ID NO:151.
PN WO2003076642-A2.
PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35.6; DB 10; Length 2066;
Best Local Similarity 57.0%; Pred. No. 71;
RESULT 953
ID ADH41892 standard; DNA; 2066 BP.
DE Novel human nucleic acid NOV36a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35.6; DB 12; Length 2066;


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Best Local Similarity 57.0%; Pred. No. 71;
RESULT 954
ID ADJ79059 standard; DNA; 2066 BP.
DE Human NOVX protein Nov45F gene sequence.
PN US2004014053-A1.
PD 22-JAN-2004.
PA (ZERRH/) ZERHUSEN B D.
PA (PATR/) PATURAJAN M.
PA (KEKU/) KEKUDA R.
PA (MILL/) MILLER C E.
PA (RIEG/) RIEGER D K.
PA (PENNA) PENNA C B A.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (BERG/) BERGHS C.
PA (ZHON/) ZHONG M.
PA (CASM/) CASHMAN S J.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (PADI/) PADIGARU M.
PA (SMIT/) SMITHSON G.
PA (JIMW/) JI W.
PA (GORM/) GORMAN L.
PA (VERN/) VERNET C A M.
PA (LEIT/) LEITE M W.
PA (GUOX/) GUO X S.
PA (ANDE/) ANDERSON D W.
PA (SEPT/) SPYTEK K A.
PA (GERL/) GERLACH V.
PA (BURC/) BURGESS C E.
PA (KHRA/) KHRAMTSOV N V.
PA (ORTT/) ORT T.
PA (ELER/) ELIERMAN K.
PA (RAST/) RASTELLI L.
PA (AGEE/) AGEE M L.
PA (CHAU/) CHAUDHURI A.
PA (CHAN/) CHANT U S.
PA (DIP/) DIPPEO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A J.
PA (GANG/) GANGOLLI E A.
PA (GIOT/) GIOT L.
PA (IOTC/) IOTI C E.
PA (ROTH/) ROTHENBERG M E.
PA (SPAD/) SPADERNA S K.
PA (HJAL/) HJALT T.
PA (LIUX/) LIU X.
PA (TAUP/) TAUPIER R J.
PA (CATT/) CATTERTON E.
PA (SHEN/) SHENOY S G.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 12; Length 2066;
RESULT 955
ID ADO54827 standard; DNA; 2136 BP.
DE Human macrophage stimulating protein (MSP) DNA SegID 1.
PN KR2003003840-A.
PD 14-JAN-2003.
PA (PANG-) PANGENOMICS CO LTD.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 11; Length 2136;
RESULT 956
ID AAC48435 standard; DNA; 2173 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57468.
PN EP1033405-A2.
PD 06-SEP-2000.
PA
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 3; Length 2173;
RESULT 957
ID AD745831 standard; cDNA; 2205 BP.
DE Bacterial polynucleotide #20582.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 13; Length 2205;
RESULT 958
ID AAT7149 standard; cDNA; 2213 BP.
DE Macrophage stimulating protein C672X deletion variant cDNA.
PN EP750040-A2.
PD 27-DEC-1996.
PA (TOYM) TOYO BOSEKI KK.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 2; Length 2213;
RESULT 959
ID AAT7145 standard; cDNA; 2216 BP.
DE Macrophage stimulating protein C672X variant cDNA.
PN EP750040-A2.
PD 27-DEC-1996.
PA (TOYM) TOYO BOSEKI KK.
Query Match
Best Local Similarity 57.0%; Pred. No. 73;
RESULT 960
ID AAV72083 standard; cDNA; 2216 BP.
DE Human MSP cDNA.
PN WO9855141-A1.
PD 10-DEC-1998.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 2; Length 2216;
RESULT 961
ID ABV75112 standard; cDNA; 2216 BP.
DE Human hepatocyte growth factor-like protein (HGFL) encoding cDNA.
PN WO200283074-A2.
PD 24-OCT-2002.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 8; Length 2216;
RESULT 962
ID AAQ79724 standard; cDNA to mRNA; 2219 BP.
DE Human I5/3 tumour suppressor gene (Phe214 polymorphism).
PN US5315000-A.
PD 24-MAY-1994.
PA (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 2; Length 2219;
RESULT 963
ID AAQ79723 standard; cDNA to mRNA; 2219 BP.
DE Human I5/3 tumour suppressor gene (Cye214 polymorphism).
PN US5315000-A.
PD 24-MAY-1994.
PA (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 2; Length 2219;
RESULT 964
ID AAT62436 standard; cDNA to mRNA; 2219 BP.
DE Human I5/3 partial clone #33 polymorphism #1.
PN US5606029-A.
PD 25-FEB-1997.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 2; Length 2219;
RESULT 965
ID AAT62437 standard; cDNA to mRNA; 2219 BP.
DE Human I5/3 partial clone #33 polymorphism #2.
PN US5606029-A.
PD 25-FEB-1997.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 2; Length 2219;
RESULT 966
ID ABV94342 standard; cDNA; 2219 BP.
DE Breast carcinoma related nucleotide sequence SEQ ID NO:333.
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PN WO200246467-A2.
PD 13-JUN-2002.
PA (IPSO-) IPSOGEN.
Query Match 2.4%; Score 35.6; DB 6; Length 2219;
Best Local Similarity 57.0%; Pred. No. 73;
RESULT 967
ID AD084917 standard; cDNA; 2220 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1731.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH-) GENENTECH INC.
PA (WOTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.4%; Score 35.6; DB 13; Length 2220;
Best Local Similarity 57.0%; Pred. No. 73;
RESULT 968
ID AA079729 standard; cDNA; 2262 BP.
DE Full-length human I5/3 tumour suppressor gene cDNA.
PN US531500-A.
PD 24-MAY-1994.
PA (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.
Query Match 2.4%; Score 35.6; DB 2; Length 2262;
Best Local Similarity 57.0%; Pred. No. 74;
RESULT 969
ID AAT62439 standard; cDNA to mRNA; 2262 BP.
DE Human I5/3 construct gene.
PN US5606029-A.
PD 25-FEB-1997.
PA (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.
Query Match 2.4%; Score 35.6; DB 2; Length 2262;
Best Local Similarity 57.0%; Pred. No. 74;
RESULT 970
ID ADF81916 standard; DNA; 2292 BP.
DE Leukemia-related DNA sequence #2472.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 2.4%; Score 35.6; DB 10; Length 2292;
Best Local Similarity 57.0%; Pred. No. 74;
RESULT 971
ID ACC42371 standard; DNA; 2440 BP.
DE Human extracellular messenger, EXMES-11, coding sequence.
PN WO2003018612-A2.
PD 06-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 35.6; DB 8; Length 2440;
Best Local Similarity 57.0%; Pred. No. 77;
RESULT 972
ID AA159516 standard; cDNA; 2482 BP.
DE Human polynucleotide SEQ ID NO 1719.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35.6; DB 4; Length 2482;
Best Local Similarity 47.0%; Pred. No. 77;
RESULT 973
ID ACN41133 standard; cDNA; 2493 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:8.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.4%; Score 35.6; DB 13; Length 2493;
Best Local Similarity 57.0%; Pred. No. 78;
RESULT 974
ID ACC42370 standard; DNA; 2573 BP.
DE Human extracellular messenger, EXMES-10, coding sequence.
PN WO2003018612-A2.
PD 06-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 2.4%; Score 35.6; DB 8; Length 2573;
Best Local Similarity 57.0%; Pred. No. 79;
RESULT 975
ID ADS56284 standard; cDNA; 2586 BP.
DE Bacterial polynucleotide #8271.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SIATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.4%; Score 35.6; DB 13; Length 2586;
Best Local Similarity 55.7%; Pred. No. 79;
RESULT 976
ID ACN41131 standard; cDNA; 2589 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:6.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.4%; Score 35.6; DB 13; Length 2589;
Best Local Similarity 57.0%; Pred. No. 79;
RESULT 977
ID AAL51943 standard; DNA; 2598 BP.
DE Human extracellular messenger gene #1.
PN WO2003002610-A1.
PD 09-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 35.6; DB 8; Length 2598;
Best Local Similarity 57.0%; Pred. No. 79;
RESULT 978
ID AAI17666 standard; cDNA; 2666 BP.
DE Human cDNA sequence SEQ ID NO:17576.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.4%; Score 35.6; DB 4; Length 2666;
Best Local Similarity 47.0%; Pred. No. 80;
RESULT 979
ID ACC42374 standard; DNA; 2769 BP.
DE Human extracellular messenger, EXMES-14, coding sequence.
PN WO2003018612-A2.
PD 06-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 35.6; DB 8; Length 2769;
Best Local Similarity 57.0%; Pred. No. 82;
RESULT 980
ID ACN41130 standard; cDNA; 3140 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:5.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.4%; Score 35.6; DB 13; Length 3140;
Best Local Similarity 57.0%; Pred. No. 87;
RESULT 981
ID AA865913 standard; cDNA; 4029 BP.
DE DNA encoding novel human diagnostic protein #1717.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35.6; DB 5; Length 4029;
Best Local Similarity 51.2%; Pred. No. 98;
RESULT 982
ID ADD29793 standard; mRNA; 6997 BP.
DE Human tumour suppressor mRNA SEQ ID NO:251.
PN WO2003058201-A2.
PD 17-JUL-2003.
PA (QUAR-) QUARK BIOTECH INC.
PA (CLEV-) CLEVELAND CLINIC FOUND.
Query Match 2.4%; Score 35.6; DB 10; Length 6997;
Best Local Similarity 51.2%; Pred. No. 1.3e+02;
RESULT 983
ID AAQ25975 standard; DNA; 15377 BP.

DE MH mutant porcine ryanodine receptor cDNA.
PN WO211387-A1.
PD 09-JUL-1992.
PA (UTOR) UNIV TORONTO INNOVATIONS FOUND.
PA (UTG) UNIV GUELPH.
Query Match 2.4%; Score 35.6; DB 2; Length 15377;
Best Local Similarity 55.7%; Pred. No. 1.9e+02;
RESULT 984
ID ADO59365 standard; DNA; 49087 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:1.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 12; Length 49087;
Best Local Similarity 53.6%; Pred. No. 3.4e+02;
RESULT 985
ID ABD32540 standard; DNA; 49175 BP.
DE Human cancer-associated genomic DNA HD7-023.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 13; Length 49175;
Best Local Similarity 46.7%; Pred. No. 3.4e+02;
RESULT 986
ID ADS73531 standard; cDNA; 73882 BP.
DE tcp gene cluster.
Query Match 2.4%; Score 35.6; DB 13; Length 73882;
Best Local Similarity 46.4%; Pred. No. 4.2e+02;
RESULT 987
ID ADQ97278 standard; DNA; 86149 BP.
DE Human cancer associated sequence HD08-025, SEQ ID 254.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 12; Length 86149;
Best Local Similarity 57.0%; Pred. No. 4.5e+02;
RESULT 988
ID ABD33589 standard; DNA; 92219 BP.
DE Murine cancer-associated (CA) gene MD07-119.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 13; Length 92219;
Best Local Similarity 54.6%; Pred. No. 4.7e+02;
RESULT 989
Query Match 2.4%; Score 35.6; DB 10; Length 110000;
Best Local Similarity 57.0%; Pred. No. 5.1e+02;
RESULT 990
Query Match 2.4%; Score 35.6; DB 10; Length 110000;
Best Local Similarity 57.0%; Pred. No. 5.1e+02;
RESULT 991
ID ACN44586 standard; DNA; 118931 BP.
DE Human genomic sequence hCG30014.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 11; Length 118931;
Best Local Similarity 54.6%; Pred. No. 5.3e+02;
RESULT 992
ID ABD32827 standard; DNA; 129381 BP.
DE Human cancer-associated genomic DNA HD17-008.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 13; Length 129381;
Best Local Similarity 54.6%; Pred. No. 5.5e+02;
RESULT 993
ID ADO97526 standard; DNA; 151052 BP.
DE Mouse cancer associated sequence MD09-009, SEQ ID 503.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 12; Length 151052;

Best Local Similarity 48.1%; Pred. No. 5.9e+02;
RESULT 994
ID ABK83568 standard; DNA; 201143 BP.
DE Human DNA differentially expressed in granulocytic cells #139.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.4%; Score 35.6; DB 6; Length 201143;
Best Local Similarity 54.6%; Pred. No. 6.8e+02;
RESULT 995
ID ABK38848 standard; cDNA; 385 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4013.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.4%; Score 35.4; DB 8; Length 385;
Best Local Similarity 47.2%; Pred. No. 35;
RESULT 996
ID AAS90684 standard; cDNA; 393 BP.
DE DNA encoding novel human diagnostic protein #26488.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35.4; DB 5; Length 393;
Best Local Similarity 48.3%; Pred. No. 35;
RESULT 997
ID ABX42580 standard; cDNA; 413 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #7745.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.4%; Score 35.4; DB 8; Length 413;
Best Local Similarity 47.2%; Pred. No. 36;
RESULT 998
ID ABX36854 standard; cDNA; 416 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2019.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.4%; Score 35.4; DB 8; Length 416;
Best Local Similarity 47.2%; Pred. No. 36;
RESULT 999
ID ABD11421 standard; DNA; 423 BP.
DE Pseudomonas aeruginosa polynucleotide #10025.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 35.4; DB 11; Length 423;
Best Local Similarity 49.8%; Pred. No. 36;
RESULT 1000
ID ABX37512 standard; cDNA; 428 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2677.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.4%; Score 35.4; DB 8; Length 428;
Best Local Similarity 47.2%; Pred. No. 37;
RESULT 1001
ID ADR46439 standard; DNA; 428 BP.
DE B napus caltractin-like protein coding sequence SEQ ID NO: 5.
PN WO2004070035-A2.

PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 2.4%; Score 35.4; DB 13; Length 428;
Best Local Similarity 48.7%; Pred. No. 37;
RESULT 1002
ID ABX35170 standard; cDNA; 450 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #335.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYATT) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.4%; Score 35.4; DB 8; Length 450;
Best Local Similarity 47.2%; Pred. No. 38;
RESULT 1003
ID ACH14525 standard; cDNA; 492 BP.
DE Human adult brain cDNA #1737.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.4%; Score 35.4; DB 9; Length 492;
Best Local Similarity 47.2%; Pred. No. 39;
RESULT 1004
ID ADA69809 standard; DNA; 579 BP.
DE Rice gene, SEQ ID 3132.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 35.4; DB 8; Length 579;
Best Local Similarity 48.3%; Pred. No. 43;
RESULT 1005
ID ADE76270 standard; DNA; 701 BP.
DE Human BSK-36-8 complementary strand DNA.
PN EP1310567-A2.
PD 14-MAY-2003.
PA (OLIG-) OLIGENE GMBH.
Query Match 2.4%; Score 35.4; DB 10; Length 701;
Best Local Similarity 47.2%; Pred. No. 47;
RESULT 1006
ID ACFO4830 standard; DNA; 1008 BP.
DE M lichenicola melithiazol synthesis gene ORF 5.
PN WO2003080828-A2.
PD 02-OCT-2003.
PA (GBFB) GBF GES BIOTECH FORSCHUNG GMBH.
Query Match 2.4%; Score 35.4; DB 10; Length 1008;
Best Local Similarity 49.2%; Pred. No. 56;
RESULT 1007
ID ADO83950 standard; cDNA; 1525 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #764.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.4%; Score 35.4; DB 12; Length 1525;
Best Local Similarity 47.2%; Pred. No. 69;
RESULT 1008
ID ADO85345 standard; cDNA; 1525 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2159.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.4%; Score 35.4; DB 13; Length 1525;
Best Local Similarity 47.2%; Pred. No. 69;
RESULT 1009
ID ACF34491 standard; DNA; 1526 BP.

DE Gene encoding angiogenesis protein BN0112.
PN WO2003027285-A1.
PD 03-APR-2003.
PA (BION-) BIONOMICS LTD.
Query Match 2.4%; Score 35.4; DB 8; Length 1526;
Best Local Similarity 47.2%; Pred. No. 69;
RESULT 1010
ID ACC50093 standard; cDNA; 1526 BP.
DE Breast cancer associated cDNA sequence SEQ ID NO:34.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.4%; Score 35.4; DB 8; Length 1526;
Best Local Similarity 47.2%; Pred. No. 69;
RESULT 1011
ID ADF81420 standard; DNA; 1526 BP.
DE Leukaemia-related DNA sequence #1976.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (TYLU-) UNITV LUDWIG MAXIMILIANS.
PA (HAPE/) HAPELACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 2.4%; Score 35.4; DB 10; Length 1526;
Best Local Similarity 47.2%; Pred. No. 69;
RESULT 1012
ID ACN39732 standard; cDNA; 1526 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325923, SEQ ID NO:4063.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 35.4; DB 13; Length 1526;
Best Local Similarity 47.2%; Pred. No. 69;
RESULT 1013
ID AAT91855 standard; cDNA; 1559 BP.
DE DUB-1 enhancer/promoter.
PN WO9706247-A2.
PD 20-FEB-1997.
PA (DAND) DNA PARBER CANCER INST INC.
Query Match 2.4%; Score 35.4; DB 2; Length 1559;
Best Local Similarity 51.6%; Pred. No. 70;
RESULT 1014
ID ACA39654 standard; DNA; 1770 BP.
DE Prokaryotic essential gene #21311.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.4%; Score 35.4; DB 8; Length 1770;
Best Local Similarity 52.3%; Pred. No. 74;
RESULT 1015
ID ACN92807 standard; DNA; 3535 BP.
DE Breast cancer related marker, seq id 13957.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.4%; Score 35.4; DB 11; Length 3535;
Best Local Similarity 47.2%; Pred. No. 1e+02;
RESULT 1016
ID AD124476 standard; cDNA; 3718 BP.
DE Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:26.
PN WO2004004785-A1.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 2.4%; Score 35.4; DB 12; Length 3718;
Best Local Similarity 47.2%; Pred. No. 1.1e+02;
RESULT 1017
ID ACC46250 standard; cDNA; 3978 BP.
DE Human dthp intracellular signalling protein-encoding cDNA.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 35.4; DB 8; Length 3978;

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Best Local Similarity 47.2%; Pred. No. 1.1e+02;
RESULT 1018
ID AAT74034 standard; cDNA; 4621 BP.
DE Mouse male-enhanced antigen-2 encoding cDNA.
PN UF09121869-A.
PD 13-MAY-1997.
PA (ITOH-) ITO HAM KK.
Query Match 2.4%; Score 35.4; DB 2; Length 4621;
Best Local Similarity 51.2%; Pred. No. 1.2e+02;
RESULT 1019
ID AAX04132 standard; cDNA; 4621 BP.
DE Mouse male enhanced antigen 2 encoding cDNA.
PN JP1018622-A.
PD 26-JAN-1999.
PA (ITOH-) ITO HAM KK.
Query Match 2.4%; Score 35.4; DB 2; Length 4621;
Best Local Similarity 51.2%; Pred. No. 1.2e+02;
RESULT 1020
ID ABD32920 standard; cDNA; 5012 BP.
DE Human cancer-associated cDNA HR18-043.9.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 5012;
Best Local Similarity 59.7%; Pred. No. 1.2e+02;
RESULT 1021
ID ABD32918 standard; cDNA; 5099 BP.
DE Human cancer-associated cDNA HR18-043.7.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 5099;
Best Local Similarity 59.7%; Pred. No. 1.3e+02;
RESULT 1022
ID ABD32919 standard; cDNA; 5186 BP.
DE Human cancer-associated cDNA HR18-043.8.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 5186;
Best Local Similarity 59.7%; Pred. No. 1.3e+02;
RESULT 1023
ID ABD33393 standard; DNA; 24318 BP.
DE Human cancer-associated (CA) gene HD07-073.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 24318;
Best Local Similarity 46.2%; Pred. No. 2.7e+02;
RESULT 1024
ID AAD52172 standard; DNA; 26000 BP.
DE Human interferon gamma receptor 1 (IFNGR1) gene.
PN WO200288162-A1.
PD 07-NOV-2002.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.4%; Score 35.4; DB 10; Length 26000;
Best Local Similarity 53.2%; Pred. No. 2.8e+02;
RESULT 1025
ID ADG97945 standard; DNA; 39414 BP.
DE Mouse cancer associated sequence MD11-027, SEQ ID 922.
PN WO2004060304-A2.
PD 22-JUN-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 12; Length 39414;
Best Local Similarity 51.6%; Pred. No. 3.5e+02;
RESULT 1026
ID ABD32684 standard; DNA; 41991 BP.
DE Human cancer-associated genomic DNA HD13-117.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 41991;
Best Local Similarity 53.2%; Pred. No. 3.6e+02;

RESULT 1027
ID ACF04818 standard; DNA; 51855 BP.
DE Melithiazol biosynthetic gene cluster.
PN WO2003080828-A2.
PD 02-OCT-2003.
PA (GBRB-) GBR GBS BIOTECH FORSCHUNG GMBH.
Query Match 2.4%; Score 35.4; DB 10; Length 51855;
Best Local Similarity 49.2%; Pred. No. 4e+02;
RESULT 1028
ID ABD33551 standard; DNA; 84410 BP.
DE Murine cancer-associated (CA) gene MD07-110.
PN WO2004058146-A2.
PD 15-JUN-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 84410;
Best Local Similarity 54.1%; Pred. No. 5.1e+02;
RESULT 1029
ID ACN44000 standard; DNA; 90026 BP.
DE Mouse genomic sequence mCG12663.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 11; Length 90026;
Best Local Similarity 47.5%; Pred. No. 5.3e+02;
RESULT 1030
ID ADC85287 standard; DNA; 96596 BP.
DE Mouse fish genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 10; Length 96596;
Best Local Similarity 51.6%; Pred. No. 5.4e+02;
RESULT 1031
ID ADX02807 standard; DNA; 96597 BP.
DE Mouse fish carcinoma associated gene, SEQ ID NO.1325.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 9; Length 96597;
Best Local Similarity 51.6%; Pred. No. 5.4e+02;
RESULT 1032
ID ADB72545 standard; DNA; 96597 BP.
DE Mouse fish gene.
PN WO200308583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 10; Length 96597;
Best Local Similarity 51.6%; Pred. No. 5.4e+02;
RESULT 1033
ID ADM74402 standard; DNA; 96597 BP.
DE Murine carcinoma associated (CA) nucleic acid #37.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR-) MORRIS D W.
Query Match 2.4%; Score 35.4; DB 12; Length 96597;
Best Local Similarity 51.6%; Pred. No. 5.4e+02;
RESULT 1034
ID ABX16390 standard; DNA; 659158 BP.
DE Mouse high growth region.
PN US2002155564-A1.
PD 24-OCT-2002.
PA (REGC-) UNIV CALIFORNIA.
Query Match 2.4%; Score 35.4; DB 8; Length 110000;
Best Local Similarity 56.4%; Pred. No. 5.8e+02;
RESULT 1035
ID ADG70184 standard; DNA; 379652 BP.
DE DNA of BAC BA236m15-00303.
PN WO2003000727-A2.
PD 03-JAN-2003.
PA (ISIS-) ISIS INNOVATIONS LTD.
Query Match 2.4%; Score 35.4; DB 10; Length 110000;
Best Local Similarity 47.2%; Pred. No. 5.8e+02;
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RESULT 1036
ID AD097050 standard; DNA; 687411 BP.
DE Human cancer associated sequence HD08-001, SEQ ID 26.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 12; Length 110000;
Best Local Similarity 50.9%; Pred. No. 5.8e+02;
RESULT 1037
Query Match 2.4%; Score 35.4; DB 13; Length 110000;
Best Local Similarity 50.9%; Pred. No. 5.8e+02;
RESULT 1038
ID ABD32911 standard; DNA; 783062 BP.
DE Human cancer-associated genomic DNA HD18-043.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 110000;
Best Local Similarity 59.7%; Pred. No. 5.8e+02;
RESULT 1039
ID ABD32886 standard; DNA; 117328 BP.
DE Mouse cancer-associated genomic DNA MD18-013.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 117328;
Best Local Similarity 55.2%; Pred. No. 6e+02;
RESULT 1040
ID ADP80536 standard; DNA; 118788 BP.
DE Human HPC2/ELAC2 gene SeqID1.
PN JP2004166565-A.
PD 17-JUN-2004.
PA (TAKA/) TAKAHASHI H.
PA (WATA/) WATANABE M.
PA (FURU/) FURUSATO M.
PA (HONS) YAKULT HONSHA KK.
Query Match 2.4%; Score 35.4; DB 12; Length 118788;
Best Local Similarity 46.2%; Pred. No. 6e+02;
RESULT 1041
ID ABR63573 standard; cDNA; 130263 BP.
DE Human cDNA differentially expressed in granulocytic cells #144.
PN WO200228939-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.4%; Score 35.4; DB 6; Length 130263;
Best Local Similarity 63.5%; Pred. No. 6.3e+02;
RESULT 1042
ID ABR39880 standard; cDNA; 406 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #5045.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATN/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.4%; Score 35.2; DB 8; Length 406;
Best Local Similarity 48.1%; Pred. No. 41;
RESULT 1043
ID ADA48417 standard; DNA; 500 BP.
DE Rice gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 35.2; DB 9; Length 500;
Best Local Similarity 48.1%; Pred. No. 45;
RESULT 1044
ID ADN73638 standard; cDNA; 510 BP.
DE Thale cress cDNA repressed in E2fe/Dpa expressing plants SeqID 1533.
PN WO2004035798-A2.
PD 23-APR-2004.
PA (CROP-) CROPPESIGN NV.
Query Match 2.4%; Score 35.2; DB 12; Length 510;
Best Local Similarity 46.1%; Pred. No. 46;

RESULT 1045
ID ADA9332 standard; cDNA; 557 BP.
DE Bacterial polynucleotide #4075.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.4%; Score 35.2; DB 13; Length 557;
Best Local Similarity 60.4%; Pred. No. 48;
RESULT 1046
ID AAC6937 standard; DNA; 594 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO. 51958.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.4%; Score 35.2; DB 3; Length 594;
Best Local Similarity 48.1%; Pred. No. 49;
RESULT 1047
ID ABX98560 standard; cDNA; 615 BP.
DE Rice leaf specific expression label sequence #12.
PN CN1364933-A.
PD 21-AUG-2002.
PA (UYZH-) UNIV ZHEJIANG.
Query Match 2.4%; Score 35.2; DB 8; Length 615;
Best Local Similarity 53.3%; Pred. No. 50;
RESULT 1048
ID ADC75910 standard; DNA; 632 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 834.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match 2.4%; Score 35.2; DB 10; Length 632;
Best Local Similarity 52.0%; Pred. No. 51;
RESULT 1049
ID ACU20023 standard; DNA; 674 BP.
DE DNA clone originating in barley containing SNP encoding sequence #10014.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 2.4%; Score 35.2; DB 9; Length 674;
Best Local Similarity 53.7%; Pred. No. 52;
RESULT 1050
ID ACI20017 standard; DNA; 708 BP.
DE DNA clone originating in barley containing SNP encoding sequence #10008.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 2.4%; Score 35.2; DB 9; Length 708;
Best Local Similarity 53.7%; Pred. No. 54;
RESULT 1051
ID ABR62083 standard; cDNA; 1010 BP.
DE Human cDNA encoding novel secreted protein LP218.
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 2.4%; Score 35.2; DB 6; Length 1010;
Best Local Similarity 50.0%; Pred. No. 64;
RESULT 1052
ID AAF61042 standard; DNA; 2250 BP.
DE P. putida KT2440-associated DNA ORF06553.
PN DE19935086-A1.
PD 01-FEB-2001.
PA (TIGR-) TIGR INST GENOMIC RES.
PA (QUIA-) QUIAGEN GMBH.
PA (GAPF) GFS BIOTECHNOLOGISCHE FORSCHUNG MBH.
PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
PA (MEDT-) MEDIZINISCHE HOCHSCHULE HANNOVER.
Query Match 2.4%; Score 35.2; DB 4; Length 2250;
Best Local Similarity 49.0%; Pred. No. 95;
RESULT 1053
ID ADA02845 standard; cDNA; 2403 BP.

DE Mouse Fgf3 carcinoma associated coding sequence, SEQ ID NO:1363.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 9; Length 2403;
Best Local Similarity 51.2%; Pred. No. 98;
RESULT 1054
ID ADB72583 standard; cDNA; 2403 BP.
DE Mouse Fgf3 cDNA.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 10; Length 2403;
Best Local Similarity 51.2%; Pred. No. 98;
RESULT 1055
ID ADC85324 standard; DNA; 2403 BP.
DE Mouse Fgf3 mRNA sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 10; Length 2403;
Best Local Similarity 51.2%; Pred. No. 98;
RESULT 1056
ID ADM74440 standard; DNA; 2403 BP.
DE Murine carcinoma associated (CA) nucleic acid #57.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 2.4%; Score 35.2; DB 12; Length 2403;
Best Local Similarity 51.2%; Pred. No. 98;
RESULT 1057
ID AA209484 standard; DNA; 2606 BP.
DE Bovine retina 1h ion channel DNA fragment.
PN WO9942574-A1.
PD 26-AUG-1999.
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
Query Match 2.4%; Score 35.2; DB 2; Length 2606;
Best Local Similarity 57.1%; Pred. No. 1e+02;
RESULT 1058
ID ADK06684 standard; DNA; 2692 BP.
DE HOMO protein encoding sequence #31.
PN WO2004014946-A1.
PD 19-FEB-2004.
PA (NEWO-) NEWORGEN LTD.
Query Match 2.4%; Score 35.2; DB 12; Length 2692;
Best Local Similarity 48.1%; Pred. No. 1e+02;
RESULT 1059
ID ADA02844 standard; cDNA; 2887 BP.
DE Mouse Fgf3 carcinoma associated cDNA, SEQ ID NO:1362.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 9; Length 2887;
Best Local Similarity 51.2%; Pred. No. 1.1e+02;
RESULT 1060
ID ADB72582 standard; mRNA; 2887 BP.
DE Mouse Fgf3 mRNA.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 10; Length 2887;
Best Local Similarity 51.2%; Pred. No. 1.1e+02;
RESULT 1061
ID ADC85323 standard; DNA; 2887 BP.
DE Mouse Fgf3 genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 10; Length 2887;
Best Local Similarity 51.2%; Pred. No. 1.1e+02;
RESULT 1062
ID ADM74439 standard; DNA; 2887 BP.

DE Murine carcinoma associated (CA) nucleic acid #56.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 2.4%; Score 35.2; DB 12; Length 2887;
Best Local Similarity 51.2%; Pred. No. 1.1e+02;
RESULT 1063
ID AA209467 standard; DNA; 2922 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 13216.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
Query Match 2.4%; Score 35.2; DB 2; Length 2922;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
RESULT 1064
ID ABL20561 standard; DNA; 3318 BP.
DE Human fibroblast growth factor receptor 3 (FGFR3) mutant cDNA.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Query Match 2.4%; Score 35.2; DB 4; Length 3318;
Best Local Similarity 46.4%; Pred. No. 1.2e+02;
RESULT 1065
ID AAD34802 standard; cDNA; 8083 BP.
DE Mouse fibroblast growth factor receptor 3 (FGFR3) mutant cDNA.
PN US6256532-B1.
PD 24-JUL-2001.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (PROCC-) PROCHON BIOTECH LTD.
Query Match 2.4%; Score 35.2; DB 5; Length 8083;
Best Local Similarity 51.2%; Pred. No. 1.8e+02;
RESULT 1066
ID ABL33718 standard; DNA; 17934 BP.
DE Human immune system associated gene SEQ ID NO: 1691.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPICENOMICS AG.
Query Match 2.4%; Score 35.2; DB 6; Length 17934;
Best Local Similarity 50.9%; Pred. No. 2.7e+02;
RESULT 1067
ID ADR66967 standard; DNA; 34571 BP.
DE Mouse cancer associated gene genomic sequence SEQ ID NO:13.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.2; DB 13; Length 34571;
Best Local Similarity 54.7%; Pred. No. 3.7e+02;
RESULT 1068
ID ACN44230 standard; DNA; 66973 BP.
DE Human genomic sequence hCG21559.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 11; Length 66973;
Best Local Similarity 52.0%; Pred. No. 5.2e+02;
RESULT 1070
ID ADS73531 standard; cDNA; 73882 BP.
DE tcp gene cluster.
Query Match 2.4%; Score 35.2; DB 13; Length 73882;
Best Local Similarity 52.0%; Pred. No. 5.4e+02;
RESULT 1071
ID ACN44380 standard; DNA; 76846 BP.
DE Mouse genomic sequence mCG18525.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 11; Length 76846;
Best Local Similarity 58.7%; Pred. No. 5.5e+02;
RESULT 1072

ID ADC86916 standard; DNA; 349989 BP.
DE Human GPCR gene SEQ ID NO:1369.
PN EPI270724-A2.
PD 02-JAN-2003.
PA (NADAC-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ABSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 2.4%; Score 35.2; DB 10; Length 349989;
Best Local Similarity 65.0%; Pred. No. 1.1e+03;
RESULT 1073

ID ADA58745 standard; cDNA; 224 BP.
DE Maize sucrose synthase EST #389.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.4%; Score 35; DB 9; Length 224;
Best Local Similarity 55.3%; Pred. No. 34;
RESULT 1074

ID ADA58686 standard; cDNA; 235 BP.
DE Maize sucrose synthase EST #330.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.4%; Score 35; DB 9; Length 235;
Best Local Similarity 55.3%; Pred. No. 35;
RESULT 1075

ID ADA58541 standard; cDNA; 270 BP.
DE Maize sucrose synthase EST #185.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.4%; Score 35; DB 9; Length 270;
Best Local Similarity 55.3%; Pred. No. 38;
RESULT 1076

ID ADA49273 standard; DNA; 339 BP.
DE Maize gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 35; DB 9; Length 339;
Best Local Similarity 48.7%; Pred. No. 42;
RESULT 1077

ID ABX40527 standard; cDNA; 344 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #5692.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARB/) WARREN W C.
Query Match 2.4%; Score 35; DB 8; Length 344;
Best Local Similarity 45.5%; Pred. No. 43;
RESULT 1078

ID ADO19577 standard; DNA; 393 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2396.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.4%; Score 35; DB 12; Length 393;
Best Local Similarity 50.3%; Pred. No. 45;
RESULT 1079

ID ACH44942 standard; cDNA; 487 BP.
DE Human foetal brain cDNA #5667.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.

PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.4%; Score 35; DB 9; Length 487;
Best Local Similarity 61.5%; Pred. No. 51;
RESULT 1080

ID AAH10073 standard; cDNA; 547 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:6908.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.4%; Score 35; DB 4; Length 547;
Best Local Similarity 50.9%; Pred. No. 54;
RESULT 1081

ID ACH72546 standard; DNA; 598 BP.
DE Human genome derived single exon probe #5741.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 2.4%; Score 35; DB 12; Length 598;
Best Local Similarity 59.6%; Pred. No. 56;
RESULT 1082

ID ADA68731 standard; DNA; 805 BP.
DE Rice gene, SEQ ID 2054.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 35; DB 8; Length 805;
Best Local Similarity 47.8%; Pred. No. 65;
RESULT 1083

ID AAS44974 standard; cDNA; 814 BP.
DE cDNA encoding novel human secretory protein, Seq ID No 55.
PN WO200166689-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35; DB 5; Length 814;
Best Local Similarity 46.2%; Pred. No. 65;
RESULT 1084

ID ADT43885 standard; cDNA; 870 BP.
DE Bacterial polynucleotide #18636.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.4%; Score 35; DB 13; Length 870;
Best Local Similarity 48.7%; Pred. No. 68;
RESULT 1085

ID ADP28033 standard; DNA; 1176 BP.
DE Human secreted protein encoding sequence SEQ ID #31.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.4%; Score 35; DB 12; Length 1176;
Best Local Similarity 61.5%; Pred. No. 78;
RESULT 1086

ID ADM47892 standard; DNA; 1216 BP.
DE Polynucleotide sequence #310 useful in producing transgenic plants.
PN US200233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 2.4%; Score 35; DB 12; Length 1216;
Best Local Similarity 47.5%; Pred. No. 80;
RESULT 1087

ID ABD08729 standard; DNA; 1488 BP.
DE Pseudomonas aeruginosa polynucleotide #7333.
PN US6551795-B1.
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 35; DB 11; Length 1488;
Best Local Similarity 50.3%; Pred. No. 88;
RESULT 1088
ID ADE76934 standard; cDNA; 1498 BP.
DE Human cDNA differentially expressed in a liver disorder #71.
PN US200310871-A1.
PD 12-JUN-2003.
PA (KASE-) KASER M R.
Query Match 2.4%; Score 35; DB 12; Length 1498;
Best Local Similarity 61.5%; Pred. No. 88;
RESULT 1089
ID AA190669 standard; cDNA; 1520 BP.
DE Human polynucleotide SEQ ID NO 10729.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35; DB 4; Length 1520;
Best Local Similarity 59.6%; Pred. No. 89;
RESULT 1090
ID ABD08808 standard; DNA; 1593 BP.
DE Pseudomonas aeruginosa polynucleotide #7412.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 35; DB 11; Length 1593;
Best Local Similarity 50.3%; Pred. No. 91;
RESULT 1091
ID ADP28053 standard; DNA; 1692 BP.
DE Human secreted protein encoding sequence SEQ ID #51.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.4%; Score 35; DB 12; Length 1692;
Best Local Similarity 61.5%; Pred. No. 94;
RESULT 1092
ID ADP28010 standard; DNA; 1692 BP.
DE Human secreted protein encoding sequence SEQ ID #8.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.4%; Score 35; DB 12; Length 1692;
Best Local Similarity 61.5%; Pred. No. 94;
RESULT 1093
ID ADE47787 standard; DNA; 1698 BP.
DE Human NOV45e gene SEQ ID NO:149.
PN WO2003076642-A2.
PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 10; Length 1698;
Best Local Similarity 56.5%; Pred. No. 94;
RESULT 1094
ID ADH41894 standard; DNA; 1698 BP.
DE Novel human nucleic acid NOV36b.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 12; Length 1698;
Best Local Similarity 56.5%; Pred. No. 94;
RESULT 1095
ID ADJ79057 standard; DNA; 1698 BP.
DE Human NOVX protein NOV45E gene sequence.
PN US2004014053-A1.
PD 22-JAN-2004.
PA (ZERH-) ZERHUSEN B D.
PA (PAT/) PATURAJAN M.
PA (KEKU/) KEKUDA R.
PA (MILL/) MILLER C E.
PA (RIEG/) RIEGER D K.
PA (PENNA/) PENNA C B A.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (BERG/) BERGHS C.

PA (ZHON/) ZHONG M.
PA (CASW/) CASMAN S J.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (PADI/) PADIGARU M.
PA (SMIT/) SMITHSON G.
PA (JTW/) JI W.
PA (GORM/) GORMAN L.
PA (VERN/) VERNET C A M.
PA (LEIT/) LEITE M W.
PA (GUOX/) GUO X S.
PA (ANDE/) ANDERSON D W.
PA (SPYT/) SPYTEK K A.
PA (GERL/) GERLACH V.
PA (BURG/) BURGESS C E.
PA (KIRA/) KRAMTSOV N V.
PA (ORTY/) ORT T.
PA (ELLE/) ELLERMAN K.
PA (RAST/) RASTELLI L.
PA (AGEE/) AGE E M L.
PA (CHAU/) CHAUDHURI A.
PA (CHAN/) CHANT J S.
PA (DIP/) DIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A J.
PA (GANG/) GANGOLLI E A.
PA (GIOT/) GIOT L.
PA (OOIC/) OOI C E.
PA (ROTH/) ROTHENBERG M E.
PA (SPAD/) SPADERNA S K.
PA (HJAL/) HJALT T.
PA (LIUX/) LIU X.
PA (TAUP/) TAUPFER R J.
PA (CAT/) CATTERTON R.
PA (SHEN/) SHENDY S G.
Query Match 2.4%; Score 35; DB 12; Length 1698;
Best Local Similarity 56.5%; Pred. No. 94;
RESULT 1096
ID AAH17389 standard; cDNA; 1851 BP.
DE Human cDNA sequence SEQ ID NO:16827.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.4%; Score 35; DB 4; Length 1851;
Best Local Similarity 50.3%; Pred. No. 98;
RESULT 1097
ID ABA08292 standard; cDNA; 1890 BP.
DE Human equine herpesvirus p24 homologue-encoding cDNA, SEQ ID NO:68.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35; DB 4; Length 1890;
Best Local Similarity 49.7%; Pred. No. 99;
RESULT 1098
ID ABR08324 standard; DNA; 2011 BP.
DE Human NOV7 gene sequence.
PN WO200246408-A2.
PD 13-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 6; Length 2011;
Best Local Similarity 61.5%; Pred. No. 1e+02;
RESULT 1099
ID ABS59330 standard; DNA; 2011 BP.
DE Human macrophage stimulating protein precursor-like gene.
PN WO200233087-A2.
PD 25-APR-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 6; Length 2011;
Best Local Similarity 61.5%; Pred. No. 1e+02;
RESULT 1100
ID ADJ38433 standard; cDNA; 2011 BP.
DE Human cDNA encoding protein NOV5.
PN US2003212256-A1.

PD 13-NOV-2003.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLER I.
PA (PEYM/) PEYMAN J A.
PA (STON/) STONE D J.
PA (GUNT/) GUNTHER E.
PA (ELLE/) ELLERMAN K.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (GUOX/) GUO X.
PA (PAT/) PATTURAJAN M.
PA (TAUP/) TAUPIER R J.
PA (BURG/) BURGESS C E.
PA (ZERR/) ZERRHOSEN B D.
PA (KERU/) KERUDA R.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (GORM/) GORMAN L.
Query Match
Best Local Similarity 2.4%; Score 35; DB 10; Length 2011;
RESULT 1101
ID AAS83813 standard; cDNA; 2052 BP.
DE DNA encoding novel human diagnostic protein #19617.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.4%; Score 35; DB 5; Length 2052;
RESULT 1102
ID AD74313 standard; cDNA; 2139 BP.
DE Bacterial polynucleotide #18064.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 2.4%; Score 35; DB 13; Length 2139;
RESULT 1103
ID ABR92065 standard; DNA; 2200 BP.
DE DNA encoding novel hepatocyte growth factor-like protein #2.
PN WO200229058-A2.
PD 11-APR-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.4%; Score 35; DB 6; Length 2200;
RESULT 1104
ID ABR92064 standard; DNA; 2200 BP.
DE DNA encoding novel hepatocyte growth factor-like protein #1.
PN WO200229058-A2.
PD 11-APR-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.4%; Score 35; DB 6; Length 2200;
RESULT 1105
ID AAD26582 standard; cDNA; 2200 BP.
DE Human MSP precursor-like protein, POLY13 encoding cDNA.
PN WO200185767-A2.
PD 15-NOV-2001.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.4%; Score 35; DB 6; Length 2200;
RESULT 1106
ID ADE47779 standard; DNA; 2200 BP.
DE Human NOV45a gene seq ID NO:141.
PN WO2003076642-A2.

PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.4%; Score 35; DB 10; Length 2200;
RESULT 1107
ID ADH41896 standard; DNA; 2200 BP.
DE Novel human nucleic acid NOV36c.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.4%; Score 35; DB 12; Length 2200;
RESULT 1108
ID ADJ79049 standard; DNA; 2200 BP.
DE Human NOVX protein NOV45a gene sequence.
PN US2004014053-A1.
PD 22-JAN-2004.
PA (ZERR/) ZERRHOSEN B D.
PA (PAT/) PATTURAJAN M.
PA (KERU/) KERUDA R.
PA (MILL/) MILLER C E.
PA (RIEG/) RIEGER D K.
PA (PENA/) PENNA C E A.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (BERG/) BERGHS C.
PA (ZHON/) ZHONG M.
PA (CASM/) CASHMAN S J.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (PADI/) PADIGARU M.
PA (SMIT/) SMITHSON G.
PA (JTWI/) JI W.
PA (GORM/) GORMAN L.
PA (VERN/) VERNET C A M.
PA (LEIT/) LEITE M W.
PA (GUOX/) GUO X S.
PA (ANDE/) ANDERSON D W.
PA (SPYT/) SPYTEK K A.
PA (GERL/) GERLACH V.
PA (BURG/) BURGESS C E.
PA (KERA/) KHRAMTSOV N V.
PA (ORTT/) ORT T.
PA (ELLE/) ELLERMAN K.
PA (RAST/) RASTELI L.
PA (AGEE/) AGEE M L.
PA (CHAU/) CHAUDHURI A.
PA (CHAN/) CHANT J S.
PA (DIP/) DIPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A J.
PA (GANG/) GANGOLLI E A.
PA (GIOT/) GIOT L.
PA (OOIC/) OOI C E.
PA (ROTH/) ROTHENBERG M E.
PA (SPAD/) SPADERNA S K.
PA (HUAL/) HUALT T.
PA (LITUX/) LITUX.
PA (TAUP/) TAUPIER R J.
PA (CAT/) CATERTON E.
PA (SHEN/) SHENOV S G.
Query Match
Best Local Similarity 2.4%; Score 35; DB 12; Length 2200;
RESULT 1109
ID AAS83814 standard; cDNA; 2296 BP.
DE DNA encoding novel human diagnostic protein #19618.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.4%; Score 35; DB 5; Length 2296;
RESULT 1110
ID ACN41132 standard; cDNA; 2533 BP.

DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:7.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.4%; Score 35; DB 13; Length 2533;
Best Local Similarity 61.5%; Pred. No. 1.1e+02;
RESULT 1111
ID ADQ25501 standard; DNA; 2768 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8321.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.4%; Score 35; DB 12; Length 2768;
Best Local Similarity 44.3%; Pred. No. 1.2e+02;
RESULT 1112
ID ADK18361 standard; DNA; 3570 BP.
DE Human NOVX protein encoding gene #8.
PN WO2003057854-A2.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 10; Length 3570;
Best Local Similarity 55.3%; Pred. No. 1.4e+02;
RESULT 1113
ID ADK18363 standard; DNA; 4775 BP.
DE Human NOVX protein encoding gene #9.
PN WO2003057854-A2.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 10; Length 4775;
Best Local Similarity 55.3%; Pred. No. 1.6e+02;
RESULT 1114
ID AAS83815 standard; cDNA; 5635 BP.
DE DNA encoding novel human diagnostic protein #19619.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HISE-) HISEQ INC.
Query Match 2.4%; Score 35; DB 5; Length 5635;
Best Local Similarity 61.5%; Pred. No. 1.7e+02;
RESULT 1115
ID ADK18365 standard; DNA; 5760 BP.
DE Human NOVX protein encoding gene #10.
PN WO2003057854-A2.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 10; Length 5760;
Best Local Similarity 55.3%; Pred. No. 1.7e+02;
RESULT 1116
ID ADK18367 standard; DNA; 6008 BP.
DE Human NOVX protein encoding gene #11.
PN WO2003057854-A2.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 10; Length 6008;
Best Local Similarity 55.3%; Pred. No. 1.8e+02;
RESULT 1117
ID ADP13461 standard; DNA; 6008 BP.
DE Renal cell carcinoma differentially expressed gene #197.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP-) WYETH.
PA (TWIN-) TWINE N C.
PA (BURC-) BURCZYNSKI M E.
PA (TREP-) TREPICCHIO W L.
PA (DORN-) DORNER A.
PA (STOV-) STOVER U A.
PA (SLON-) SLONI D K.
Query Match 2.4%; Score 35; DB 12; Length 6008;
Best Local Similarity 55.3%; Pred. No. 1.8e+02;
RESULT 1118
ID ADC86968 standard; DNA; 6269 BP.
DE Human GPCR gene SEQ ID NO:1421.
PN EP1270724-A2.
PD 02-JAN-2003.

PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 2.4%; Score 35; DB 10; Length 6269;
Best Local Similarity 46.8%; Pred. No. 1.8e+02;
RESULT 1119
ID AAU05754 standard; DNA; 6647 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8442.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.4%; Score 35; DB 4; Length 6647;
Best Local Similarity 59.6%; Pred. No. 1.9e+02;
RESULT 1120
ID ABA20362 standard; DNA; 6647 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12693.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.4%; Score 35; DB 5; Length 6647;
Best Local Similarity 59.6%; Pred. No. 1.9e+02;
RESULT 1121
ID ADS52723 standard; DNA; 6957 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3265.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.4%; Score 35; DB 10; Length 6957;
Best Local Similarity 51.6%; Pred. No. 1.9e+02;
RESULT 1122
ID ADC86850 standard; DNA; 8360 BP.
DE Human GPCR gene SEQ ID NO:1303.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 2.4%; Score 35; DB 10; Length 8360;
Best Local Similarity 48.7%; Pred. No. 2.1e+02;
RESULT 1123
ID ADQ91701 standard; DNA; 10287 BP.
DE Polypeptide synthase ORF11, SEQ ID 24.
PN WO2004065401-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOPITA BIOSCIENCES INC.
Query Match 2.4%; Score 35; DB 13; Length 10287;
Best Local Similarity 57.9%; Pred. No. 2.3e+02;
RESULT 1124
ID AAU05755 standard; DNA; 16579 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8443.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.4%; Score 35; DB 4; Length 16579;
Best Local Similarity 59.6%; Pred. No. 2.9e+02;
RESULT 1125
ID ABA20363 standard; DNA; 16579 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12694.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.4%; Score 35; DB 5; Length 16579;
Best Local Similarity 59.6%; Pred. No. 2.9e+02;
RESULT 1126
ID ACN44588 standard; DNA; 33454 BP.
DE Mouse genomic sequence mCG22056.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35; DB 11; Length 33454;
Best Local Similarity 52.4%; Pred. No. 4.1e+02;
RESULT 1128

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ID AAK83781 standard; DNA; 37664 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38593.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCL INC.
Query Match 2.4%; Score 35; DB 4; Length 37664;
Best Local Similarity 54.2%; Pred. No. 4.4e+02;
RESULT 1129
ID ACN44064 standard; DNA; 44748 BP.
DE Mouse genomic sequence MCG13520.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35; DB 11; Length 44748;
Best Local Similarity 47.9%; Pred. No. 4.8e+02;
RESULT 1130
ID ACN44456 standard; DNA; 56258 BP.
DE Mouse genomic sequence MCG19337.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35; DB 11; Length 56258;
Best Local Similarity 54.2%; Pred. No. 5.4e+02;
RESULT 1131
ID AAK83782 standard; DNA; 61710 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38594.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCL INC.
Query Match 2.4%; Score 35; DB 4; Length 61710;
Best Local Similarity 54.2%; Pred. No. 5.6e+02;
RESULT 1132
ID ADA02747 standard; DNA; 96599 BP.
DE Mouse Irf2 carcinoma associated gene, SEQ ID NO:1265.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35; DB 9; Length 96599;
Best Local Similarity 54.2%; Pred. No. 7e+02;
RESULT 1133
ID ADB72485 standard; DNA; 96599 BP.
DE Mouse Irf2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35; DB 10; Length 96599;
Best Local Similarity 54.2%; Pred. No. 7e+02;
RESULT 1134
ID ADC85227 standard; DNA; 96599 BP.
DE Mouse Irf2 genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35; DB 10; Length 96599;
Best Local Similarity 54.2%; Pred. No. 7e+02;
RESULT 1135
ID ADM74342 standard; DNA; 96599 BP.
DE Murine carcinoma associated (CA) nucleic acid #7.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 2.4%; Score 35; DB 12; Length 96599;
Best Local Similarity 54.2%; Pred. No. 7e+02;
RESULT 1136
ID ADN30326 standard; DNA; 121434 BP.
DE Human Nuclech2 genomic DNA region #1.
PN US2004101847-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.4%; Score 35; DB 12; Length 121434;
Best Local Similarity 52.4%; Pred. No. 7.8e+02;
RESULT 1137

ID ADQ59431 standard; DNA; 154504 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:67.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35; DB 12; Length 154504;
Best Local Similarity 52.4%; Pred. No. 8.8e+02;
RESULT 1138
ID ADQ97691 standard; DNA; 155083 BP.
DE Mouse cancer associated sequence MD11-020, SEQ ID 868.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35; DB 12; Length 155083;
Best Local Similarity 57.9%; Pred. No. 8.8e+02;
RESULT 1139
ID ADQ91695 standard; DNA; 164051 BP.
DE Polyketide synthase related DNA contig 2, SEQ ID 18.
PN WO2004065401-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 2.4%; Score 35; DB 13; Length 164051;
Best Local Similarity 57.9%; Pred. No. 9e+02;
RESULT 1140
ID ADQ97362 standard; DNA; 215126 BP.
DE Mouse cancer associated sequence MD08-038, SEQ ID 339.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35; DB 12; Length 215126;
Best Local Similarity 30.6%; Pred. No. 1e+03;
RESULT 1141
ID ADA70687 standard; DNA; 410 BP.
DE Rice gene, SEQ ID 4010.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.3%; Score 34.8; DB 8; Length 410;
Best Local Similarity 48.9%; Pred. No. 53;
RESULT 1142
ID AA182119 standard; cDNA; 415 BP.
DE Human polynucleotide SEQ ID NO 2179.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34.8; DB 4; Length 415;
Best Local Similarity 48.9%; Pred. No. 53;
RESULT 1143
ID AAC10054 standard; cDNA; 530 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 14129.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 2.3%; Score 34.8; DB 3; Length 530;
Best Local Similarity 42.0%; Pred. No. 60;
RESULT 1144
ID ABX56967 standard; DNA; 568 BP.
DE Arabidopsis thaliana polynucleotide #319.
PN US2002040489-A1.
PD 04-APR-2002.
PA (GORL/) GORLACH J.
PA (ANYV/) AN Y.
PA (HAMT/) HAMILTON C M.
PA (ERIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYV/) YU Y.
PA (RAME/) RAMEKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
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PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 10; Length 568;
RESULT 1145
ID ADL12630 standard; cDNA; 694 BP.
DE Human steroid-induced C3A liver cell cDNA #359.
PN US673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 12; Length 694;
RESULT 1146
ID ADU42637 standard; cDNA; 747 BP.
DE Plant cDNA #3637.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MORG/) MORGANER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZERBOOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVANT N.
PA (RICK/) RICE D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 12; Length 747;
RESULT 1147
ID AAC39827 standard; DNA; 751 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 26049.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 3; Length 751;
RESULT 1148
ID ABL13473 standard; cDNA; 935 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 34901.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE/) PE CORP NY.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 4; Length 935;
RESULT 1149
ID AAT70982 standard; cDNA; 1176 BP.
DE Rat histamine H4 receptor cDNA.
PN WO200192485-A1.
PD 06-DEC-2001.
PA (ORRH/) ORTHO-MCNEIL PHARM INC.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 6; Length 1176;
RESULT 1150
ID ADA49077 standard; DNA; 1290 BP.
DE Wheat gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN/) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 9; Length 1290;
RESULT 1151
ID AAX90405 standard; DNA; 1375 BP.
DE Actinomadura sp. DSM43186 35 kDa xylanase encoding DNA.
PN US935836-A.
PD 10-AUG-1999.
PA (ROHG/) ROEHM ENZYME FINLAND OY.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 2; Length 1375;
PA 49.5%; Pred. No. 96;

RESULT 1152
ID AAT64930 standard; DNA; 1375 BP.
DE Actinomadura flexuosa 35 kDa (AM35) xylanase encoding DNA.
PN WO9727306-A1.
PD 31-JUL-1997.
PA (ALKO-) ALKO GROUP LTD.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 2; Length 1375;
RESULT 1153
ID AAC59256 standard; cDNA; 1607 BP.
DE Human secreted protein cDNA sequence #42.
PN WO200055199-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 3; Length 1607;
RESULT 1154
ID ACA27405 standard; DNA; 1837 BP.
DE Prokaryotic essential gene #9062.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 8; Length 1837;
RESULT 1155
ID ADO35997 standard; DNA; 1956 BP.
DE Novel mouse gene sequence #670.
PN WO2004046310-A2.
PD 03-JUN-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 12; Length 1956;
RESULT 1156
ID AAS68016 standard; cDNA; 1999 BP.
DE DNA encoding novel human diagnostic protein #3820.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 5; Length 1999;
RESULT 1157
ID ACA27342 standard; DNA; 2028 BP.
DE Prokaryotic essential gene #8999.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 8; Length 2028;
RESULT 1158
ID ADB63067 standard; cDNA; 2077 BP.
DE Human cDNA encoding clone SMINT20007470.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 10; Length 2077;
RESULT 1159
ID AAS83500 standard; cDNA; 2484 BP.
DE DNA encoding novel human diagnostic protein #19304.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 5; Length 2484;
RESULT 1160
ID AOT45909 standard; cDNA; 2484 BP.
DE Bacterial polynucleotide #20660.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.3%; Score 34.8; DB 13; Length 2484;
Best Local Similarity 49.5%; Pred. No. 1.3e+02;
RESULT 1161
ID AAS56030 standard; DNA; 2679 BP.
DE Salmonella typhi DNA for cellular proliferation protein #63.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.3%; Score 34.8; DB 4; Length 2679;
Best Local Similarity 58.8%; Pred. No. 1.3e+02;
RESULT 1162
ID ACAS1586 standard; DNA; 2679 BP.
DE Prokaryotic essential gene #33243.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.3%; Score 34.8; DB 8; Length 2679;
Best Local Similarity 58.8%; Pred. No. 1.3e+02;
RESULT 1163
ID ABZ23911 standard; DNA; 3108 BP.
DE Human 3OST4 polypeptide encoding DNA.
PN WO200292849-A2.
PD 21-NOV-2002.
PA (ASTR-) ASTRAZENCA UK LTD.
Query Match 2.3%; Score 34.8; DB 8; Length 3108;
Best Local Similarity 53.7%; Pred. No. 1.4e+02;
RESULT 1164
ID ACF04819 standard; DNA; 3153 BP.
DE M lichenicola melithiazol synthesis gene Mel B.
PN WO2003080828-A2.
PD 02-OCT-2003.
PA (GEPB) GEP GES BIOTECH FORSCHUNG GMBH.
Query Match 2.3%; Score 34.8; DB 10; Length 3153;
Best Local Similarity 50.6%; Pred. No. 1.5e+02;
RESULT 1165
ID ADS47373 standard; cDNA; 3237 BP.
DE Bacterial polynucleotide #2116.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.3%; Score 34.8; DB 13; Length 3237;
Best Local Similarity 52.0%; Pred. No. 1.5e+02;
RESULT 1166
ID AAX37250 standard; DNA; 3658 BP.
DE Human 3-OST-4 encoding DNA.
PN WO9922005-A2.
PD 06-MAY-1999.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 2.3%; Score 34.8; DB 2; Length 3658;
Best Local Similarity 53.7%; Pred. No. 1.6e+02;
RESULT 1167
ID ABA15504 standard; DNA; 4034 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7835.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 5; Length 4034;
Best Local Similarity 54.8%; Pred. No. 1.6e+02;
RESULT 1168
ID ABA16206 standard; DNA; 4034 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8537.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 5; Length 4034;
Best Local Similarity 54.8%; Pred. No. 1.6e+02;
RESULT 1169
ID AAX37251 standard; DNA; 4045 BP.
DE Human 3-OST-4 5' promoter and exon sequence.
PN WO9922005-A2.
PD 06-MAY-1999.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 2.3%; Score 34.8; DB 2; Length 4045;
Best Local Similarity 53.7%; Pred. No. 1.6e+02;
RESULT 1170
ID AAS28590 standard; DNA; 4172 BP.
DE Genomic sequence #430 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 4; Length 4172;
Best Local Similarity 57.3%; Pred. No. 1.7e+02;
RESULT 1171
ID ADG41786 standard; DNA; 4172 BP.
DE Human respiratory system associated genomic DNA seq id 1024.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 10; Length 4172;
Best Local Similarity 57.3%; Pred. No. 1.7e+02;
RESULT 1172
ID ADI97560 standard; DNA; 4172 BP.
DE Human respiratory system associated polypeptide-related DNA SeqID1024.
PN US200307704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 11; Length 4172;
Best Local Similarity 57.3%; Pred. No. 1.7e+02;
RESULT 1173
ID AAI10263 standard; DNA; 11883 BP.
DE Bordetella pertussis filamentous haemagglutinin gene, fHAB.
PN US6036960-A.
PD 14-MAR-2000.
PA (RELM/) RELMAN D A.
PA (DOME/) DOMENIGHINI M.
PA (RAIP/) RAIPULI R.
PA (FALK/) FALKOW S.
Query Match 2.3%; Score 34.8; DB 3; Length 11883;
Best Local Similarity 49.5%; Pred. No. 2.8e+02;
RESULT 1174
ID AAQ04668 standard; DNA; 12036 BP.
DE FHA structural gene, fHAB.
PN WO9904641-A.
PD 03-MAY-1990.
PA (STRD) UNIV IELAND STANFORD JUNIOR.
PA (ISTS) SCLAVO SPA.
Query Match 2.3%; Score 34.8; DB 2; Length 12036;
Best Local Similarity 49.5%; Pred. No. 2.8e+02;
RESULT 1175
ID ABZ23912 standard; DNA; 12277 BP.
DE Human 3OST4 genomic DNA fragment.
PN WO200292849-A2.
PD 21-NOV-2002.
PA (ASTR-) ASTRAZENCA AB.
PA (ASTR-) ASTRAZENCA UK LTD.
Query Match 2.3%; Score 34.8; DB 8; Length 12277;
Best Local Similarity 53.7%; Pred. No. 2.9e+02;
RESULT 1176
ID AEN97984 standard; DNA; 13695 BP.
DE FMR2 coding sequence.
PN WO9967395-A1.
PD 29-DEC-1999.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 2.3%; Score 34.8; DB 3; Length 13695;
Best Local Similarity 48.5%; Pred. No. 3e+02;
RESULT 1177
ID AAK89020 standard; DNA; 32152 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2596.
PN WO200155314-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 4; Length 32152;
Best Local Similarity 55.9%; Pred. No. 4.6e+02;
RESULT 1178
ID AAK1534 standard; DNA; 32152 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 5110.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 4; Length 32152;
Best Local Similarity 55.9%; Pred. No. 4.6e+02;
RESULT 1179
ID AAI57791 standard; DNA; 32152 BP.
DE Human colorectal cancer antigen coding sequence SEQ ID NO: 328.
PN WO200155350-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 4; Length 32152;
Best Local Similarity 55.9%; Pred. No. 4.6e+02;
RESULT 1180
ID AAS39621 standard; DNA; 32152 BP.
DE Genomic sequence #40 encoding human colon associated polypeptide.
PN WO200155302-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 5; Length 32152;
Best Local Similarity 55.9%; Pred. No. 4.6e+02;
RESULT 1181
ID ABS99968 standard; DNA; 32152 BP.
DE Genomic DNA #172 encoding human colorectal cancer related protein.
PN US2002119919-A1.
PD 29-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.3%; Score 34.8; DB 6; Length 32152;
Best Local Similarity 55.9%; Pred. No. 4.6e+02;
RESULT 1182
ID ADB32581 standard; DNA; 32152 BP.
DE Human novel colon related polypeptide DNA SEQ ID NO 518.
PN US2003050231-A1.
PD 13-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.3%; Score 34.8; DB 9; Length 32152;
Best Local Similarity 55.9%; Pred. No. 4.6e+02;
RESULT 1183
ID ADB93121 standard; DNA; 32152 BP.
DE Human colorectal cancer related polypeptide DNA #172.
PN US2003054420-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 10; Length 32152;
Best Local Similarity 55.9%; Pred. No. 4.6e+02;
RESULT 1184
ID AAK6362 standard; DNA; 36933 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21174.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 4; Length 36933;
Best Local Similarity 55.9%; Pred. No. 5e+02;
RESULT 1185
ID AAX23520 standard; DNA; 45546 BP.
DE Human kidney aminopeptidase P genomic DNA fragment 4.
PN WO9911799-A2.
PD 11-MAR-1999.
PA (MEDI-) MEDICAL COLLEGE GEORGIA RES INST.
Query Match 2.3%; Score 34.8; DB 2; Length 45546;
Best Local Similarity 54.8%; Pred. No. 5.5e+02;
RESULT 1186

ID ACP04818 standard; DNA; 51855 BP.
DE Melithiazol biosynthetic gene cluster.
PN WO2003080828-A2.
PD 02-OCT-2003.
PA (GBFB) GBF GRS BIOTECH FORSCHUNG GMBH.
Query Match 2.3%; Score 34.8; DB 10; Length 51855;
Best Local Similarity 50.6%; Pred. No. 5.9e+02;
RESULT 1187
ID ADQ97340 standard; DNA; 60202 BP.
DE Mouse cancer associated sequence MD08-035, SEQ ID 317.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.8; DB 12; Length 60202;
Best Local Similarity 46.1%; Pred. No. 6.3e+02;
RESULT 1188
ID ACN44284 standard; DNA; 71678 BP.
DE Mouse genomic sequence mCG16994.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.8; DB 11; Length 71678;
Best Local Similarity 54.8%; Pred. No. 6.9e+02;
RESULT 1189
ID ACN44560 standard; DNA; 94672 BP.
DE Mouse genomic sequence mCG21419.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.8; DB 11; Length 94672;
Best Local Similarity 53.7%; Pred. No. 7.9e+02;
RESULT 1190
ID ACN43984 standard; DNA; 493631 BP.
DE Mouse genomic sequence mCG12182.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.8; DB 11; Length 110000;
Best Local Similarity 55.9%; Pred. No. 8.5e+02;
RESULT 1191
ID ACN44560 standard; DNA; 94672 BP.
DE Mouse genomic sequence mCG21419.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.8; DB 13; Length 110000;
Best Local Similarity 48.1%; Pred. No. 8.5e+02;
RESULT 1192
ID ACN44560 standard; DNA; 94672 BP.
DE Mouse genomic sequence mCG21419.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.8; DB 13; Length 110000;
Best Local Similarity 48.1%; Pred. No. 8.5e+02;
RESULT 1193
ID ADQ17592 standard; DNA; 116561 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 409.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.3%; Score 34.8; DB 12; Length 116561;
Best Local Similarity 54.8%; Pred. No. 8.7e+02;
RESULT 1194
ID ABD33312 standard; DNA; 138115 BP.
DE Murine cancer-associated (CA) gene MD07-056.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.8; DB 13; Length 138115;
Best Local Similarity 52.0%; Pred. No. 9.4e+02;
RESULT 1195
ID ADL13775 standard; DNA; 173805 BP.
DE Osteoarthritis-associated polymorphic nucleotide #307.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCYT) INCYTE GENOMICS INC.
Query Match 2.3%; Score 34.8; DB 10; Length 173805;
Best Local Similarity 53.7%; Pred. No. 1.1e+03;
RESULT 1196
ID ACN44002 standard; DNA; 228139 BP.
DE Human genomic sequence hCG37553.
PN WO2003073826-A2.

PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.8; DB 11; Length 228139;
Best Local Similarity 48.1%; Pred. No. 1.2e+03;
RESULT 1197
ID AAR43643 standard; cDNA; 267 BP.
DE SSG #9.
PN WO200175169-A2.
PD 11-OCT-2001.
PA (DIAD-) DIADEXUS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 267;
Best Local Similarity 53.3%; Pred. No. 49;
RESULT 1198
ID AAI13112 standard; DNA; 422 BP.
DE Probe #3045 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1199
ID ABA54811 standard; DNA; 422 BP.
DE Human foetal liver single exon nucleic acid probe #3116.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1200
ID AAI34463 standard; DNA; 422 BP.
DE Probe #3149 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1201
ID ABA44357 standard; DNA; 422 BP.
DE Human breast cell single exon nucleic acid probe #3052.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1202
ID ABA24575 standard; DNA; 422 BP.
DE Probe #3041 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1203
ID AAK28539 standard; DNA; 422 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 3096.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1204
ID AAK03087 standard; DNA; 422 BP.
DE Human brain expressed single exon probe SEQ ID NO: 3078.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1205
ID ABA28139 standard; DNA; 422 BP.
DE Human liver single exon probe, SEQ ID NO 3129.
PN WO200157273-A2.
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1206
ID AAI03015 standard; DNA; 422 BP.
DE Probe #3006 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 5; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1207
ID ABS03051 standard; DNA; 422 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 3042.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 6; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1208
ID AAC35781 standard; DNA; 497 BP.
DE Zea mays DNA fragment SEQ ID NO: 11399.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.3%; Score 34.6; DB 3; Length 497;
Best Local Similarity 53.3%; Pred. No. 66;
RESULT 1209
ID ADA71021 standard; DNA; 500 BP.
DE Rice gene, SEQ ID 4344.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.
Query Match 2.3%; Score 34.6; DB 8; Length 500;
Best Local Similarity 47.1%; Pred. No. 66;
RESULT 1210
ID ABA22262 standard; DNA; 615 BP.
DE Schwann cell specific enhancer consensus SCE1 nucleotide sequence #2.
PN WO200288352-A2.
PD 07-NOV-2002.
PA (UTMC-) UNIV MCGILL.
Query Match 2.3%; Score 34.6; DB 8; Length 615;
Best Local Similarity 18.9%; Pred. No. 73;
RESULT 1211
ID ADA42630 standard; cDNA; 740 BP.
DE Plant cDNA #3630.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOF/) GOF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
PA (ZHUT/) ZHU T.
Query Match 2.3%; Score 34.6; DB 12; Length 740;
Best Local Similarity 48.3%; Pred. No. 81;
RESULT 1212
ID ADC12755 standard; DNA; 933 BP.
DE Human GPCR gene, SEQ ID No 87.
PN WO200300893-A2.
PD 03-JAN-2003.
PA (DECO-) DECODE GENETICS BHF.
Query Match 2.3%; Score 34.6; DB 10; Length 933;
Best Local Similarity 53.3%; Pred. No. 90;
RESULT 1213
ID ABD03694 standard; DNA; 984 BP.
DE Pseudomonas aeruginosa polynucleotide #2298.
PN US651795-B1.
PD 22-APR-2003.

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PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 34.6; DB 11; Length 984;
Best Local Similarity 49.7%; Pred. No. 93;
RESULT 1214
ID AB222275 standard; DNA; 997 BP.
DE Mouse and human consensus SCE1 nucleotide sequence #2.
PN WO200288352-A2.
PD 07-NOV-2002.
PA (UYWC-) UNIV MCGILL.
Query Match 2.3%; Score 34.6; DB 8; Length 997;
Best Local Similarity 18.9%; Pred. No. 93;
RESULT 1215
ID ADR18583 standard; cDNA; 1083 BP.
DE Human GPCR 14273 coding sequence, SEQ ID 2.
PN WO2004065960-A1.
PD 05-AUG-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 2.3%; Score 34.6; DB 13; Length 1083;
Best Local Similarity 53.3%; Pred. No. 97;
RESULT 1216
ID ABR04869 standard; cDNA; 1086 BP.
DE Human G protein coupled receptor hRUP31 coding sequence.
PN WO200242461-A2.
PD 30-MAY-2002.
PA (AREN-) ARENA PHARM INC.
Query Match 2.3%; Score 34.6; DB 6; Length 1086;
Best Local Similarity 53.3%; Pred. No. 98;
RESULT 1217
ID AB573399 standard; DNA; 1086 BP.
DE DNA encoding human GPCR HF1948 mutant E135N.
PN WO200268600-A2.
PD 06-SEP-2002.
PA (AREN-) ARENA PHARM INC.
Query Match 2.3%; Score 34.6; DB 6; Length 1086;
Best Local Similarity 53.3%; Pred. No. 98;
RESULT 1218
ID AB573343 standard; cDNA; 1086 BP.
DE cDNA encoding human GPCR HF1948.
PN WO200268600-A2.
PD 06-SEP-2002.
PA (AREN-) ARENA PHARM INC.
Query Match 2.3%; Score 34.6; DB 6; Length 1086;
Best Local Similarity 53.3%; Pred. No. 98;
RESULT 1219
ID ACA60998 standard; cDNA; 1086 BP.
DE cDNA encoding novel human G protein coupled receptor HGPRBM18.
PN US2003022186-A1.
PD 30-JAN-2003.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
Query Match 2.3%; Score 34.6; DB 8; Length 1086;
Best Local Similarity 53.3%; Pred. No. 98;
RESULT 1220
ID ADB47641 standard; cDNA; 1086 BP.
DE Human cDNA encoding GPCR, HGPRBM18.
PN US2003129653-A1.
PD 10-JUL-2003.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
Query Match 2.3%; Score 34.6; DB 9; Length 1086;
Best Local Similarity 53.3%; Pred. No. 98;
RESULT 1221
ID ADR40535 standard; cDNA; 1086 BP.
DE Human G-protein coupled receptor HGPRBM18 cDNA.
PN US2004161823-A1.
PD 19-AUG-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
PA (HAWK/) HAWKEN D R.

Query Match 2.3%; Score 34.6; DB 13; Length 1086;
Best Local Similarity 53.3%; Pred. No. 98;
RESULT 1222
ID ABR10627 standard; DNA; 1160 BP.
DE DNA encoding human orphan SNORF49 receptor.
PN US2002151705-A1.
PD 17-OCT-2002.
PA (SMIT/) SMITH K E.
PA (OUAN/) OUAN Y.
Query Match 2.3%; Score 34.6; DB 8; Length 1160;
Best Local Similarity 53.3%; Pred. No. 1e+02;
RESULT 1223
ID ADT46979 standard; cDNA; 1278 BP.
DE Bacterial polynucleotide #21730.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.3%; Score 34.6; DB 13; Length 1278;
Best Local Similarity 45.2%; Pred. No. 1.1e+02;
RESULT 1224
ID AAD08854 standard; cDNA; 1321 BP.
DE Human G-protein coupled receptor-20 (GCREC-20) cDNA.
PN WO200142288-A2.
PD 14-JUN-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 1321;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1225
ID ADT44390 standard; cDNA; 1368 BP.
DE Bacterial polynucleotide #19141.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.3%; Score 34.6; DB 13; Length 1368;
Best Local Similarity 49.2%; Pred. No. 1.1e+02;
RESULT 1226
ID ADR67380 standard; DNA; 1372 BP.
DE Human GPCR gene SEQ ID NO:1833.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 2.3%; Score 34.6; DB 10; Length 1372;
Best Local Similarity 46.5%; Pred. No. 1.1e+02;
RESULT 1227
ID AA166039 standard; cDNA; 1458 BP.
DE Human G protein-coupled receptor encoding cDNA SEQ ID NO 2.
PN JP2001211885-A.
PD 07-AUG-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 2.3%; Score 34.6; DB 4; Length 1458;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1228
ID ADR01275 standard; DNA; 1599 BP.
DE Farnesyl dibenzodiazepinone biosynthetic ORF32 protein HOYH DNA.
PN WO2004065591-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 2.3%; Score 34.6; DB 13; Length 1599;
Best Local Similarity 52.4%; Pred. No. 1.2e+02;
RESULT 1229
ID AA64346 standard; DNA; 1743 BP.
DE DNA encoding a human G-protein coupled receptor designated 14273.
PN WO200050596-A2.
PD 31-AUG-2000.
```

PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.3%; Score 34.6; DB 3; Length 1743;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1230
ID AB081226 standard; cDNA, 1743 BP.
DE Human 14723 nucleic acid, associated with metabolic disorder.
PN WO200267868-A2.
PD 06-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.3%; Score 34.6; DB 6; Length 1743;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1231
ID ADF70511 standard; DNA, 1800 BP.
DE Orphan receptor ligand-related human protein gene SeqID134.
PN WO2003071272-A1.
PD 28-AUG-2003.
PA (TAKE) TAKEEDA CHEM IND LTD.
Query Match 2.3%; Score 34.6; DB 10; Length 1800;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 1232
ID ADB58993 standard; DNA, 2034 BP.
DE Toxicity-related gene, SEQ ID 4019.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.3%; Score 34.6; DB 10; Length 2034;
Best Local Similarity 51.6%; Pred. No. 1.3e+02;
RESULT 1233
ID ADB53747 standard; DNA, 2034 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4289.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.3%; Score 34.6; DB 10; Length 2034;
Best Local Similarity 51.6%; Pred. No. 1.3e+02;
RESULT 1234
ID ABD1675 standard; DNA, 2073 BP.
DE Pseudomonas aeruginosa polynucleotide #10279.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 34.6; DB 11; Length 2073;
Best Local Similarity 47.8%; Pred. No. 1.3e+02;
RESULT 1235
ID ADO28989 standard; cDNA, 2081 BP.
DE Human novel GPCR PGR4 polynucleotide, SEQ ID NO:88.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 2.3%; Score 34.6; DB 12; Length 2081;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 1236
ID ADA70561 standard; DNA, 2145 BP.
DE Rice gene, SEQ ID 3884.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.3%; Score 34.6; DB 8; Length 2145;
Best Local Similarity 49.2%; Pred. No. 1.4e+02;
RESULT 1237
ID ACA50840 standard; DNA, 2355 BP.
DE Prokaryotic essential gene #32497.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.3%; Score 34.6; DB 8; Length 2355;
Best Local Similarity 46.5%; Pred. No. 1.4e+02;
RESULT 1238
ID ADB63556 standard; cDNA, 2650 BP.
DE Human cDNA encoding clone TEST120287760.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.

PA (REAS-) REAS ASSOC BIOTECHNOLOGY.
Query Match 2.3%; Score 34.6; DB 10; Length 2650;
Best Local Similarity 56.6%; Pred. No. 1.5e+02;
RESULT 1239
ID ABD1973 standard; DNA, 2772 BP.
DE Pseudomonas aeruginosa polynucleotide #10577.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 34.6; DB 11; Length 2772;
Best Local Similarity 47.8%; Pred. No. 1.6e+02;
RESULT 1240
ID AAF62205 standard; DNA, 2890 BP.
DE Melon ethylene receptor gene promoter.
PN JP2001037484-A.
PD 13-FEB-2001.
PA (IBAR-) IBARAKI PREFECTURE.
Query Match 2.3%; Score 34.6; DB 5; Length 2890;
Best Local Similarity 56.6%; Pred. No. 1.6e+02;
RESULT 1241
ID AAL51205 standard; DNA, 3083 BP.
DE Human gene sequence #3.
PN WO20029103-A1.
PD 12-DEC-2002.
PA (KAZU-) KAZUSA DNA RES INST FOUND.
Query Match 2.3%; Score 34.6; DB 8; Length 3083;
Best Local Similarity 55.4%; Pred. No. 1.6e+02;
RESULT 1242
ID ADO23587 standard; DNA, 3141 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6407.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.3%; Score 34.6; DB 12; Length 3141;
Best Local Similarity 55.4%; Pred. No. 1.7e+02;
RESULT 1243
ID AAL51404 standard; cDNA, 3537 BP.
DE Human secreted protein coding sequence, SEQ ID No 1.
PN WO200292621-A1.
PD 21-NOV-2002.
PA (PEKE) PE CORP NY.
PA (SHAO/) SHAO W.
PA (GONG/) GONG F.
PA (DPRR/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 2.3%; Score 34.6; DB 8; Length 3537;
Best Local Similarity 55.4%; Pred. No. 1.8e+02;
RESULT 1244
ID AAF62217 standard; DNA, 3797 BP.
DE Melon ethylene receptor gene promoter-related sequence.
PN JP2001037484-A.
PD 13-FEB-2001.
PA (IBAR-) IBARAKI PREFECTURE.
Query Match 2.3%; Score 34.6; DB 5; Length 3797;
Best Local Similarity 56.6%; Pred. No. 1.8e+02;
RESULT 1245
ID ADR01273 standard; DNA, 5960 BP.
DE Farnesyl dibenzodiazepinone biosynthetic locus Contig 2, SEQ ID 64.
PN WO2004065591-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOPITA BIOSCIENCES INC.
Query Match 2.3%; Score 34.6; DB 13; Length 5960;
Best Local Similarity 52.4%; Pred. No. 2.3e+02;
RESULT 1246
ID AAA10594 standard; DNA, 10732 BP.
DE Gene encoding a subunit of cellulose synthase.
PN JP2000060568-A.
PD 29-FEB-2000.
PA (MIZU/) MIZUNO K.
PA (OJIP) OJI PAPER CO.
Query Match 2.3%; Score 34.6; DB 3; Length 10732;
Best Local Similarity 13.4%; Pred. No. 3e+02;

RESULT 1247
ID AAS59569 standard; DNA; 29139 BP.
DE Propionibacterium acnes immunogenic protein encoding DNA #64.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.3%; Score 34.6; DB 4; Length 29139;
Best Local Similarity 51.6%; Pred. No. 5e+02;
RESULT 1248
ID AC644498 standard; DNA; 29139 BP.
DE Propionibacterium acnes DNA contig sequence #64.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 2.3%; Score 34.6; DB 8; Length 29139;
Best Local Similarity 51.6%; Pred. No. 5e+02;
RESULT 1249
ID ABD32614 standard; DNA; 34245 BP.
DE Mouse cancer-associated genomic DNA MD12-027.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.6; DB 13; Length 34245;
Best Local Similarity 54.3%; Pred. No. 5.4e+02;
RESULT 1250
ID ADP31997 standard; DNA; 39949 BP.
DE Full length cosmid 2A7.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVERT-) AVERTIS PHARM INC.
Query Match 2.3%; Score 34.6; DB 12; Length 39949;
Best Local Similarity 54.3%; Pred. No. 5.9e+02;
RESULT 1251
ID ADF31998 standard; DNA; 48200 BP.
DE Cosmid 2A7.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVERT-) AVERTIS PHARM INC.
Query Match 2.3%; Score 34.6; DB 12; Length 48200;
Best Local Similarity 54.3%; Pred. No. 6.4e+02;
RESULT 1252
ID ABD33307 standard; DNA; 53828 BP.
DE Murine cancer-associated (CA) gene MD07-055.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.6; DB 13; Length 53828;
Best Local Similarity 50.9%; Pred. No. 6.8e+02;
RESULT 1253
ID ABN87364 standard; cDNA; 55155 BP.
DE Human lipase encoding gene sequence SEQ ID NO:3.
PN US2002052034-A1.
PD 02-MAY-2002.
PA (GUEG/) GUEGLER K.
PA (WEBB/) WEBSTER M.
PA (KERC/) KETCHUM K A.
PA (DRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 2.3%; Score 34.6; DB 6; Length 55155;
Best Local Similarity 61.8%; Pred. No. 6.9e+02;
RESULT 1254
ID AD097700 standard; DNA; 86804 BP.
DE Mouse cancer associated sequence MD10-031, SEQ ID 677.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.6; DB 12; Length 86804;
Best Local Similarity 50.9%; Pred. No. 8.6e+02;
RESULT 1255
ID AAH87704 standard; DNA; 160755 BP.
DE Human DNA sequence SEQ ID 544.
PN WO200151659-A2.
PD 19-JUL-2001.

PA (GERT-) GENSET.
Query Match 2.3%; Score 34.6; DB 4; Length 160755;
Best Local Similarity 55.4%; Pred. No. 1.2e+03;
RESULT 1256
ID ACN44110 standard; DNA; 223556 BP.
DE Human genomic sequence hCG38337.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.6; DB 11; Length 223556;
Best Local Similarity 53.3%; Pred. No. 1.3e+03;
RESULT 1257
ID ACN44068 standard; DNA; 295096 BP.
DE Mouse genomic sequence mCG13636.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.6; DB 11; Length 295096;
Best Local Similarity 48.7%; Pred. No. 1.5e+03;
RESULT 1258
ID AD048726 standard; DNA; 316 BP.
DE Novel canine microarray-related DNA sequence SeqID28.
PN WO2004063524-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PRIZ-) PRIZER PROD INC.
Query Match 2.3%; Score 34.4; DB 13; Length 316;
Best Local Similarity 56.8%; Pred. No. 60;
RESULT 1259
ID AAD03892 standard; DNA; 340 BP.
DE Human target of methylation-induced silencing-1 (TMS1) exon1 DNA.
PN WO200129235-A2.
PD 26-APR-2001.
PA (UTEM-) UNIV EMORY.
Query Match 2.3%; Score 34.4; DB 4; Length 340;
Best Local Similarity 46.0%; Pred. No. 62;
RESULT 1260
ID AAS90909 standard; cDNA; 379 BP.
DE DNA encoding novel human diagnostic protein #26713.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34.4; DB 5; Length 379;
Best Local Similarity 47.6%; Pred. No. 66;
RESULT 1261
ID AAS75428 standard; cDNA; 379 BP.
DE DNA encoding novel human diagnostic protein #11232.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34.4; DB 5; Length 379;
Best Local Similarity 47.6%; Pred. No. 66;
RESULT 1262
ID ADB09716 standard; DNA; 379 BP.
DE Novel DNA-related contig nucleotide sequence #438.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34.4; DB 10; Length 379;
Best Local Similarity 47.6%; Pred. No. 66;
RESULT 1263
ID AAD03907 standard; cDNA; 405 BP.
DE Alternatively spliced form of human TMS1 cDNA (lacking exon3).
PN WO200129235-A2.
PD 26-APR-2001.
PA (UTEM-) UNIV EMORY.
Query Match 2.3%; Score 34.4; DB 4; Length 405;
Best Local Similarity 46.0%; Pred. No. 68;
RESULT 1264
ID AAC98638 standard; cDNA; 432 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:648.
PN WO200055351-A1.
PD 21-SEP-2000.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 3; Length 432;
Best Local Similarity 46.0%; Pred. No. 70;
RESULT 1265
ID ABX37280 standard; cDNA; 434 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2445.
PN US200237139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.3%; Score 34.4; DB 8; Length 434;
Best Local Similarity 46.0%; Pred. No. 70;
RESULT 1266
ID AAC36571 standard; DNA; 449 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 14294.
PN EP1033405-A2.
PD 06-SEP-2000.
PA
Query Match 2.3%; Score 34.4; DB 3; Length 449;
Best Local Similarity 53.8%; Pred. No. 71;
RESULT 1267
ID AAD03891 standard; DNA; 626 BP.
DE CpG island of human TMS1 gene.
PN WO200129235-A2.
PD 26-APR-2001.
PA (UYEM-) UNIV EMORY.
Query Match 2.3%; Score 34.4; DB 4; Length 626;
Best Local Similarity 46.0%; Pred. No. 84;
RESULT 1268
ID AAD03906 standard; cDNA; 713 BP.
DE Alternatively spliced form of human TMS1 cDNA (lacking exon2).
PN WO200129235-A2.
PD 26-APR-2001.
PA (UYEM-) UNIV EMORY.
Query Match 2.3%; Score 34.4; DB 4; Length 713;
Best Local Similarity 46.0%; Pred. No. 90;
RESULT 1269
ID AAF30007 standard; cDNA; 740 BP.
DE Human CARD-5 cDNA.
PN WO200100826-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 2.3%; Score 34.4; DB 4; Length 740;
Best Local Similarity 46.0%; Pred. No. 92;
RESULT 1270
ID ABR87966 standard; cDNA; 740 BP.
DE Human caspase recruitment domain-5 (CARD-5) cDNA.
PN WO200244354-A2.
PD 06-JUN-2002.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 2.3%; Score 34.4; DB 6; Length 740;
Best Local Similarity 46.0%; Pred. No. 92;
RESULT 1271
ID ABR87967 standard; DNA; 740 BP.
DE Human caspase recruitment domain-5 (CARD-5) cDNA complementary strand.
PN WO200244354-A2.
PD 06-JUN-2002.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 2.3%; Score 34.4; DB 6; Length 740;
Best Local Similarity 46.0%; Pred. No. 92;
RESULT 1272
ID ABS56032 standard; cDNA; 740 BP.
DE cDNA encoding human caspase recruitment domain-5 (CARD-5).
PN US2002128198-A1.
PD 12-SEP-2002.
PA (BERT/) BERTIN J.
Query Match 2.3%; Score 34.4; DB 8; Length 740;
Best Local Similarity 46.0%; Pred. No. 92;
RESULT 1273
ID AAS59817 standard; cDNA; 745 BP.
DE Human novel cytokine encoding cDNA 790CIP2B_1 #1.
PN WO200175093-A1.

PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34.4; DB 4; Length 745;
Best Local Similarity 46.0%; Pred. No. 92;
RESULT 1274
ID AAD03890 standard; cDNA; 770 BP.
DE Human target of methylation-induced silencing-1 (TMS1) cDNA.
PN WO200129235-A2.
PD 26-APR-2001.
PA (UYEM-) UNIV EMORY.
Query Match 2.3%; Score 34.4; DB 4; Length 770;
Best Local Similarity 46.0%; Pred. No. 93;
RESULT 1275
ID AA233631 standard; cDNA; 779 BP.
DE Human breast tumour-associated EST 21.
PN DE1981839-A1.
PD 23-SEP-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 2.3%; Score 34.4; DB 2; Length 779;
Best Local Similarity 46.0%; Pred. No. 94;
RESULT 1276
ID AA47126 standard; DNA; 782 BP.
DE Pyrin domain containing protein Pycard coding sequence.
PN WO200240668-A2.
PD 23-MAY-2002.
PA (APOT-) APOTTECH RES & DEV LTD.
Query Match 2.3%; Score 34.4; DB 6; Length 782;
Best Local Similarity 46.0%; Pred. No. 94;
RESULT 1277
ID ADF90785 standard; DNA; 796 BP.
DE Human hepatic-fibrosis disease marker SEQ ID 247.
PN JP2003259877-A.
PD 16-SEP-2003.
PA (SOMU) SOMITOMO SEIYAKU KK.
Query Match 2.3%; Score 34.4; DB 10; Length 796;
Best Local Similarity 46.0%; Pred. No. 95;
RESULT 1278
ID AAH34052 standard; cDNA; 806 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1134.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 4; Length 806;
Best Local Similarity 46.0%; Pred. No. 96;
RESULT 1279
ID AAC77884 standard; cDNA; 811 BP.
DE Human cancer associated gene sequence SEQ ID NO:278.
PN WO20005350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 3; Length 811;
Best Local Similarity 46.0%; Pred. No. 96;
RESULT 1280
ID ADR01252 standard; DNA; 825 BP.
DE Farnesyl dibenzodiazepinone biosynthetic ORF21 protein ALDB DNA.
PN WO2004065591-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOPHA BIOSCIENCES INC.
Query Match 2.3%; Score 34.4; DB 13; Length 825;
Best Local Similarity 54.8%; Pred. No. 97;
RESULT 1281
ID ADN05025 standard; cDNA; 936 BP.
DE Antipeptidic cDNA sequence #727.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.3%; Score 34.4; DB 12; Length 936;
Best Local Similarity 46.0%; Pred. No. 1e+02;
RESULT 1282
ID ADP07316 standard; DNA; 936 BP.
DE Human TMS1 DNA.
PN DE10255104-A1.
PD 11-MAR-2004.

PA (EPIC-) EPIGENOMICS AG.
Query Match 2.3%; Score 34.4; DB 12; Length 936;
Best Local Similarity 46.0%; Pred. No. 1e+02;
RESULT 1283
ID ADP56277 standard; cDNA; 936 BP.
DE Human PRO cDNA sequence SEQ ID NO:2253.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GENTH) GENTECH INC.
Query Match 2.3%; Score 34.4; DB 13; Length 936;
Best Local Similarity 46.0%; Pred. No. 1e+02;
RESULT 1284
ID AAI97783 standard; cDNA; 1049 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 3858.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREPCTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 2.3%; Score 34.4; DB 4; Length 1049;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
RESULT 1285
ID ADT46829 standard; cDNA; 1164 BP.
DE Bacterial polynucleotide #21580.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATTER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.3%; Score 34.4; DB 13; Length 1164;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
RESULT 1286
ID AAS54218 standard; DNA; 1470 BP.
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #349.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.3%; Score 34.4; DB 4; Length 1470;
Best Local Similarity 46.0%; Pred. No. 1.3e+02;
RESULT 1287
ID AAS27365 standard; cDNA; 1619 BP.
DE cDNA encoding novel signal transduction pathway protein, Seq ID 400.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 4; Length 1619;
Best Local Similarity 50.6%; Pred. No. 1.4e+02;
RESULT 1288
ID AAS34830 standard; cDNA; 1619 BP.
DE cDNA encoding novel human neoplastic disease associated polypeptide #64.
PN WO200155163-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 4; Length 1619;
Best Local Similarity 50.6%; Pred. No. 1.4e+02;
RESULT 1289
ID ADB93543 standard; cDNA; 1619 BP.
DE Human cDNA encoding a novel protein #390.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.3%; Score 34.4; DB 10; Length 1619;
Best Local Similarity 50.6%; Pred. No. 1.4e+02;
RESULT 1290
ID ADC45988 standard; cDNA; 1619 BP.
DE Human neoplastic disease-associated gene 64 cDNA #1.
PN US2003082758-A1.
PD 01-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 10; Length 1619;

Best Local Similarity 50.6%; Pred. No. 1.4e+02;
RESULT 1291
ID ADF30323 standard; cDNA; 2525 BP.
DE Human cancer suppressing protein PP10443-encoding cDNA, SEQ.10 and 12.
PN CN1368508-A.
PD 11-SEP-2002.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match 2.3%; Score 34.4; DB 10; Length 2525;
Best Local Similarity 52.9%; Pred. No. 1.7e+02;
RESULT 1292
ID AAS27013 standard; cDNA; 2686 BP.
DE cDNA encoding novel signal transduction pathway protein, Seq ID 48.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 4; Length 2686;
Best Local Similarity 50.6%; Pred. No. 1.7e+02;
RESULT 1293
ID ADB93191 standard; cDNA; 2686 BP.
DE Human cDNA encoding a novel protein #38.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.3%; Score 34.4; DB 10; Length 2686;
Best Local Similarity 50.6%; Pred. No. 1.7e+02;
RESULT 1294
ID ADU50974 standard; cDNA; 2768 BP.
DE Human cDNA encoding NOV15a.
PN US2004030096-A1.
PD 12-FEB-2004.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (EDIN/) EDINGER S R.
PA (PADI/) PADIGARU M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (ZHON/) ZHONG M.
PA (PATY/) PATTRABAN M.
PA (MITL/) MITLER C E.
PA (JTWI/) JI W.
PA (PENNA/) PENNA C E A.
PA (BURG/) BURGESS C E.
PA (SCIO/) SCIORE P.
PA (STON/) STONE D J.
PA (TAUP/) TAUPETER R J.
PA (CASM/) CASMAN S J.
PA (ROTH/) ROTHENBERG M E.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
Query Match 2.3%; Score 34.4; DB 12; Length 2768;
Best Local Similarity 50.6%; Pred. No. 1.8e+02;
RESULT 1295
ID AAD03989 standard; DNA; 2821 BP.
DE Human target of methylation-induced silencing-1 (TMS1) genomic DNA.
PN WO200129235-A2.
PD 26-APR-2001.
PA (UTEM-) UNIV EMORY.
Query Match 2.3%; Score 34.4; DB 4; Length 2821;
Best Local Similarity 46.0%; Pred. No. 1.8e+02;
RESULT 1296
ID AAS44718 standard; DNA; 3321 BP.
DE Human full-length polynucleotide sequence #143.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34.4; DB 4; Length 3321;
Best Local Similarity 50.6%; Pred. No. 1.9e+02;
RESULT 1297
ID AEX14762 standard; cDNA; 3380 BP.
DE cDNA encoding novel human ras-like protein.
PN US2002132291-A1.

PD 19-SEP-2002.
PA (YELU/) YE J.
DE (KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BRAS/) BRASLEY E M.
Query Match 2.3%; Score 34.4; DB 8; Length 3380;
Best Local Similarity 50.6%; Pred. No. 2e+02;
RESULT 1298
ID AAL26787 standard; cDNA; 3399 BP.
DE Human breast cancer expressed polynucleotide 19244.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.3%; Score 34.4; DB 4; Length 3399;
Best Local Similarity 52.9%; Pred. No. 2e+02;
RESULT 1299
ID ACN88722 standard; DNA; 3411 BP.
DE Breast cancer related marker, seq id 9872.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.3%; Score 34.4; DB 11; Length 3411;
Best Local Similarity 52.9%; Pred. No. 2e+02;
RESULT 1300
ID ADH61306 standard; DNA; 3420 BP.
DE INTSIG encoding DNA 7512389CB1, SEQ ID 23.
PN WO2004001005-A2.
PD 31-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 2.3%; Score 34.4; DB 12; Length 3420;
Best Local Similarity 49.4%; Pred. No. 2e+02;
RESULT 1301
ID ADK65790 standard; DNA; 3438 BP.
DE Angiogenesis-differentially expressed gene ANH0423.
PN WO200306831-A2.
PD 14-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 2.3%; Score 34.4; DB 10; Length 3438;
Best Local Similarity 50.6%; Pred. No. 2e+02;
RESULT 1302
ID AAV15181 standard; cDNA to mRNA; 3955 BP.
DE Human serrate 2 encoding cDNA.
PN WO9802458-A1.
PD 22-JAN-1998.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 2.3%; Score 34.4; DB 2; Length 3955;
Best Local Similarity 51.3%; Pred. No. 2.1e+02;
RESULT 1303
ID ADR24345 standard; DNA; 4670 BP.
DE Breast cancer prognosis marker #206.
PN WO200406545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 2.3%; Score 34.4; DB 13; Length 4670;
Best Local Similarity 50.6%; Pred. No. 2.3e+02;
RESULT 1304
ID ABR95047 standard; DNA; 4702 BP.
DE Gene #1545 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.3%; Score 34.4; DB 6; Length 4702;
Best Local Similarity 51.3%; Pred. No. 2.3e+02;
RESULT 1305
ID AAL06946 standard; DNA; 12232 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9634.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 4; Length 12232;
Best Local Similarity 59.0%; Pred. No. 3.7e+02;
RESULT 1306

ID AAX83006 standard; DNA; 16442 BP.
DE Partial mouse WRN genomic sequence #2.
PN WO9724435-A1.
PD 10-JUL-1997.
PA (DARW-) DARWIN MOLECULAR CORP.
Query Match 2.3%; Score 34.4; DB 2; Length 16442;
Best Local Similarity 47.6%; Pred. No. 4.3e+02;
RESULT 1307
ID AUB33201 standard; DNA; 36312 BP.
DE Murine cancer-associated (CA) gene MD07-031.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.4; DB 13; Length 36312;
Best Local Similarity 44.2%; Pred. No. 6.4e+02;
RESULT 1308
ID ADR01210 standard; DNA; 36602 BP.
DE Farnesyl dibenzodiazepine biosynthetic locus Contlg 1, SEQ ID 1.
PN WO2004065591-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOPHA BIOSCIENCES INC.
Query Match 2.3%; Score 34.4; DB 13; Length 36602;
Best Local Similarity 54.8%; Pred. No. 6.4e+02;
RESULT 1309
ID ACN45024 standard; DNA; 68370 BP.
DE Mouse genomic sequence mCG7008.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.4; DB 11; Length 68370;
Best Local Similarity 55.0%; Pred. No. 8.7e+02;
RESULT 1310
ID ACN44818 standard; DNA; 116704 BP.
DE Human genomic sequence hCG30155.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.4; DB 11; Length 116704;
Best Local Similarity 54.8%; Pred. No. 1.1e+03;
RESULT 1311
ID ADQ97651 standard; DNA; 127943 BP.
DE Human cancer associated sequence HD10-021, SEQ ID 628.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.4; DB 12; Length 127943;
Best Local Similarity 54.8%; Pred. No. 1.2e+03;
RESULT 1312
ID AAH41223 standard; DNA; 349980 BP.
DE Pyrococcus abyssi genomic fragment #2.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 2.3%; Score 34.4; DB 5; Length 349980;
Best Local Similarity 53.8%; Pred. No. 1.9e+03;
RESULT 1313
ID ADC86916 standard; DNA; 349989 BP.
DE Human GPCR gene SEQ ID NO:1369.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 2.3%; Score 34.4; DB 10; Length 349989;
Best Local Similarity 57.4%; Pred. No. 1.9e+03;
RESULT 1314
ID ADS67678 standard; cDNA; 238 BP.
DE Corn seedling-derived polynucleotide (cpds), SEQ ID 2694.
PN US200237110-A9.
PD 25-DEC-2003.
PA (INCY-) INCYTE PHARM INC.
Query Match 2.3%; Score 34.2; DB 7; Length 238;
Best Local Similarity 60.0%; Pred. No. 59;

RESULT 1315
ID ADP94454 standard; cDNA; 283 BP.
DE Cotton expressed sequence tag, EST, #3465.
PN US200412338-A1.
PD 24-JUN-2004.
PA (FINC/) FINCHER K L.
Query Match 2.3%; Score 34.2; DB 12; Length 283;
Best Local Similarity 46.2%; Pred. No. 65;
RESULT 1316
ID ABV38474 standard; cDNA; 398 BP.
DE Human prostate expression marker cDNA 38465.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.3%; Score 34.2; DB 5; Length 398;
Best Local Similarity 55.5%; Pred. No. 77;
RESULT 1317
ID ABT07648 standard; cDNA; 420 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 127.
PN WO200264611-A1.
PD 22-AUG-2002.
PA (DIDAD-) DIDDEXUS INC.
Query Match 2.3%; Score 34.2; DB 6; Length 420;
Best Local Similarity 52.4%; Pred. No. 79;
RESULT 1318
ID AAF07736 standard; cDNA; 567 BP.
DE Fusarium venenatum EST SEQ ID NO:259.
PN WO200056762-A2.
PD 28-SEP-2000.
PA (NOVO) NOVO NORDISK BIOTECH INC.
Query Match 2.3%; Score 34.2; DB 3; Length 567;
Best Local Similarity 47.4%; Pred. No. 91;
RESULT 1319
ID AAH42837 standard; cDNA; 645 BP.
DE Nucleotide sequence of a human metastasis associated 1 gene.
PN WO200153524-A2.
PD 26-JUL-2001.
PA (UNIV-) UNIV NOTTINGHAM TRENT.
Query Match 2.3%; Score 34.2; DB 5; Length 645;
Best Local Similarity 53.8%; Pred. No. 97;
RESULT 1320
ID ABU87669 standard; cDNA; 695 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:10647.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.3%; Score 34.2; DB 6; Length 695;
Best Local Similarity 61.4%; Pred. No. 1e+02;
RESULT 1321
ID AAS69547 standard; cDNA; 708 BP.
DE DNA encoding novel human diagnostic protein #5351.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSB-) HYSBQ INC.
Query Match 2.3%; Score 34.2; DB 5; Length 708;
Best Local Similarity 44.7%; Pred. No. 1e+02;
RESULT 1322
ID AAS75461 standard; cDNA; 708 BP.
DE DNA encoding novel human diagnostic protein #11265.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSB-) HYSBQ INC.
Query Match 2.3%; Score 34.2; DB 5; Length 708;
Best Local Similarity 44.7%; Pred. No. 1e+02;
RESULT 1323
ID ADA69917 standard; DNA; 978 BP.
DE Rice gene, SEQ ID 3240.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.3%; Score 34.2; DB 8; Length 978;
Best Local Similarity 54.3%; Pred. No. 1.2e+02;

RESULT 1324
ID AAQ67210 standard; DNA; 1423 BP.
DE Human corticosteroid binding globulin cDNA.
PN CA2111656-A.
PD 17-JUN-1994.
PA (ALIX) ALLELIX BIOPHARMACEUTICALS INC.
Query Match 2.3%; Score 34.2; DB 2; Length 1423;
Best Local Similarity 47.6%; Pred. No. 1.4e+02;
RESULT 1325
ID AAX22095 standard; DNA; 1767 BP.
DE Cellobiohydrolase CBH B coding sequence.
PN WO9906574-A1.
PD 11-FEB-1999.
PA (KONN) GIST-BROCADES BV.
Query Match 2.3%; Score 34.2; DB 2; Length 1767;
Best Local Similarity 54.3%; Pred. No. 1.6e+02;
RESULT 1326
ID ADT48680 standard; cDNA; 2226 BP.
DE Bacterial polynucleotide #23431.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.3%; Score 34.2; DB 13; Length 2226;
Best Local Similarity 47.4%; Pred. No. 1.8e+02;
RESULT 1327
ID AAH27266 standard; cDNA; 3371 BP.
DE Human cervical cancer marker nucleic acid 4040.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.3%; Score 34.2; DB 4; Length 3371;
Best Local Similarity 53.3%; Pred. No. 2.2e+02;
RESULT 1328
ID ADP25090 standard; cDNA; 3674 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:2268.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GERTH) GENENTECH INC.
Query Match 2.3%; Score 34.2; DB 13; Length 3674;
Best Local Similarity 52.4%; Pred. No. 2.3e+02;
RESULT 1329
ID ADR83544 standard; DNA; 6999 BP.
DE Human sidekick homologue 1 DNA, target gene of miRNA.
PN WO2004076622-A2.
PD 10-SEP-2004.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 2.3%; Score 34.2; DB 13; Length 6999;
Best Local Similarity 56.8%; Pred. No. 3.2e+02;
RESULT 1330
ID ADC26983 standard; DNA; 11358 BP.
DE Sorangium cellulosum tmba gene cluster tmbC DNA.
PN US2003054547-A1.
PD 20-MAR-2003.
PA (JULI/) JULIEN B.
Query Match 2.3%; Score 34.2; DB 10; Length 11358;
Best Local Similarity 56.8%; Pred. No. 4.1e+02;
RESULT 1331
ID AAK69400 standard; DNA; 11456 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24212.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.2; DB 4; Length 11456;
Best Local Similarity 52.4%; Pred. No. 4.1e+02;
RESULT 1332
ID AAX66357 standard; DNA; 16009 BP.
DE Rat smooth muscle myosin heavy chain gene sequence.
PN WO936101-A1.
PD 22-JUL-1999.

PA (UVVI-) UNIV VIRGINIA PATENT FOUND.
Query Match 2.3%; Score 34.2; DB 2; Length 16009;
Best Local Similarity 56.8%; Pred. No. 4.8e+02;
RESULT 1333
ID ABB84504 standard; DNA; 16011 BP.
DE Rat smooth muscle myosin heavy chain gene (-4216 to +11795).
PN WO200259270-A2.
PD 01-AUG-2002.
PA (OWEN/) OWENS G K.
PA (MANA/) MANABE I.
Query Match 2.3%; Score 34.2; DB 6; Length 16011;
Best Local Similarity 56.8%; Pred. No. 4.8e+02;
RESULT 1334
ID ACA60861 standard; DNA; 16011 BP.
DE Rat smooth muscle myosin heavy chain gene fragment.
PN US2003017549-A1.
PD 23-JAN-2003.
PA (OWEN/) OWENS G K.
Query Match 2.3%; Score 34.2; DB 6; Length 16011;
Best Local Similarity 56.8%; Pred. No. 4.8e+02;
RESULT 1335
ID ACN37218 standard; DNA; 20001 BP.
DE Human periodontal disease related gene PTGDS SEQ ID NO:128.
PN WO2004042054-A1.
PD 21-MAY-2004.
PA (HUBI-) HUBIT GENOMIX INC.
PA (KMOI/) KMOI K.
Query Match 2.3%; Score 34.2; DB 13; Length 20001;
Best Local Similarity 60.0%; Pred. No. 5.4e+02;
RESULT 1336
ID ADC26981 standard; DNA; 20922 BP.
DE Sorangium cellulosum tmbA gene cluster tmbB DNA.
PN US2003054547-A1.
PD 20-MAR-2003.
PA (JULI/) JULIEN B.
Query Match 2.3%; Score 34.2; DB 10; Length 20922;
Best Local Similarity 56.8%; Pred. No. 5.5e+02;
RESULT 1337
ID AAO10190 standard; DNA; 23666 BP.
DE Cephalosporin antibiotic biosynthetic genes.
PN JP02291274-A.
PD 03-DEC-1990.
PA (TAKE) TAKEIDA CHEM IND LTD.
Query Match 2.3%; Score 34.2; DB 2; Length 23666;
Best Local Similarity 45.6%; Pred. No. 5.8e+02;
RESULT 1338
ID ACN44414 standard; DNA; 24492 BP.
DE Human genomic sequence hCG1780827.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.2; DB 11; Length 24492;
Best Local Similarity 60.0%; Pred. No. 5.9e+02;
RESULT 1339
ID AAF88314 standard; DNA; 25360 BP.
DE S. spinoza DNA fragment SEQ ID 3.
PN DE19957268-A1.
PD 08-MAR-2001.
PA (FARB) BAYER AG.
Query Match 2.3%; Score 34.2; DB 4; Length 25360;
Best Local Similarity 47.8%; Pred. No. 6e+02;
RESULT 1340
ID AAF88317 standard; DNA; 29366 BP.
DE S. spinoza DNA fragment SEQ ID 6.
PN DE19957268-A1.
PD 08-MAR-2001.
PA (FARB) BAYER AG.
Query Match 2.3%; Score 34.2; DB 4; Length 29736;
Best Local Similarity 47.8%; Pred. No. 6.5e+02;
RESULT 1341
ID AAD56078 standard; DNA; 32069 BP.
DE Mouse Map3k6 carcinoma associated (CA) gene.
PN WO2003035637-A2.
PD 01-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.2; DB 8; Length 32069;
Best Local Similarity 46.4%; Pred. No. 6.8e+02;
RESULT 1342
ID ADA02440 standard; DNA; 32069 BP.
DE Mouse Map3k6 carcinoma associated gene, SEQ ID NO:959.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.2; DB 9; Length 32069;
Best Local Similarity 46.4%; Pred. No. 6.8e+02;
RESULT 1343
ID ADB72179 standard; DNA; 32069 BP.
DE Mouse Map3k6 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.2; DB 10; Length 32069;
Best Local Similarity 46.4%; Pred. No. 6.8e+02;
RESULT 1344
ID AAS17367 standard; DNA; 33529 BP.
DE DNA sequence of S. cellulosum polyketide synthase cosmId. PKOS28-26.
PN US6280999-B1.
PD 28-AUG-2001.
PA (KOSA-) KOSAN BIOSCIENCE.
Query Match 2.3%; Score 34.2; DB 5; Length 33529;
Best Local Similarity 56.8%; Pred. No. 6.9e+02;
RESULT 1345
ID AAS12439 standard; DNA; 37590 BP.
DE DNA encoding l-aminocyclopropane carboxylate synthase #10.
PN WO2001068879-A2.
PD 20-SEP-2001.
PA (FARB) BAYER AG.
Query Match 2.3%; Score 34.2; DB 4; Length 37590;
Best Local Similarity 52.4%; Pred. No. 7.4e+02;
RESULT 1346
ID ADQ97084 standard; DNA; 38690 BP.
DE Human cancer associated sequence HD10-004, SEQ ID 60.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.2; DB 12; Length 38690;
Best Local Similarity 54.3%; Pred. No. 7.5e+02;
RESULT 1347
ID ADA37416 standard; DNA; 41907 BP.
DE Human rDNA repeat unit.
PN US2003108914-A1.
PD 12-JUN-2003.
PA (HADL/) HADLACZKY G.
Query Match 2.3%; Score 34.2; DB 9; Length 41907;
Best Local Similarity 47.4%; Pred. No. 7.8e+02;
RESULT 1348
ID ACN45116 standard; DNA; 42772 BP.
DE Mouse genomic sequence mCG8527.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.2; DB 11; Length 42772;
Best Local Similarity 48.7%; Pred. No. 7.8e+02;
RESULT 1349
ID ADA14747 standard; DNA; 42998 BP.
DE Human ribosomal DNA complete repeating unit.
PN US2002160970-A1.
PD 31-OCT-2002.
PA (HADL/) HADLACZKY G.
PA (SZAL/) SZALAY A A.
Query Match 2.3%; Score 34.2; DB 8; Length 42998;
Best Local Similarity 47.4%; Pred. No. 7.9e+02;
RESULT 1350
ID ABB65032 standard; DNA; 42999 BP.
DE Invertebrate foraging behaviour associated human DNA sequence #12.
PN WO200259370-A2.

PD 01-AUG-2002.
PA (NEUR-) NEUROSCIENCES RES FOUND INC.
Query Match 2.3%; Score 34.2; DB 6; Length 42999;
Best Local Similarity 47.4%; Pred. No. 7.9e+02;
RESULT 1351
ID AAD61411 standard; DNA; 42999 BP.
DE Human ribosomal DNA (rDNA) repeat region.
PN US2003101480-A1.
PD 29-MAY-2003.
PA (HADL/) HADJACZKY G.
PA (SZAL/) SZALAY A A.
Query Match 2.3%; Score 34.2; DB 10; Length 42999;
Best Local Similarity 47.4%; Pred. No. 7.9e+02;
RESULT 1352
ID ADR43949 standard; DNA; 42999 BP.
DE Human ribosomal DNA complete repeating unit.
PN US2004163147-A1.
PD 19-AUG-2004.
PA (HADL/) HADJACZKY G.
Query Match 2.3%; Score 34.2; DB 13; Length 42999;
Best Local Similarity 47.4%; Pred. No. 7.9e+02;
RESULT 1353
ID ADP64151 standard; DNA; 57082 BP.
DE Human CA125 genomic DNA amino terminal sequence SegID 1.
PN WO2004045553-A2.
PD 03-JUN-2004.
PA (UYAR-) UNIV ARKANSAS.
Query Match 2.3%; Score 34.2; DB 12; Length 57082;
Best Local Similarity 52.4%; Pred. No. 9.1e+02;
RESULT 1354
ID ADQ97534 standard; DNA; 58687 BP.
DE Mouse cancer associated sequence MD09-010, SEQ ID 511.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.2; DB 12; Length 58687;
Best Local Similarity 54.3%; Pred. No. 9.2e+02;
RESULT 1355
ID ADC26995 standard; DNA; 67251 BP.
DE Sorangium cellulosum tmbA gene cluster.
PN US2003054547-A1.
PD 20-MAR-2003.
PA (JULI/) JULIEN B.
Query Match 2.3%; Score 34.2; DB 10; Length 67251;
Best Local Similarity 56.8%; Pred. No. 9.8e+02;
RESULT 1356
ID ABD32576 standard; DNA; 80423 BP.
DE Mouse cancer-associated genomic DNA MD7-205.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.2; DB 13; Length 80423;
Best Local Similarity 58.3%; Pred. No. 1.1e+03;
RESULT 1357
ID ABX14763 standard; DNA; 88191 BP.
DE Genomic DNA encoding novel human ras-like protein.
PN US2002132291-A1.
PD 19-SEP-2002.
PA (YEJU/) YE J.
PA (KETC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 2.3%; Score 34.2; DB 8; Length 88191;
Best Local Similarity 51.7%; Pred. No. 1.1e+03;
RESULT 1358
ID ADA03083 standard; DNA; 93483 BP.
DE Mouse mCG17918 carcinoma associated gene, SEQ ID NO:1601.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.2; DB 9; Length 93483;
Best Local Similarity 53.3%; Pred. No. 1.1e+03;
RESULT 1359

ID ADA66367 standard; DNA; 93483 BP.
DE Mouse mCG17918 gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.2; DB 9; Length 93483;
Best Local Similarity 53.3%; Pred. No. 1.1e+03;
RESULT 1360
ID ADR72821 standard; DNA; 93483 BP.
DE Mouse mCG17918 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.2; DB 10; Length 93483;
Best Local Similarity 53.3%; Pred. No. 1.1e+03;
RESULT 1361
ID ADL27161 standard; DNA; 93483 BP.
DE Mouse genomic sequence for mCG17918.
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 2.3%; Score 34.2; DB 11; Length 93483;
Best Local Similarity 53.3%; Pred. No. 1.1e+03;
RESULT 1362
ID ABD33157 standard; DNA; 109559 BP.
DE Murine cancer-associated (CA) gene MD07-021.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.2; DB 13; Length 109559;
Best Local Similarity 50.9%; Pred. No. 1.2e+03;
RESULT 1363
Query Match 2.3%; Score 34.2; DB 13; Length 110000;
Best Local Similarity 54.3%; Pred. No. 1.2e+03;
RESULT 1364
ID ABN95044 standard; DNA; 110096 BP.
DE Gene #1542 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.3%; Score 34.2; DB 6; Length 110096;
Best Local Similarity 45.2%; Pred. No. 1.2e+03;
RESULT 1365
ID ADL13512 standard; DNA; 178870 BP.
DE Osteoarthritis-associated polymorphic nucleotide #44.
PN WO2003058166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.3%; Score 34.2; DB 10; Length 178870;
Best Local Similarity 50.9%; Pred. No. 1.6e+03;
RESULT 1366
ID ABD32841 standard; DNA; 227448 BP.
DE Mouse cancer-associated genomic DNA MD17-014.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.2; DB 13; Length 227448;
Best Local Similarity 55.5%; Pred. No. 1.7e+03;
RESULT 1367
ID ADF51132 standard; DNA; 243428 BP.
DE Human P-Rex1 genomic DNA sequence.
PN WO2003080664-A1.
PD 02-OCT-2003.
PA (BAHR-) BARAHAM INST.
Query Match 2.3%; Score 34.2; DB 12; Length 243428;
Best Local Similarity 55.5%; Pred. No. 1.8e+03;
RESULT 1368
ID ADP75180 standard; DNA; 304905 BP.
DE Human Endophilin 2 gene.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 2.3%; Score 34.2; DB 11; Length 304905;
Best Local Similarity 55.5%; Pred. No. 2e+03;
RESULT 1369
ID AAG08244 standard; cDNA to mRNA; 234 BP.
DE Exon 4 of rice pyruvate orthophosphate dikinase gene.
FN JP07184657-A.
PD 25-JUL-1995.
PA (NITRA-) JAPAN TAFU GURASU KK.
Query Match 2.3%; Score 34; DB 2; Length 234;
Best Local Similarity 61.1%; Pred. No. 67;
RESULT 1370
ID ADG95503 standard; DNA; 280 BP.
DE Kidney disease-associated gene-related mouse DNA sequence SeqID633.
FN WO2003091427-A1.
PD 06-NOV-2003.
PA (KANS-) KANSAS TECHNOLOGY LICENSING ORG CO LTD.
Query Match 2.3%; Score 34; DB 12; Length 280;
Best Local Similarity 47.2%; Pred. No. 73;
RESULT 1371
ID ADI45208 standard; cDNA; 378 BP.
DE Rice isoprenoid biosynthesis-associated cDNA #70.
FN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGSEMIAN M.
PA (GHAS/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICK D.
PA (ZHUT/) ZHU T.
Query Match 2.3%; Score 34; DB 12; Length 378;
Best Local Similarity 60.5%; Pred. No. 85;
RESULT 1372
ID AAS69541 standard; cDNA; 390 BP.
DE DNA encoding novel human diagnostic protein #5345.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34; DB 5; Length 390;
Best Local Similarity 47.6%; Pred. No. 86;
RESULT 1373
ID AA184784 standard; cDNA; 400 BP.
DE Human polynucleotide SEQ ID NO 4844.
FN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34; DB 4; Length 400;
Best Local Similarity 47.6%; Pred. No. 87;
RESULT 1374
ID ABD16714 standard; DNA; 429 BP.
DE Pseudomonas aeruginosa polynucleotide #15318.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 34; DB 11; Length 429;
Best Local Similarity 49.4%; Pred. No. 90;
RESULT 1375
ID ABR6216 standard; cDNA; 455 BP.
DE cDNA sequence #607 encoding novel human secreted protein.
FN WO200177289-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.3%; Score 34; DB 6; Length 455;
Best Local Similarity 52.0%; Pred. No. 93;
RESULT 1376
ID ACH73361 standard; DNA; 510 BP.
DE Human genome derived single exon probe #6556.
FN US2003194704-A1.

PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 2.3%; Score 34; DB 12; Length 510;
Best Local Similarity 50.0%; Pred. No. 98;
RESULT 1377
ID ADE83517 standard; DNA; 521 BP.
DE Rat gene AA799755, SEQ ID NO 11114.
FN WO2003016475-A2.
PD 27-FEB-2003.
PA (GERO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 2.3%; Score 34; DB 10; Length 521;
Best Local Similarity 52.9%; Pred. No. 1e+02;
RESULT 1378
ID ABD16760 standard; DNA; 726 BP.
DE Pseudomonas aeruginosa polynucleotide #15364.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 34; DB 11; Length 726;
Best Local Similarity 49.4%; Pred. No. 1.2e+02;
RESULT 1379
ID ABV06518 standard; cDNA; 793 BP.
DE Human prostate expression marker cDNA 6509.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.3%; Score 34; DB 5; Length 793;
Best Local Similarity 46.6%; Pred. No. 1.2e+02;
RESULT 1380
ID ADR46465 standard; DNA; 895 BP.
DE Tobacco caltractin-like protein coding sequence SEQ ID NO: 31.
FN WO2004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 2.3%; Score 34; DB 13; Length 895;
Best Local Similarity 46.9%; Pred. No. 1.3e+02;
RESULT 1381
ID AAS90702 standard; cDNA; 1167 BP.
DE DNA encoding novel human diagnostic protein #26506.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34; DB 5; Length 1167;
Best Local Similarity 46.3%; Pred. No. 1.5e+02;
RESULT 1382
ID ABD16865 standard; DNA; 1383 BP.
DE Pseudomonas aeruginosa polynucleotide #15469.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 34; DB 11; Length 1383;
Best Local Similarity 49.4%; Pred. No. 1.6e+02;
RESULT 1383
ID ABD16805 standard; DNA; 1503 BP.
DE Pseudomonas aeruginosa polynucleotide #15409.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 34; DB 11; Length 1503;
Best Local Similarity 49.4%; Pred. No. 1.7e+02;
RESULT 1384
ID AAK52313 standard; cDNA; 1627 BP.
DE Human polynucleotide SEQ ID NO 858.
FN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34; DB 4; Length 1627;
Best Local Similarity 57.5%; Pred. No. 1.8e+02;
RESULT 1385
ID ABX05202 standard; cDNA; 2154 BP.

DE Human novel polynucleotide #217.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34; DB 8; Length 2154;
RESULT 1386 Best Local Similarity 54.9%; Pred. No. 2e+02;
ID ADO87317 standard; cDNA; 2192 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4194.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.3%; Score 34; DB 13; Length 2192;
RESULT 1387 Best Local Similarity 54.9%; Pred. No. 2e+02;
ID ADO87554 standard; cDNA; 2192 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4432.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.3%; Score 34; DB 13; Length 2192;
RESULT 1388 Best Local Similarity 54.9%; Pred. No. 2e+02;
ID ADA53499 standard; cDNA; 2338 BP.
DE Human coding sequence, SEQ ID 1067.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.3%; Score 34; DB 10; Length 2338;
RESULT 1389 Best Local Similarity 52.1%; Pred. No. 2.1e+02;
ID ADM03650 standard; cDNA; 2404 BP.
DE Human cDNA of the invention SEQ ID NO:2335.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.3%; Score 34; DB 11; Length 2404;
RESULT 1390 Best Local Similarity 57.5%; Pred. No. 2.1e+02;
ID AAT35233 standard; cDNA; 2823 BP.
DE Natural killer lytic associated protein cDNA.
PN WO9626744-A1.
PD 06-SEP-1996.
PA (UYAR-) UNIV ARKANSAS.
Query Match 2.3%; Score 34; DB 2; Length 2823;
RESULT 1391 Best Local Similarity 50.0%; Pred. No. 2.3e+02;
ID ADO36980 standard; DNA; 2844 BP.
DE Cell proliferation-related nucleic acid sequence #70.
PN WO2004061122-A2.
PD 22-JUL-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.3%; Score 34; DB 12; Length 2844;
RESULT 1392 Best Local Similarity 61.1%; Pred. No. 2.3e+02;
ID ADQ15650 standard; DNA; 2844 BP.
DE Rice stress-related protein coding sequence #30.
PN WO2004061080-A2.
PD 22-JUL-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.3%; Score 34; DB 12; Length 2844;
RESULT 1393 Best Local Similarity 61.1%; Pred. No. 2.3e+02;
ID AAL04774 standard; DNA; 3051 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7462.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 2.3%; Score 34; DB 4; Length 3051;
RESULT 1394 Best Local Similarity 48.0%; Pred. No. 2.4e+02;
ID ABK95303 standard; cDNA; 3809 BP.
DE Human prostate specific gene sequence DEX0283_68.
PN WO200242329-A2.
PD 30-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 2.3%; Score 34; DB 6; Length 3809;
RESULT 1395 Best Local Similarity 47.2%; Pred. No. 2.7e+02;
ID ADS48518 standard; cDNA; 3851 BP.
DE Bacterial polynucleotide #3261.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.3%; Score 34; DB 13; Length 3851;
RESULT 1396 Best Local Similarity 63.4%; Pred. No. 2.7e+02;
ID AAC64438 standard; DNA; 3896 BP.
DE Arabidopsis thaliana PDAT genomic DNA SEQ ID NO:11.
PN WO20060095-A2.
PD 12-OCT-2000.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 2.3%; Score 34; DB 3; Length 3896;
RESULT 1397 Best Local Similarity 52.9%; Pred. No. 2.7e+02;
ID AAC64448 standard; DNA; 3896 BP.
DE Arabidopsis thaliana PDAT genomic DNA SEQ ID NO:10b.
PN WO20060095-A2.
PD 12-OCT-2000.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 2.3%; Score 34; DB 3; Length 3896;
RESULT 1398 Best Local Similarity 52.9%; Pred. No. 2.7e+02;
ID AAR26524 standard; cDNA; 4182 BP.
DE Human proton/oligonucleotide transporter hPHT2 gene intron 1.
PN WO200160854-A1.
PD 23-AUG-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 2.3%; Score 34; DB 4; Length 4182;
RESULT 1399 Best Local Similarity 50.0%; Pred. No. 2.8e+02;
ID AAQ98237 standard; DNA; 8626 BP.
DE Partial rice pyruvate orthophosphate dikinase gene.
PN JP07184657-A.
PD 25-JUL-1995.
PA (NITA-) JAPAN TAFU GURASU KK.
Query Match 2.3%; Score 34; DB 2; Length 8626;
RESULT 1400 Best Local Similarity 61.1%; Pred. No. 4e+02;
ID ACC48896 standard; DNA; 8766 BP.
DE Rhodococcus ruber eth gene cluster involved in ETBE degradation.
PN EP1270722-A1.
PD 02-JAN-2003.
PA (INSE) INST PASTEUR.
PA (INSE) INST FRANCAIS DU PETROLE.
Query Match 2.3%; Score 34; DB 8; Length 8766;
RESULT 1401 Best Local Similarity 51.5%; Pred. No. 4.1e+02;
ID ABI15220 standard; cDNA; 10479 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40142.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.3%; Score 34; DB 4; Length 10479;
RESULT 1402 Best Local Similarity 45.5%; Pred. No. 4.4e+02;
ID ACC48895 standard; DNA; 12342 BP.

DE Rhodococcus ruber eth gene cluster deleted region.
PN EPI270722-A1.
PD 02-JAN-2003.
PA (INSP) INST PASTEUR.
PA (INSP) INST FRANCAIS DU PETROLE.
Query Match 2.3%; Score 34; DB 8; Length 12342;
Best Local Similarity 51.5%; Pred. No. 4.8e+02;
RESULT 1403
ID AB074539 standard; DNA; 19321 BP.
DE Human transglutaminase-A gene sequence SEQ ID NO:4.
PN WO200259285-A2.
PD 01-AUG-2002.
PA (DECO-) DECODE GENETICS INC.
Query Match 2.3%; Score 34; DB 6; Length 19321;
Best Local Similarity 63.4%; Pred. No. 6e+02;
RESULT 1404
ID ADA14746 standard; DNA; 22118 BP.
DE Mouse 45S rRNA gene.
PN US2002160970-A1.
PD 31-OCT-2002.
PA (HADL/) HADLACZKY G.
PA (SZAL/) SZALAY A A.
Query Match 2.3%; Score 34; DB 8; Length 22118;
Best Local Similarity 56.0%; Pred. No. 6.4e+02;
RESULT 1405
ID ADA37415 standard; DNA; 22118 BP.
DE Origin of replication DNA.
PN US2003108914-A1.
PD 12-JUN-2003.
PA (HADL/) HADLACZKY G.
Query Match 2.3%; Score 34; DB 9; Length 22118;
Best Local Similarity 56.0%; Pred. No. 6.4e+02;
RESULT 1406
ID AAD61410 standard; DNA; 22118 BP.
DE Mouse ribosomal DNA (rDNA) repeat region.
PN US2003101480-A1.
PD 29-MAY-2003.
PA (HADL/) HADLACZKY G.
PA (SZAL/) SZALAY A A.
Query Match 2.3%; Score 34; DB 10; Length 22118;
Best Local Similarity 56.0%; Pred. No. 6.4e+02;
RESULT 1407
ID ADP10518 standard; DNA; 22118 BP.
DE Mouse ribosomal RNA gene repeat unit.
PN WO2003093469-A2.
PD 13-NOV-2003.
PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
Query Match 2.3%; Score 34; DB 10; Length 22118;
Best Local Similarity 56.0%; Pred. No. 6.4e+02;
RESULT 1408
ID ACC44629 standard; DNA; 22118 BP.
DE Mouse ribosomal RNA gene (rDNA) nucleotide sequence SEQ ID NO:18.
PN WO200297059-A2.
PD 05-DEC-2002.
PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
Query Match 2.3%; Score 34; DB 10; Length 22118;
Best Local Similarity 56.0%; Pred. No. 6.4e+02;
RESULT 1409
ID ADR43948 standard; DNA; 22118 BP.
DE Mouse pre rRNA gene.
PN US2004163147-A1.
PD 19-AUG-2004.
PA (HADL/) HADLACZKY G.
Query Match 2.3%; Score 34; DB 13; Length 22118;
Best Local Similarity 56.0%; Pred. No. 6.4e+02;
RESULT 1410
ID ACC48894 standard; DNA; 23656 BP.
DE Rhodococcus ruber eth gene region involved in ETBE degradation.
PN EPI270722-A1.
PD 02-JAN-2003.
PA (INSP) INST PASTEUR.
PA (INSP) INST FRANCAIS DU PETROLE.
Query Match 2.3%; Score 34; DB 8; Length 23656;
Best Local Similarity 51.5%; Pred. No. 6.6e+02;
RESULT 1411
ID AAK90279 standard; DNA; 25423 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3855.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34; DB 4; Length 25423;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1412
ID AA157656 standard; DNA; 25423 BP.
DE Human colorectal cancer antigen coding sequence SEQ ID NO: 193.
PN WO200155350-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34; DB 4; Length 25423;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1413
ID ABS99833 standard; DNA; 25423 BP.
DE Genomic DNA #37 encoding human colorectal cancer related protein.
PN US2002119919-A1.
PD 29-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.3%; Score 34; DB 6; Length 25423;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1414
ID ADB92986 standard; DNA; 25423 BP.
DE Human colorectal cancer related polypeptide DNA #37.
PN US2003054420-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34; DB 10; Length 25423;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1415
ID AAK90280 standard; DNA; 25424 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3856.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34; DB 4; Length 25424;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1416
ID AA157657 standard; DNA; 25424 BP.
DE Human colorectal cancer antigen coding sequence SEQ ID NO: 194.
PN WO200155350-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34; DB 4; Length 25424;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1417
ID ABS99834 standard; DNA; 25424 BP.
DE Genomic DNA #38 encoding human colorectal cancer related protein.
PN US2002119919-A1.
PD 29-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.3%; Score 34; DB 6; Length 25424;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1418
ID ADB92987 standard; DNA; 25424 BP.
DE Human colorectal cancer related polypeptide DNA #38.
PN US2003054420-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34; DB 10; Length 25424;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1419
ID AAK68605 standard; DNA; 26555 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23417.
PN WO200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 2.3%; Score 34; DB 4; Length 26555;
Best Local Similarity 50.0%; Pred. No. 7e+02;
RESULT 1420
ID AAK68372 standard; DNA; 26555 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:23184.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 2.3%; Score 34; DB 4; Length 26555;
Best Local Similarity 50.0%; Pred. No. 7e+02;
RESULT 1421
ID AAI62833 standard; DNA; 26555 BP.
DE Human genomic DNA SEQ ID NO 161.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 2.3%; Score 34; DB 4; Length 26555;
Best Local Similarity 50.0%; Pred. No. 7e+02;
RESULT 1422
ID AAL56704 standard; DNA; 36604 BP.
DE Chimpanzee adenovirus serotype Pan6 genomic DNA.
PN WO2003046124-A2.
PD 05-JUN-2003.
PA (UTPE-) UNIV PENNSYLVANIA.
Query Match 2.3%; Score 34; DB 8; Length 36604;
Best Local Similarity 50.0%; Pred. No. 8.3e+02;
RESULT 1423
ID ACN44568 standard; DNA; 43799 BP.
DE Mouse genomic sequence MCC21498.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 11; Length 43799;
Best Local Similarity 22.4%; Pred. No. 9e+02;
RESULT 1424
ID AAD36070 standard; DNA; 45993 BP.
DE Human liver glucokinase genomic DNA.
PN WO200224741-A2.
PD 28-MAR-2002.
PA (RYAN/) RYAN J W.
Query Match 2.3%; Score 34; DB 6; Length 45993;
Best Local Similarity 46.3%; Pred. No. 9.2e+02;
RESULT 1425
ID ADA02729 standard; DNA; 50396 BP.
DE Mouse Gnb1 carcinoma associated gene, SEQ ID NO:1247.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 9; Length 50396;
Best Local Similarity 54.9%; Pred. No. 9.7e+02;
RESULT 1426
ID ADA02732 standard; DNA; 50396 BP.
DE Human GNB1 carcinoma associated gene, SEQ ID NO:1250.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 9; Length 50396;
Best Local Similarity 54.9%; Pred. No. 9.7e+02;
RESULT 1427
ID ADB72470 standard; DNA; 50396 BP.
DE Human GNB1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 10; Length 50396;
Best Local Similarity 54.9%; Pred. No. 9.7e+02;
RESULT 1428
ID ADB72467 standard; DNA; 50396 BP.
DE Mouse Gnb1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 10; Length 50396;
Best Local Similarity 54.9%; Pred. No. 9.7e+02;
RESULT 1429
ID ADE95977 standard; DNA; 50396 BP.
DE Mouse Gnb1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 10; Length 50396;
Best Local Similarity 54.9%; Pred. No. 9.7e+02;
RESULT 1430
ID ADE95980 standard; DNA; 50396 BP.
DE Human GNB1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 10; Length 50396;
Best Local Similarity 54.9%; Pred. No. 9.7e+02;
RESULT 1431
ID ADP64454 standard; DNA; 76994 BP.
DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.
PN WO2004053065-A2.
PD 24-JUN-2004.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 2.3%; Score 34; DB 12; Length 76994;
Best Local Similarity 59.2%; Pred. No. 1.2e+03;
RESULT 1432
ID ACN44076 standard; DNA; 77834 BP.
DE Mouse genomic sequence MCC14020.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 11; Length 77834;
Best Local Similarity 52.1%; Pred. No. 1.2e+03;
RESULT 1433
ID ABX09143 standard; DNA; 86114 BP.
DE Mycobacterium tuberculosis H37Rv BAC clone BAC-RV265.
PN WO200274803-A2.
PD 26-SEP-2002.
PA (INSP) INST PASTEUR.
Query Match 2.3%; Score 34; DB 6; Length 86114;
Best Local Similarity 48.0%; Pred. No. 1.3e+03;
RESULT 1434
ID ADO17634 standard; DNA; 96276 BP.
DE Human bovt tissue sarcoma-upregulated DNA - SEQ ID 451.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.3%; Score 34; DB 12; Length 96276;
Best Local Similarity 54.9%; Pred. No. 1.3e+03;
RESULT 1435
ID ADA02501 standard; DNA; 96597 BP.
DE Mouse Bach2 carcinoma associated gene, SEQ ID NO:1019.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 9; Length 96597;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1436
ID ADB72239 standard; DNA; 96597 BP.
DE Mouse Bach2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 10; Length 96597;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1437
ID ADE95749 standard; DNA; 96597 BP.
DE Mouse Bach2 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 2.3%; Score 34; DB 10; Length 96597;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1438
Query Match 2.3%; Score 34; DB 4; Length 110000;
Best Local Similarity 48.0%; Pred. No. 1.4e+03;
RESULT 1439
Query Match 2.3%; Score 34; DB 4; Length 110000;
Best Local Similarity 48.0%; Pred. No. 1.4e+03;
RESULT 1440
Query Match 2.3%; Score 34; DB 6; Length 110000;
Best Local Similarity 52.1%; Pred. No. 1.4e+03;
RESULT 1441
Query Match 2.3%; Score 34; DB 6; Length 110000;
Best Local Similarity 52.1%; Pred. No. 1.4e+03;
RESULT 1442
Query Match 2.3%; Score 34; DB 12; Length 110000;
Best Local Similarity 52.1%; Pred. No. 1.4e+03;
RESULT 1443
Query Match 2.3%; Score 34; DB 12; Length 110000;
Best Local Similarity 52.1%; Pred. No. 1.4e+03;
RESULT 1444
Query Match 2.3%; Score 34; DB 12; Length 110000;
Best Local Similarity 52.1%; Pred. No. 1.4e+03;
RESULT 1445
Query Match 2.3%; Score 34; DB 12; Length 110000;
Best Local Similarity 52.1%; Pred. No. 1.4e+03;
RESULT 1446
Query Match 2.3%; Score 34; DB 12; Length 110000;
Best Local Similarity 52.1%; Pred. No. 1.4e+03;
RESULT 1447
Query Match 2.3%; Score 34; DB 12; Length 110000;
Best Local Similarity 52.1%; Pred. No. 1.4e+03;
RESULT 1448
Query Match 2.3%; Score 34; DB 12; Length 110000;
Best Local Similarity 52.1%; Pred. No. 1.4e+03;
RESULT 1449
ID AAK53491 standard; DNA; 114955 BP.
DE Human adenosine A1 receptor antisense oligonucleotide fragment.
PN WO9913886-A1.
PD 25-MAR-1999.
PA (UTEC-) UNIV EAST CAROLINA.
Query Match 2.3%; Score 34; DB 13; Length 110000;
Best Local Similarity 47.2%; Pred. No. 1.4e+03;
RESULT 1450
ID ABR35015 standard; cDNA; 136328 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 127.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match 2.3%; Score 34; DB 6; Length 136328;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
RESULT 1451
ID ADO59449 standard; DNA; 153740 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:85.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34; DB 12; Length 153740;
Best Local Similarity 52.1%; Pred. No. 1.6e+03;
RESULT 1452
ID ADI13501 standard; DNA; 167932 BP.
DE Osteoarthritis-associated polymorphic nucleotide #33.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.3%; Score 34; DB 10; Length 167932;
Best Local Similarity 57.5%; Pred. No. 1.7e+03;
RESULT 1453

ID ADO97146 standard; DNA; 348101 BP.
DE Human cancer associated sequence HD08-007, SEQ ID 122.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34; DB 12; Length 348101;
Best Local Similarity 47.2%; Pred. No. 2.3e+03;
RESULT 1454
ID ADA58581 standard; cDNA; 270 BP.
DE Maize sucrose synthase EST #225.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LITU/) LITU J.
Query Match 2.3%; Score 33.8; DB 9; Length 270;
Best Local Similarity 58.4%; Pred. No. 82;
RESULT 1455
ID ACN87596 standard; DNA; 383 BP.
DE Breast cancer related marker, seq id 8746.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNium PHARM INC.
Query Match 2.3%; Score 33.8; DB 11; Length 383;
Best Local Similarity 48.7%; Pred. No. 97;
RESULT 1456
ID ABR34899 standard; cDNA; 409 BP.
DE Human cDNA encoding secreted protein #37.
PN WO200177288-A2.
PD 18-OCT-2001.
PA (GENY) GENETICS INST INC.
Query Match 2.3%; Score 33.8; DB 6; Length 409;
Best Local Similarity 54.4%; Pred. No. 1e+02;
RESULT 1457
ID ABR37415 standard; cDNA; 415 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2580.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.3%; Score 33.8; DB 8; Length 415;
Best Local Similarity 48.7%; Pred. No. 1e+02;
RESULT 1458
ID ABD16662 standard; DNA; 438 BP.
DE Pseudomonas aeruginosa polynucleotide #15266.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 33.8; DB 11; Length 438;
Best Local Similarity 49.7%; Pred. No. 1e+02;
RESULT 1459
ID ABA59121 standard; DNA; 454 BP.
DE Human foetal liver single exon nucleic acid probe #7426.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 33.8; DB 4; Length 454;
Best Local Similarity 50.3%; Pred. No. 1.1e+02;
RESULT 1460
ID AA138867 standard; DNA; 454 BP.
DE Probe #7553 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 33.8; DB 4; Length 454;
Best Local Similarity 50.3%; Pred. No. 1.1e+02;
RESULT 1461
ID AAK33067 standard; DNA; 454 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 7624.
PN WO200157276-A2.
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 33.8; DB 4; Length 454;
Best Local Similarity 50.3%; Pred. No. 1.1e+02;
RESULT 1462
ID AAK07302 standard; DNA; 454 BP.
DE Human brain expressed single exon probe SEQ ID NO: 7293.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 33.8; DB 4; Length 454;
Best Local Similarity 50.3%; Pred. No. 1.1e+02;
RESULT 1463
ID AB832802 standard; DNA; 454 BP.
DE Human liver single exon probe, SEQ ID NO 7792.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 33.8; DB 4; Length 454;
Best Local Similarity 50.3%; Pred. No. 1.1e+02;
RESULT 1464
ID AB807882 standard; DNA; 454 BP.
DE Human genome-derived single exon probe from lung SEQ ID NO 7873.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 33.8; DB 6; Length 454;
Best Local Similarity 50.3%; Pred. No. 1.1e+02;
RESULT 1465
ID ACH15828 standard; cDNA; 473 BP.
DE Human adult heart cDNA #142.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DNA/) DRMANC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.3%; Score 33.8; DB 9; Length 473;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
RESULT 1466
ID AAI88625 standard; cDNA; 512 BP.
DE Human polynucleotide SEQ ID NO 8685.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 33.8; DB 4; Length 512;
Best Local Similarity 54.4%; Pred. No. 1.1e+02;
RESULT 1467
ID ADD16019 standard; cDNA; 517 BP.
DE cDNA (SeqID 87) that confers an altered visual phenotype in plants.
PN WO2003020741-A1.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
PA (DOMC) DOW AGROSCIENCES LLC.
Query Match 2.3%; Score 33.8; DB 10; Length 517;
Best Local Similarity 53.4%; Pred. No. 1.1e+02;
RESULT 1468
ID ADL45106 standard; DNA; 531 BP.
DE Human ovarian cancer DNA marker #18996.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.3%; Score 33.8; DB 5; Length 531;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
RESULT 1469
ID AAH1011 standard; cDNA; 572 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:7846.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.3%; Score 33.8; DB 4; Length 572;
Best Local Similarity 46.0%; Pred. No. 1.2e+02;
RESULT 1470
ID ABK89970 standard; cDNA; 619 BP.
DE Expressed sequence tag (EST) #5 encoding human alanine aminotransferase.
PN WO200255712-A2.
PD 18-JUL-2002.
PA (FARB) BAYER AG.
Query Match 2.3%; Score 33.8; DB 6; Length 619;
Best Local Similarity 53.4%; Pred. No. 1.2e+02;
RESULT 1471
ID ABK89969 standard; cDNA; 631 BP.
DE Expressed sequence tag (EST) #4 encoding human alanine aminotransferase.
PN WO200255712-A2.
PD 18-JUL-2002.
PA (FARB) BAYER AG.
Query Match 2.3%; Score 33.8; DB 6; Length 631;
Best Local Similarity 53.4%; Pred. No. 1.2e+02;
RESULT 1472
ID AB065930 standard; DNA; 654 BP.
DE Arabidopsis thaliana polynucleotide SEQ ID NO 507.
PN US2002059663-A1.
PD 16-MAY-2002.
PA (GORL/) GORLACH J.
PA (ANYV/) AN Y.
PA (HAMT/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYV/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATTHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SIAT/) SIATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 2.3%; Score 33.8; DB 6; Length 654;
Best Local Similarity 47.4%; Pred. No. 1.3e+02;
RESULT 1473
ID ABD17092 standard; DNA; 672 BP.
DE Pseudomonas aeruginosa polynucleotide #15696.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 33.8; DB 11; Length 672;
Best Local Similarity 46.4%; Pred. No. 1.3e+02;
RESULT 1474
ID AAC38557 standard; DNA; 716 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 21405.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.3%; Score 33.8; DB 3; Length 716;
Best Local Similarity 47.4%; Pred. No. 1.3e+02;
RESULT 1475
ID AAV15437 standard; DNA; 753 BP.
DE Human gene fragment D13C10 causing carboxydehydrogenase activity.
PN JP10057062-A.
PD 03-MAR-1998.
PA (RITA) RITAGAKU KENKYUSHO.
Query Match 2.3%; Score 33.8; DB 2; Length 753;
Best Local Similarity 50.3%; Pred. No. 1.4e+02;
RESULT 1476
ID AAH03867 standard; cDNA; 765 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:702.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.3%; Score 33.8; DB 4; Length 765;
Best Local Similarity 52.5%; Pred. No. 1.4e+02;
RESULT 1477

ID AAc4956 standard; DNA; 774 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44762.
 PA EPI033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 47.4%; Pred. No. 1.4e+02;
 RESULT 1478
 ID ABA99115 standard; DNA; 777 BP.
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 883.
 PN US2002023281-A1.
 PD 21-FEB-2002.
 PA (GORL/) GORLACH J.
 PA (ANYV/) AN Y.
 PA (HAMJ/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUYV/) YU Y.
 PA (RAME/) RAMEKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHW A V.
 PA (LEDF/) LEDFORD B L.
 PA (MOES/) MOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 Query Match
 Best Local Similarity 49.2%; Pred. No. 1.4e+02;
 RESULT 1479
 ID ADI42806 standard; DNA; 820 BP.
 DE Plant transcription factor polynucleotide #811.
 PN US2004019927-A1.
 PD 29-JAN-2004.
 PA (SHER/) SHERMAN B K.
 PA (RIEC/) RIECHMANN J L.
 PA (JIAN/) JIANG C.
 PA (HEAR/) HEARD J E.
 PA (HNAK/) HNAKE V.
 PA (CREE/) CREELMAN R A.
 PA (RATC/) RATCLIFFE O.
 PA (ADAM/) ADAM L J.
 PA (KEUB/) REUBER T L.
 PA (KEDJ/) KEDDIE J.
 PA (BROU/) BROUD P E.
 PA (PILG/) PILGRIM M L.
 PA (DUBE/) DUBBEL A N.
 PA (PINE/) PINEDA O.
 PA (YUGG/) YU G.
 Query Match
 Best Local Similarity 48.2%; Pred. No. 1.4e+02;
 RESULT 1480
 ID ADO03013 standard; cDNA; 820 BP.
 DE Corn orthologue of Thalecress transcription factor, cDNA #124.
 PN US2004045049-A1.
 PD 04-MAR-2004.
 PA (ZHAN/) ZHANG J.
 PA (FROM/) FROM M E.
 PA (HEAR/) HEARD J E.
 PA (RIEC/) RIECHMANN J L.
 PA (ADAM/) ADAM L J.
 PA (BROU/) BROUD P E.
 PA (PINE/) PINEDA O.
 PA (KEUB/) REUBER T L.
 PA (KEDJ/) KEDDIE J S.
 PA (YUGG/) YU G.
 PA (JIAN/) JIANG C.
 PA (SAMA/) SAMANA R S.
 PA (PILG/) PILGRIM M L.
 PA (CREE/) CREELMAN R A.

PA (DUBE/) DUBBEL A N.
 PA (RATC/) RATCLIFFE O.
 PA (KIMI/) KIMIMOTO R.
 PA (SHER/) SHERMAN B K.
 Query Match
 Best Local Similarity 48.2%; Pred. No. 1.4e+02;
 RESULT 1481
 ID ADO62434 standard; DNA; 820 BP.
 DE Transcription factor G961 orthologous sequence, SEQ ID 901.
 PN WO2004031349-A2.
 PD 15-APR-2004.
 PA (MENB-) MENDEL BIOTECHNOLOGY INC.
 Query Match
 Best Local Similarity 48.2%; Pred. No. 1.4e+02;
 RESULT 1482
 ID ABZ34722 standard; cDNA; 882 BP.
 DE Coding sequence SEQ ID 80, upregulated in osteogenesis.
 PN WO200281745-A2.
 PD 17-OCT-2002.
 PA (AVET-) AVENTIS PHARMA SA.
 Query Match
 Best Local Similarity 49.2%; Pred. No. 1.5e+02;
 RESULT 1483
 ID ABX75345 standard; cDNA; 882 BP.
 DE Human cDNA encoding secreted frizzled related protein 1.
 PN WO200277204-A2.
 PD 03-OCT-2002.
 PA (AXOR-) AXORDIA LTD.
 Query Match
 Best Local Similarity 49.2%; Pred. No. 1.5e+02;
 RESULT 1484
 ID AAD52559 standard; DNA; 882 BP.
 DE SARP 1 DNA.
 PN WO200290992-A2.
 PD 14-NOV-2002.
 PA (AXOR-) AXORDIA LTD.
 Query Match
 Best Local Similarity 49.2%; Pred. No. 1.5e+02;
 RESULT 1485
 ID ABZ81831 standard; DNA; 882 BP.
 DE FRP nucleic acid sequence.
 PN WO2003012082-A2.
 PD 13-FEB-2003.
 PA (AXOR-) AXORDIA LTD.
 Query Match
 Best Local Similarity 49.2%; Pred. No. 1.5e+02;
 RESULT 1486
 ID ADK65947 standard; DNA; 882 BP.
 DE Gene #37 for inhibitory RNA to manipulate stem cell phenotype.
 PN WO2003068961-A2.
 PD 21-AUG-2003.
 PA (AXOR-) AXORDIA LTD.
 Query Match
 Best Local Similarity 49.2%; Pred. No. 1.5e+02;
 RESULT 1487
 ID ADA69490 standard; DNA; 1002 BP.
 DE Rice gene, SEQ ID 2813.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN-) SYNGENTA PARTICIPATIONS AG.
 Query Match
 Best Local Similarity 53.4%; Pred. No. 1.6e+02;
 RESULT 1488
 ID ADL12563 standard; cDNA; 1004 BP.
 DE Human steroid-induced C3A liver cell cDNA #292.
 PN US6673549-B1.
 PD 06-JAN-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 50.3%; Pred. No. 1.6e+02;
 RESULT 1489
 ID AAV60339 standard; cDNA; 1120 BP.
 DE cDNA sequence of fibroblast growth factor-2 (FGF-2).

PN WO9837880-A1.
 PD 03-SEP-1998.
 PA (CIBL-) CIBLEX CORP.
 Query Match 2.3%; Score 33.8; DB 2; Length 1120;
 Best Local Similarity 53.4%; Pred. No. 1.7e+02;
 RESULT 1490
 ID AAAS3563 standard; cDNA; 1120 BP.
 DE Human fibroblast growth factor 2 cDNA.
 PN US6083706-A.
 PD 04-JUL-2000.
 PA (CIBL-) CIBLEX CORP.
 Query Match 2.3%; Score 33.8; DB 3; Length 1120;
 Best Local Similarity 53.4%; Pred. No. 1.7e+02;
 RESULT 1491
 ID AAS17400 standard; cDNA; 1120 BP.
 DE Full length cDNA for human fibroblast growth factor 2, FGF-2.
 PN US6306613-B1.
 PD 23-OCT-2001.
 PA (CIBL-) CIBLEX CORP.
 Query Match 2.3%; Score 33.8; DB 6; Length 1120;
 Best Local Similarity 53.4%; Pred. No. 1.7e+02;
 RESULT 1492
 ID ADP28744 standard; DNA; 1227 BP.
 DE Human secreted protein encoding sequence SEQ ID #742.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 2.3%; Score 33.8; DB 12; Length 1227;
 Best Local Similarity 50.3%; Pred. No. 1.7e+02;
 RESULT 1493
 ID ADP28745 standard; DNA; 1344 BP.
 DE Human secreted protein encoding sequence SEQ ID #743.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 2.3%; Score 33.8; DB 12; Length 1344;
 Best Local Similarity 50.3%; Pred. No. 1.8e+02;
 RESULT 1494
 ID ABK89965 standard; DNA; 1569 BP.
 DE DNA encoding human alanine aminotransferase #1.
 PN WO200255712-A2.
 PD 18-JUL-2002.
 PA (FARB) BAYER AG.
 Query Match 2.3%; Score 33.8; DB 6; Length 1569;
 Best Local Similarity 53.4%; Pred. No. 2e+02;
 RESULT 1495
 ID AAH13860 standard; cDNA; 1809 BP.
 DE Human cDNA sequence SEQ ID NO:10847.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 2.3%; Score 33.8; DB 4; Length 1809;
 Best Local Similarity 52.5%; Pred. No. 2.1e+02;
 RESULT 1496
 ID ADD18814 standard; DNA; 1809 BP.
 DE Human disease related protein DNA sequence SegID246.
 PN WO2003018621-A2.
 PD 06-MAR-2003.
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 Query Match 2.3%; Score 33.8; DB 10; Length 1809;
 Best Local Similarity 52.5%; Pred. No. 2.1e+02;
 RESULT 1497
 ID ADR25867 standard; DNA; 1809 BP.
 DE Breast cancer prognosis marker #1728.
 PN WO2004065545-A2.
 PD 05-AUG-2004.
 PA (ROSE-) ROSETTA INPHARMATICS LLC.
 Query Match 2.3%; Score 33.8; DB 13; Length 1809;
 Best Local Similarity 52.5%; Pred. No. 2.1e+02;
 RESULT 1498
 ID ADA70200 standard; DNA; 1980 BP.
 DE Rice gene, SEQ ID 3523.

PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 2.3%; Score 33.8; DB 8; Length 1980;
 Best Local Similarity 54.4%; Pred. No. 2.2e+02;
 RESULT 1499
 ID ADA48189 standard; DNA; 1980 BP.
 DE Rice gene conferring disease resistance in plants.
 PN WO2003000906-A2.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 2.3%; Score 33.8; DB 9; Length 1980;
 Best Local Similarity 54.4%; Pred. No. 2.2e+02;
 RESULT 1500
 ID ACC61932 standard; DNA; 2000 BP.
 DE Gene sequence #SEQ ID 2646.
 PN EP1258494-A1.
 PD 20-NOV-2002.
 PA (CELL-) CELLZONE AG.
 Query Match 2.3%; Score 33.8; DB 10; Length 2000;
 Best Local Similarity 58.4%; Pred. No. 2.2e+02;

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OM nucleic - nucleic search, using sw model

Run on: March 28, 2005, 20:14:09 / Search time 6688 Seconds
(without alignments)
10758.971 Million cell updates/sec

Title: US-10-015-610A-195
Perfect score: 1485
Sequence: 1 gcgcgcacacgcagcagcagc.....tgaaaaaaaaaaaaaaaaaa 1485

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1500 summaries

Database :

GenEmbl:*
1: gb_ha:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|--------|-------------|-----------|----|--------------------|
| 1 | 1485 | 100.0 | 1485 | 6 | AX358856 Sequence |
| 2 | 1485 | 100.0 | 1485 | 6 | AX362349 Sequence |
| 3 | 1485 | 100.0 | 1485 | 6 | AX454624 Sequence |
| 4 | 1485 | 100.0 | 1485 | 6 | AX491102 Sequence |
| 5 | 1485 | 100.0 | 1485 | 6 | AX697127 Sequence |
| 6 | 1485 | 100.0 | 1485 | 9 | AX359067 Sequence |
| 7 | 1462.4 | 98.5 | 3375 | 6 | BD159667 Primer fo |
| 8 | 1462.4 | 98.5 | 3375 | 6 | AX882339 Sequence |
| 9 | 1462.4 | 98.5 | 3375 | 6 | AK022845 Homo sapi |
| 10 | 1445.6 | 97.3 | 3449 | 6 | AK135358 Sequence |
| 11 | 1423.2 | 95.8 | 3470 | 6 | AX430949 Sequence |
| 12 | 1399.4 | 94.2 | 1475 | 9 | AK057789 Sequence |
| 13 | 1398.6 | 94.2 | 1446 | 9 | BC009826 Homo sapi |
| 14 | 1374.4 | 92.6 | 3451 | 6 | CO851292 Sequence |
| 15 | 1374.4 | 92.6 | 3451 | 9 | AK128526 Homo sapi |
| 16 | 1363.8 | 91.8 | 3343 | 9 | AK091912 Homo sapi |
| 17 | 1274.6 | 85.8 | 3306 | 9 | BC021253 Homo sapi |
| 18 | 994.4 | 67.0 | 197019 | 9 | AL157938 Human DNA |
| 19 | 658.4 | 44.3 | 777 | 6 | BD020049 Novel gen |

| | | | | | | | |
|-----|-------|-------|--------|--------|------------|----------------------|--------------------|
| 20: | 658.2 | 44.3 | 777 | 6 | BD099987 | BD099987 Novel gen | |
| c | 21 | 638.2 | 43.0 | 768 | 6 | BD020050 Novel gen | |
| c | 22 | 638.2 | 43.0 | 768 | 6 | BD099988 Novel gen | |
| 23 | 616 | 41.5 | 857 | 6 | BD147900 | BD147900 Primer fo | |
| 24 | 616 | 41.5 | 857 | 6 | AX867838 | AX867838 Sequence | |
| 25 | 602.8 | 40.6 | 632 | 6 | AR432559 | AR432559 Sequence | |
| 26 | 602.8 | 40.6 | 632 | 6 | BD078618 | BD078618 Human pro | |
| 27 | 453 | 30.5 | 453 | 6 | CO724408 | CO724408 Sequence | |
| 28 | 451.4 | 30.4 | 453 | 6 | BD141440 | BD141440 Novel phy | |
| 29 | 448.2 | 30.2 | 453 | 6 | E29045 | E29045 ATG-1117 (A | |
| 30 | 437.4 | 29.5 | 2967 | 10 | BC024599 | BC024599 Mus muscu | |
| 31 | 395.4 | 26.6 | 453 | 10 | AB035322 | AB035322 Mus muscu | |
| 32 | 296.6 | 20.0 | 552 | 6 | E29047 | E29047 ATG-1117 (A | |
| 33 | 278.4 | 18.7 | 393 | 6 | AX430948 | AX430948 Sequence | |
| 34 | 271.8 | 18.3 | 666 | 5 | CR523365 | CR523365 Gallus ga | |
| 35 | 253.4 | 17.1 | 1788 | 5 | AB012309 | AB012309 Cyprinus | |
| 36 | 243.4 | 16.4 | 2263 | 5 | BC059529 | BC059529 Danio rer | |
| 37 | 209 | 14.1 | 1174 | 5 | BC074259 | BC074259 Xenopus 1 | |
| 38 | 206.6 | 13.9 | 967 | 5 | BC073304 | BC073304 Xenopus 1 | |
| c | 39 | 199 | 13.4 | 201 | 11 | BV192584 sqm17502 | |
| 40 | 192.2 | 12.9 | 444 | 6 | BD141439 | BD141439 Novel phy | |
| 41 | 192.2 | 12.9 | 471 | 9 | D86438 | D86438 Homo sapien | |
| 42 | 192.2 | 12.9 | 491 | 6 | AK099732 | AK099732 Sequence | |
| 43 | 192.2 | 12.9 | 491 | 9 | HSU19713 | U19713 Human allog | |
| 44 | 192.2 | 12.9 | 635 | 6 | E28711 | E28711 Novel spllc | |
| 45 | 192.2 | 12.9 | 635 | 6 | E28719 | E28719 Novel spllc | |
| 46 | 192.2 | 12.9 | 635 | 6 | E29046 | E29046 ATG-1117 (A | |
| 47 | 192.2 | 12.9 | 635 | 9 | HUM2D18G05 | AF088038 Homo sapi | |
| 48 | 192.2 | 12.9 | 658 | 6 | AK142887 | AK142887 Sequence | |
| 49 | 192.2 | 12.9 | 687 | 9 | BC009474 | BC009474 Homo sapi | |
| 50 | 191 | 12.9 | 639 | 6 | CO861548 | CO861548 Sequence | |
| 51 | 191 | 12.9 | 639 | 6 | AX770561 | AX770561 Sequence | |
| 52 | 191 | 12.9 | 639 | 9 | HSU49392 | U49392 Human allog | |
| 53 | 189.2 | 12.7 | 441 | 6 | E49633 | E49633 Macrophage | |
| 54 | 186 | 12.5 | 658 | 6 | AX888043 | AX888043 Sequence | |
| 55 | 186 | 12.5 | 658 | 6 | BD027653 | BD027653 Sequence | |
| 56 | 185.2 | 12.5 | 592 | 10 | D86382 | D86382 Mus musculu | |
| 57 | 185.2 | 12.5 | 598 | 10 | AB013745 | AB013745 Mus muscu | |
| 58 | 185.2 | 12.5 | 610 | 10 | AF074959 | AF074959 Mus muscu | |
| 59 | 184.2 | 12.4 | 686 | 4 | AF346450 | AF346450 Bos tauru | |
| 60 | 183.6 | 12.4 | 780 | 10 | BC021539 | BC021539 Mus muscu | |
| 61 | 183.2 | 12.3 | 597 | 6 | AX899116 | AX899116 Sequence | |
| 62 | 183.2 | 12.3 | 597 | 6 | BD034649 | BD034649 Sequence | |
| 63 | 182.2 | 12.3 | 441 | 6 | E49634 | E49634 Macrophage | |
| 64 | 182 | 12.3 | 627 | 10 | RNU17919 | U17919 Rattus norv | |
| 65 | 182 | 12.3 | 653 | 10 | AB000818 | AB000818 Rattus no | |
| 66 | 180.4 | 12.1 | 627 | 6 | AR099695 | AR099695 Sequence | |
| 67 | 180.4 | 12.1 | 651 | 6 | I22424 | I22424 Sequence 4 | |
| 68 | 178.4 | 12.0 | 467 | 6 | CO684414 | CO684414 Sequence | |
| 69 | 174.4 | 11.7 | 810 | 10 | D82069 | D82069 Rat mRNA fo | |
| 70 | 173.8 | 11.7 | 414 | 4 | AF299326 | AF299326 Sus scrofa | |
| 71 | 171.6 | 11.6 | 625 | 5 | AB019540 | AB019540 Chrysophr | |
| 72 | 167.8 | 11.3 | 441 | 6 | E49639 | E49639 Macrophage | |
| 73 | 166.8 | 11.2 | 360 | 6 | E49640 | E49640 Macrophage | |
| 74 | 163.8 | 11.0 | 345 | 6 | E49635 | E49635 Macrophage | |
| 75 | 159.8 | 10.8 | 441 | 6 | E49638 | E49638 Macrophage | |
| 76 | 159 | 10.7 | 480 | 6 | CO689922 | CO689922 Sequence | |
| 77 | 154 | 10.4 | 460 | 6 | CO707654 | CO707654 Sequence | |
| 78 | 146 | 9.8 | 451 | 6 | CO683721 | CO683721 Sequence | |
| 79 | 144.8 | 9.8 | 25031 | 10 | AB094629 | AB094629 Mus muscu | |
| 80 | 144.8 | 9.8 | 203946 | 10 | AC069465 | AC069465 Mus muscu | |
| c | 81 | 144.8 | 9.8 | 235241 | 10 | AL928893 | AL928893 Mouse DNA |
| 82 | 144 | 9.7 | 372 | 6 | CO687682 | CO687682 Sequence | |
| 83 | 143.2 | 9.6 | 354 | 6 | E49636 | E49636 Macrophage | |
| 84 | 141.6 | 9.6 | 353 | 6 | CO692811 | CO692811 Sequence | |
| 85 | 141.6 | 9.5 | 223577 | 2 | AC135374 | AC135374 Rattus no | |
| 86 | 141.6 | 9.5 | 253631 | 2 | AC126155 | AC126155 Rattus no | |
| 87 | 137.4 | 9.3 | 358 | 6 | SD018439 | SD018439 Suberites d | |
| 88 | 133.2 | 9.0 | 522 | 3 | AX894754 | AX894754 Sequence | |
| 89 | 131.4 | 8.8 | 507 | 6 | BD030287 | BD030287 Sequence | |
| 90 | 131.4 | 8.8 | 579 | 6 | E28710 | E28710 Novel spllc | |
| 91 | 131.4 | 8.8 | 579 | 6 | E28710 | E28710 Novel spllc | |
| 92 | 128.2 | 8.6 | 340 | 6 | CO708190 | CO708190 Sequence | |

| | | | | | | | | | | | | | |
|-----|-------|-----|--------|----|-----------|----------------------|-----|------|-----|--------|----|-----------|---------------------|
| 93 | 127.8 | 8.6 | 273 | 6 | E49637 | E49637 Macrophe | 165 | 60.6 | 4.1 | 172 | 9 | AP299329 | AP299329 Homo sapi |
| 94 | 126.8 | 8.5 | 402 | 9 | AF162475 | AF162475 Macaca mu | 167 | 60.4 | 4.1 | 1000 | 6 | C614982 | C614982 Sequence |
| 95 | 124 | 8.4 | 1678 | 10 | RN133471 | U133471 Rattus norv | 168 | 60.4 | 4.1 | 1556 | 3 | AB081653 | AB081653 Drosophila |
| 96 | 121.8 | 8.2 | 282 | 9 | AP299327 | AP299327 Homo sapi | 169 | 60.4 | 4.1 | 1566 | 3 | AY094963 | AY094963 Drosophila |
| 97 | 120.6 | 8.1 | 1533 | 10 | BC081822 | BC081822 Rattus no | 170 | 60.2 | 4.1 | 203946 | 5 | AC069465 | AC069465 Mus muscu |
| 98 | 118.8 | 8.0 | 279 | 9 | CR542153 | CR542153 Homo sapi | 171 | 60 | 4.0 | 1978 | 5 | BX934902 | BX934902 Gallus ga |
| 99 | 117.8 | 7.9 | 424 | 10 | RN1010894 | U10894 Rattus norv | 172 | 60 | 4.0 | 125020 | 9 | AP429315 | AP429315 Homo sapi |
| 100 | 117 | 7.9 | 117 | 6 | BD141426 | BD141426 Rattus norv | 173 | 59.4 | 4.0 | 117 | 6 | BD141424 | BD141424 Homo sapi |
| 101 | 115.4 | 7.8 | 282 | 4 | AF289325 | AF289325 Sus scrof | 174 | 59.2 | 4.0 | 258901 | 2 | BD141425 | BD141425 Novel phy |
| 102 | 114.2 | 7.7 | 631 | 6 | E28718 | E28718 Novel splic | 175 | 57.8 | 3.9 | 117 | 6 | AC151944 | AC151944 Rattus no |
| 103 | 112.2 | 7.6 | 282 | 10 | AF299328 | AF299328 Rattus no | 176 | 57.4 | 3.9 | 151250 | 2 | BD141425 | BD141425 Novel phy |
| 104 | 106.6 | 7.2 | 160875 | 5 | BX571730 | BX571730 Zebrafish | 177 | 57.4 | 3.9 | 221094 | 2 | AC096618 | AC096618 Rattus no |
| 105 | 106.6 | 7.2 | 195644 | 2 | CR762385 | CR762385 Dantio rer | 178 | 57.4 | 3.9 | 261112 | 2 | AC105669 | AC105669 Rattus no |
| 106 | 104.2 | 7.0 | 117 | 6 | BD141427 | BD141427 Novel phy | 179 | 57.4 | 3.9 | 261112 | 2 | AC0614981 | AC0614981 Sequence |
| 107 | 94.8 | 6.4 | 331 | 6 | AB099692 | AB099692 Sequence | 180 | 56 | 3.8 | 10902 | 6 | AC017363 | AC017363 Drosophila |
| 108 | 94.8 | 6.0 | 117 | 6 | I22421 | I22421 Sequence 1 | 181 | 56 | 3.8 | 166918 | 3 | AC009205 | AC009205 Drosophila |
| 109 | 88.8 | 5.5 | 101248 | 4 | BX548169 | BD141428 Novel phy | 182 | 56 | 3.8 | 167777 | 3 | AC009204 | AC009204 Drosophila |
| 110 | 81 | 5.5 | 164 | 6 | E28716 | BX548169 Pig DNA s | 183 | 56 | 3.8 | 170546 | 3 | AC011756 | AC011756 Drosophila |
| 111 | 79.4 | 5.3 | 164 | 6 | E28716 | E28716 Novel splic | 184 | 56 | 3.8 | 265558 | 3 | AE003661 | AE003661 Drosophila |
| 112 | 79.4 | 5.3 | 1235 | 9 | HSU95213 | U95213 Human inter | 185 | 55.8 | 3.8 | 257681 | 5 | CR450704 | CR450704 Dantio rer |
| 113 | 79.4 | 5.3 | 1364 | 6 | CO730868 | CO730868 Sequence | 186 | 55.8 | 3.8 | 257681 | 5 | EX784025 | EX784025 Zebrafish |
| 114 | 79.4 | 5.3 | 16685 | 9 | BX248305 | BX248305 Human DNA | 187 | 55 | 3.7 | 233 | 6 | CO665525 | CO665525 Sequence |
| 115 | 79.4 | 5.3 | 16685 | 9 | HSBMT2 | Z15025 Homo sapien | 188 | 54.6 | 3.7 | 55 | 6 | AX914983 | AX914983 Sequence |
| 116 | 79.4 | 5.3 | 81800 | 9 | HSBMT2 | Y14768 Homo sapien | 189 | 54.6 | 3.7 | 7218 | 6 | BD050516 | BD050516 Sequence |
| 117 | 79.4 | 5.3 | 94667 | 2 | CR759761 | CR759761 Homo sapi | 190 | 54.6 | 3.7 | 186 | 6 | CO075916 | CO075916 Sequence |
| 118 | 79.4 | 5.3 | 99109 | 9 | AL805934 | AL805934 Human DNA | 191 | 54.4 | 3.7 | 186 | 6 | CO075916 | CO075916 Sequence |
| 119 | 79.4 | 5.3 | 99109 | 9 | AP000505 | AP000505 Homo sapi | 192 | 54.4 | 3.7 | 186 | 6 | CO075916 | CO075916 Sequence |
| 120 | 79.4 | 5.3 | 106171 | 2 | CR753892 | CR753892 Homo sapi | 193 | 54.4 | 3.7 | 186 | 6 | CO075916 | CO075916 Sequence |
| 121 | 79.4 | 5.3 | 111554 | 2 | CR753892 | CR753892 Homo sapi | 194 | 54.4 | 3.7 | 186 | 6 | CO075916 | CO075916 Sequence |
| 122 | 79.4 | 5.3 | 132330 | 9 | AL662801 | AL662801 Homo sapi | 195 | 54.4 | 3.7 | 186 | 6 | CO075916 | CO075916 Sequence |
| 123 | 79.4 | 5.3 | 135784 | 9 | AL662801 | AL662801 Human DNA | 196 | 54.4 | 3.7 | 186 | 6 | CO075916 | CO075916 Sequence |
| 124 | 79.4 | 5.3 | 182826 | 9 | AC148688 | AC148688 Macaca mu | 197 | 54.4 | 3.7 | 186 | 6 | CO075916 | CO075916 Sequence |
| 125 | 79.4 | 5.3 | 184666 | 9 | DJ201034 | AP129756 Homo sapi | 198 | 54.4 | 3.7 | 186 | 6 | CO075916 | CO075916 Sequence |
| 126 | 78 | 5.3 | 41602 | 5 | TRU50698 | Takifugu | 199 | 54.4 | 3.7 | 186 | 6 | CO075916 | CO075916 Sequence |
| 127 | 76.8 | 5.2 | 3091 | 10 | NM082932 | U8792 Mus muscu | 200 | 54.4 | 3.7 | 186 | 6 | CO075916 | CO075916 Sequence |
| 128 | 76.8 | 5.2 | 5549 | 10 | AB036423 | AB036423 Mus muscu | 201 | 54.4 | 3.7 | 346 | 6 | CO075916 | CO075916 Sequence |
| 129 | 76.8 | 5.2 | 120990 | 10 | NMHC188A7 | AF109719 Mus muscu | 202 | 54.4 | 3.7 | 500 | 6 | CO051671 | CO051671 Sequence |
| 130 | 75.4 | 5.1 | 1271 | 5 | BC059547 | BC059547 Dantio rer | 203 | 54.4 | 3.7 | 500 | 6 | CO066728 | CO066728 Sequence |
| 131 | 75.2 | 5.1 | 203633 | 2 | AC136959 | AC136959 Rattus no | 204 | 54.4 | 3.7 | 500 | 6 | CO063770 | CO063770 Sequence |
| 132 | 75.2 | 5.1 | 228453 | 2 | AC094348 | AC094348 Rattus no | 205 | 54.4 | 3.7 | 500 | 6 | CO132547 | CO132547 Sequence |
| 133 | 75.2 | 5.1 | 241558 | 2 | AC130591 | AC130591 Rattus no | 206 | 54.4 | 3.7 | 500 | 6 | CO171119 | CO171119 Sequence |
| 134 | 75.2 | 5.1 | 349047 | 10 | BX883046 | BX883046 Rattus no | 207 | 54.4 | 3.7 | 500 | 6 | CO200254 | CO200254 Sequence |
| 135 | 71.2 | 4.8 | 501 | 10 | NM056065 | AF560665 Mus muscu | 208 | 54.4 | 3.7 | 500 | 6 | CO215758 | CO215758 Sequence |
| 136 | 69.2 | 4.7 | 646 | 6 | BD150126 | BD150126 Primer fo | 209 | 54.4 | 3.7 | 500 | 6 | CO254336 | CO254336 Sequence |
| 137 | 69.2 | 4.7 | 646 | 6 | BD150126 | BD150126 Sequence | 210 | 54.4 | 3.7 | 500 | 6 | CO281370 | CO281370 Sequence |
| 138 | 68.8 | 4.6 | 1876 | 6 | BD160145 | BD160145 Primer fo | 211 | 54.4 | 3.7 | 500 | 6 | CO284473 | CO284473 Sequence |
| 139 | 68.8 | 4.6 | 1876 | 6 | AX883133 | AX883133 Sequence | 212 | 54.4 | 3.7 | 175964 | 9 | HS467K16 | HS467K16 Sequence |
| 140 | 68.8 | 4.6 | 1876 | 6 | AX883133 | AX883133 Sequence | 213 | 54.4 | 3.7 | 199763 | 2 | AL589992 | AL589992 Homo sapi |
| 141 | 68.8 | 4.6 | 1876 | 6 | AX883133 | AX883133 Sequence | 214 | 54.2 | 3.6 | 6907 | 6 | AX345468 | AX345468 Sequence |
| 142 | 68.8 | 4.6 | 1876 | 6 | AX883133 | AX883133 Sequence | 215 | 54.2 | 3.6 | 185038 | 10 | AC104894 | AC104894 Sequence |
| 143 | 68.8 | 4.6 | 1876 | 6 | AX883133 | AX883133 Sequence | 216 | 54.2 | 3.6 | 349980 | 6 | AX344556 | AX344556 Sequence |
| 144 | 68.8 | 4.6 | 1876 | 6 | AX883133 | AX883133 Sequence | 217 | 54.2 | 3.6 | 148213 | 10 | AL645731 | AL645731 Sequence |
| 145 | 66.4 | 4.5 | 1562 | 6 | CO725802 | CO725802 Sequence | 218 | 50.8 | 3.4 | 158629 | 10 | AL928591 | AL928591 Sequence |
| 146 | 66.4 | 4.5 | 1562 | 6 | CO725802 | CO725802 Sequence | 219 | 50.8 | 3.4 | 8964 | 3 | SD0410885 | SD0410885 Sequence |
| 147 | 66.4 | 4.5 | 2250 | 5 | AF193047 | AF193047 Homo sapi | 220 | 50 | 3.4 | 114458 | 10 | BX293986 | BX293986 Mouse DNA |
| 148 | 65.6 | 4.4 | 125020 | 9 | AF429315 | AF429315 Homo sapi | 221 | 49.8 | 3.4 | 70714 | 2 | AC101499 | AC101499 Sequence |
| 149 | 64.4 | 4.3 | 5813 | 5 | BC073325 | BC073325 Xenopus 1 | 222 | 49.8 | 3.4 | 114815 | 10 | BX004973 | BX004973 Mouse DNA |
| 150 | 64.4 | 4.3 | 582 | 6 | BD078619 | BD078619 Human pro | 223 | 49.8 | 3.4 | 272031 | 2 | AL772221 | AL772221 Mus muscu |
| 151 | 64.2 | 4.3 | 723 | 6 | BD078619 | BD078619 Human pro | 224 | 49.6 | 3.3 | 671 | 8 | AF042839 | AF042839 Oryza sat |
| 152 | 64.2 | 4.3 | 723 | 6 | BD078619 | BD078619 Human pro | 225 | 49.6 | 3.3 | 830 | 8 | AK119167 | AK119167 Oryza sat |
| 153 | 64.2 | 4.3 | 2264 | 9 | BC068473 | BC068473 Homo sapi | 226 | 49.6 | 3.3 | 876 | 8 | AK121606 | AK121606 Oryza sat |
| 154 | 64.2 | 4.3 | 2265 | 9 | BC014923 | BC014923 Homo sapi | 227 | 49.6 | 3.3 | 968 | 8 | AK059534 | AK059534 Oryza sat |
| 155 | 64.2 | 4.3 | 2382 | 9 | BC007233 | BC007233 Homo sapi | 228 | 49.2 | 3.3 | 213656 | 2 | AC107371 | AC107371 Mus muscu |
| 156 | 64.2 | 4.3 | 2387 | 9 | BC023611 | BC023611 Homo sapi | 229 | 49.2 | 3.3 | 599 | 10 | RATCMB | RATCMB Sequence |
| 157 | 64.2 | 4.3 | 2806 | 5 | BC076710 | BC076710 Xenopus t | 230 | 49.2 | 3.3 | 676 | 3 | AB063182 | AB063182 Halichond |
| 158 | 63.6 | 4.3 | 1100 | 6 | CR385997 | CR385997 Gallus ga | 231 | 49.2 | 3.3 | 691 | 10 | RSPRCM4 | RSPRCM4 Halichond |
| 159 | 63.2 | 4.3 | 1358 | 6 | AR379539 | AR379539 Sequence | 232 | 49.2 | 3.3 | 776 | 3 | AB063184 | AB063184 Halichond |
| 160 | 62.6 | 4.2 | 117 | 5 | BD141423 | BD141423 Novel phy | 233 | 49.2 | 3.3 | 1013 | 3 | D88976 | D88976 Brachiostr |
| 161 | 62.6 | 4.2 | 2754 | 5 | BC063917 | BC063917 Xenopus t | 234 | 49.2 | 3.3 | 1145 | 10 | BC063187 | BC063187 Rattus no |
| 162 | 62.4 | 4.2 | 1854 | 10 | AC064852 | AC064852 Homo sapi | 235 | 49.2 | 3.3 | 2000 | 6 | AX655393 | AX655393 Sequence |
| 163 | 61.2 | 4.1 | 152781 | 2 | AC064852 | AC064852 Homo sapi | 236 | 49.2 | 3.3 | 2180 | 5 | BC045298 | BC045298 Dantio rer |
| 164 | 61.2 | 4.1 | 191988 | 2 | CR388129 | CR388129 Dantio rer | 237 | 49 | 3.3 | 490 | 4 | AY575058 | AY575058 Sus scrof |
| 165 | 61 | 4.1 | 7218 | 6 | 166494 | 166494 Sequence 14 | 238 | 49 | 3.3 | 218880 | 2 | AC124750 | AC124750 Mus muscu |

| | | | | | | | | | | | |
|-------|------|-----|--------|----|-----------|-----|------|-----|--------|----|-----------|
| C 239 | 49 | 3.3 | 237712 | 9 | AC012634 | 312 | 44.8 | 3.0 | 409 | 5 | AB055386 |
| C 240 | 48.8 | 3.3 | 174095 | 10 | AC115863 | 313 | 44.8 | 3.0 | 453 | 8 | OSCALM |
| C 241 | 48.8 | 3.3 | 220247 | 10 | AC131660 | 314 | 44.8 | 3.0 | 712 | 8 | BT014541 |
| C 242 | 48.4 | 3.3 | 123678 | 10 | AC123044 | 315 | 44.8 | 3.0 | 2260 | 10 | AB050199 |
| C 243 | 48.2 | 3.2 | 295500 | 1 | AP005954 | 316 | 44.8 | 3.0 | 186125 | 10 | AC132918 |
| C 244 | 48 | 3.2 | 633 | 8 | AF441190 | 317 | 44.8 | 3.0 | 203490 | 10 | AC122851 |
| C 245 | 48 | 3.2 | 148352 | 2 | AC025309 | 318 | 44.6 | 3.0 | 643 | 5 | AY190728 |
| C 246 | 47.6 | 3.2 | 722 | 10 | MUSCALMDA | 319 | 44.6 | 3.0 | 720 | 11 | BV177505 |
| C 247 | 47.6 | 3.2 | 787 | 2 | BC071404 | 320 | 44.6 | 3.0 | 785 | 9 | BSA133727 |
| C 248 | 47.6 | 3.2 | 964 | 3 | DB8977 | 321 | 44.6 | 3.0 | 835 | 5 | AB110087 |
| C 249 | 47.6 | 3.2 | 2155 | 10 | BC050926 | 322 | 44.6 | 3.0 | 372 | 6 | AB211346 |
| C 250 | 47.4 | 3.2 | 848 | 5 | AB110086 | 323 | 44.6 | 3.0 | 3372 | 6 | AF065164 |
| C 251 | 47.4 | 3.2 | 181380 | 10 | AC115123 | 324 | 44.6 | 3.0 | 3459 | 6 | AX348086 |
| C 252 | 47.2 | 3.2 | 208443 | 10 | AC112791 | 325 | 44.6 | 3.0 | 3459 | 9 | BSA012582 |
| C 253 | 47.2 | 3.2 | 244722 | 2 | AC114788 | 326 | 44.6 | 3.0 | 38911 | 9 | AC005559 |
| C 254 | 47 | 3.2 | 161092 | 2 | AC102715 | 327 | 44.6 | 3.0 | 172171 | 10 | AL670305 |
| C 255 | 46.8 | 3.2 | 78373 | 10 | AC098641 | 328 | 44.6 | 3.0 | 185620 | 10 | AC127567 |
| C 256 | 46.8 | 3.2 | 160207 | 2 | AC130700 | 329 | 44.6 | 3.0 | 203422 | 10 | AL713863 |
| C 257 | 46.8 | 3.2 | 170340 | 10 | AC122433 | 330 | 44.6 | 3.0 | 207701 | 2 | BX545856 |
| C 258 | 46.8 | 3.2 | 226502 | 2 | AC139867 | 331 | 44.6 | 3.0 | 208399 | 2 | AC140054 |
| C 259 | 46.8 | 3.2 | 319614 | 2 | AC126905 | 332 | 44.6 | 3.0 | 217225 | 2 | AC137155 |
| C 260 | 46.6 | 3.1 | 220976 | 10 | AC132474 | 333 | 44.6 | 3.0 | 219826 | 2 | AC118183 |
| C 261 | 46.4 | 3.1 | 409 | 5 | AB055385 | 334 | 44.6 | 3.0 | 22976 | 2 | AC135869 |
| C 262 | 46.4 | 3.1 | 179862 | 9 | CNS05TEB | 335 | 44.6 | 3.0 | 236342 | 10 | AC129190 |
| C 263 | 46.4 | 3.1 | 214267 | 9 | AC008571 | 336 | 44.6 | 3.0 | 253693 | 2 | AC093997 |
| C 264 | 46.4 | 3.1 | 218171 | 2 | AC123689 | 337 | 44.6 | 3.0 | 264062 | 10 | AC095899 |
| C 265 | 46.4 | 3.1 | 344321 | 1 | BX640429 | 338 | 44.6 | 3.0 | 337486 | 2 | AC114544 |
| C 266 | 46.4 | 3.1 | 346274 | 1 | BX640443 | 339 | 44.6 | 3.0 | 347 | 6 | AF660867 |
| C 267 | 46.4 | 3.1 | 349354 | 1 | BX640416 | 340 | 44.4 | 3.0 | 787 | 6 | AF660739 |
| C 268 | 46.2 | 3.1 | 174030 | 2 | AC133936 | 341 | 44.4 | 3.0 | 1519 | 8 | MECAM |
| C 269 | 46.2 | 3.1 | 244203 | 2 | AC096313 | 342 | 44.4 | 3.0 | 116022 | 10 | AC034254 |
| C 270 | 46 | 3.1 | 924 | 3 | AB175946 | 343 | 44.4 | 3.0 | 149237 | 2 | AC139916 |
| C 271 | 46 | 3.1 | 1111 | 3 | TC04182 | 344 | 44.4 | 3.0 | 176602 | 9 | AC115665 |
| C 272 | 46 | 3.1 | 143226 | 9 | AL353802 | 345 | 44.4 | 3.0 | 177085 | 10 | AC142110 |
| C 273 | 46 | 3.1 | 146005 | 10 | AL845290 | 346 | 44.4 | 3.0 | 191255 | 10 | AL671672 |
| C 274 | 46 | 3.1 | 173929 | 2 | AC112985 | 347 | 44.4 | 3.0 | 202533 | 10 | AC099605 |
| C 275 | 46 | 3.1 | 177882 | 9 | AC013402 | 348 | 44.4 | 3.0 | 236635 | 2 | AC126737 |
| C 276 | 46 | 3.1 | 203921 | 2 | AC119460 | 349 | 44.2 | 3.0 | 450 | 8 | STU02094 |
| C 277 | 46 | 3.1 | 207812 | 2 | AC140280 | 350 | 44.2 | 3.0 | 144906 | 10 | BX682542 |
| C 278 | 46 | 3.1 | 244972 | 2 | AC106489 | 351 | 44.2 | 3.0 | 153422 | 9 | AC148715 |
| C 279 | 45.8 | 3.1 | 776 | 5 | CHK1NC | 352 | 44.2 | 3.0 | 156052 | 10 | AC104930 |
| C 280 | 45.8 | 3.1 | 1350 | 6 | BC071886 | 353 | 44.2 | 3.0 | 171011 | 10 | AC140244 |
| C 281 | 45.8 | 3.1 | 147896 | 10 | AL607145 | 354 | 44.2 | 3.0 | 177018 | 2 | AC099716 |
| C 282 | 45.8 | 3.1 | 157891 | 10 | AC133161 | 355 | 44.2 | 3.0 | 179050 | 2 | AC131108 |
| C 283 | 45.8 | 3.1 | 196150 | 10 | AC147250 | 356 | 44.2 | 3.0 | 185378 | 10 | AL772367 |
| C 284 | 45.8 | 3.1 | 21979 | 2 | AC109739 | 357 | 44.2 | 3.0 | 235250 | 2 | AC110194 |
| C 285 | 45.8 | 3.1 | 252384 | 10 | AC123071 | 358 | 44 | 3.0 | 483 | 9 | CR541864 |
| C 286 | 45.6 | 3.1 | 452 | 6 | AX885282 | 359 | 44 | 3.0 | 1251 | 6 | BD160958 |
| C 287 | 45.6 | 3.1 | 452 | 6 | BD024892 | 360 | 44 | 3.0 | 1251 | 6 | AX441273 |
| C 288 | 45.6 | 3.1 | 480 | 9 | CR541884 | 361 | 44 | 3.0 | 1290 | 12 | RN055075 |
| C 289 | 45.6 | 3.1 | 483 | 12 | BT008003 | 362 | 44 | 3.0 | 1322 | 3 | LR0291615 |
| C 290 | 45.6 | 3.1 | 547 | 6 | AX888042 | 363 | 44 | 3.0 | 2128 | 9 | BC06182 |
| C 291 | 45.6 | 3.1 | 547 | 6 | BD027652 | 364 | 44 | 3.0 | 2175 | 9 | HUMCAMA |
| C 292 | 45.6 | 3.1 | 663 | 9 | HUMTRC | 365 | 44 | 3.0 | 2181 | 9 | BC005137 |
| C 293 | 45.6 | 3.1 | 677 | 6 | CO727377 | 366 | 44 | 3.0 | 126106 | 10 | AC125051 |
| C 294 | 45.6 | 3.1 | 677 | 9 | HSTRC | 367 | 44 | 3.0 | 144000 | 2 | AC123764 |
| C 295 | 45.6 | 3.1 | 706 | 9 | BC005323 | 368 | 44 | 3.0 | 165718 | 2 | AC127508 |
| C 296 | 45.6 | 3.1 | 138179 | 9 | AC145217 | 369 | 44 | 3.0 | 168263 | 2 | AC148668 |
| C 297 | 45.6 | 3.1 | 164485 | 2 | AC026106 | 370 | 44 | 3.0 | 186596 | 2 | AC141432 |
| C 298 | 45.6 | 3.1 | 173370 | 10 | AC144629 | 371 | 44 | 3.0 | 197999 | 2 | AC134688 |
| C 299 | 45.4 | 3.1 | 892 | 5 | AB008855 | 372 | 44 | 3.0 | 207065 | 2 | AC140324 |
| C 300 | 45.4 | 3.1 | 2000 | 6 | AX655393 | 373 | 44 | 3.0 | 207822 | 2 | AC109321 |
| C 301 | 45.4 | 3.1 | 178935 | 9 | AC147339 | 374 | 44 | 3.0 | 213771 | 2 | AC109215 |
| C 302 | 45.4 | 3.1 | 202540 | 2 | AC120854 | 375 | 44 | 3.0 | 214285 | 2 | AC113532 |
| C 303 | 45.4 | 3.1 | 239297 | 10 | AC119848 | 376 | 44 | 3.0 | 221055 | 2 | AC097131 |
| C 304 | 45.4 | 3.0 | 121619 | 5 | CR354385 | 377 | 44 | 3.0 | 226167 | 2 | AC119258 |
| C 305 | 45.2 | 3.0 | 168056 | 9 | AC004458 | 378 | 44 | 3.0 | 239275 | 2 | AC113512 |
| C 306 | 45.2 | 3.0 | 184127 | 2 | AC125846 | 379 | 44 | 3.0 | 262978 | 2 | AC136272 |
| C 307 | 45 | 3.0 | 1112 | 10 | RATCAMA | 380 | 43.8 | 2.9 | 486 | 5 | AY281129 |
| C 308 | 45 | 3.0 | 136088 | 10 | EX530092 | 381 | 43.8 | 2.9 | 1644 | 5 | AF085250 |
| C 309 | 45 | 3.0 | 178027 | 2 | AC132041 | 382 | 43.8 | 2.9 | 100381 | 5 | AL672097 |
| C 310 | 45 | 3.0 | 182162 | 2 | AC102917 | 383 | 43.8 | 2.9 | 133869 | 10 | AC139157 |
| C 311 | 45 | 3.0 | 226637 | 2 | AC095337 | 384 | 43.8 | 2.9 | 177962 | 10 | AC147251 |

| | | | | | | | | | | | | |
|-------|------|-----|--------|----|----------|-------|------|-----|--------|----|-----------|--------------------|
| C 385 | 43.8 | 2.9 | 180267 | 10 | AC139324 | C 458 | 43 | 2.9 | 172344 | 2 | AC126228 | AC126228 Papio anu |
| C 386 | 43.8 | 2.9 | 183285 | 10 | AC128655 | 459 | 43 | 2.9 | 184357 | 2 | AC073728 | AC073728 Mus muscu |
| C 387 | 43.8 | 2.9 | 205642 | 2 | AC140691 | 460 | 43 | 2.9 | 205623 | 10 | AC135555 | AC123555 Mus muscu |
| C 388 | 43.8 | 2.9 | 217775 | 10 | AL592224 | 461 | 43 | 2.9 | 214060 | 2 | AC121522 | AC121522 Mus muscu |
| C 389 | 43.8 | 2.9 | 243733 | 2 | AC116381 | 462 | 43 | 2.9 | 245032 | 2 | AC109749 | AC109749 Mus muscu |
| C 390 | 43.8 | 2.9 | 267434 | 2 | AC128998 | 463 | 43 | 2.9 | 256154 | 2 | AC119386 | AC119386 Rattus no |
| C 391 | 43.6 | 2.9 | 883 | 5 | ELCCAMEL | 464 | 43 | 2.9 | 268984 | 3 | AE001274 | AE001274 Leishmani |
| C 392 | 43.6 | 2.9 | 1159 | 6 | CO727058 | 465 | 43 | 2.9 | 450 | 5 | ELCCALMA | M6168 R.electrictu |
| C 393 | 43.6 | 2.9 | 1161 | 6 | HSU31123 | 466 | 42.8 | 2.9 | 595 | 12 | SYNARBCAL | J04729 A.puncnatul |
| C 394 | 43.6 | 2.9 | 1285 | 9 | BC029515 | 467 | 42.8 | 2.9 | 743 | 8 | ZMRNCAL | X74490 Z.mays mRNA |
| C 395 | 43.6 | 2.9 | 1285 | 9 | BC029515 | 468 | 42.8 | 2.9 | 103244 | 2 | AC102394 | Continuation (4 of |
| C 396 | 43.6 | 2.9 | 68456 | 10 | BX324191 | 469 | 42.8 | 2.9 | 110000 | 1 | AE006840 | Continuation (18 o |
| C 397 | 43.6 | 2.9 | 74301 | 2 | AC137736 | 470 | 42.8 | 2.9 | 110000 | 2 | AC116271 | Continuation (2 of |
| C 398 | 43.6 | 2.9 | 110000 | 2 | AC108345 | 471 | 42.8 | 2.9 | 110000 | 2 | AC116271 | Continuation (3 of |
| C 399 | 43.6 | 2.9 | 127252 | 9 | BS000559 | 472 | 42.8 | 2.9 | 150659 | 10 | AC147159 | AC147159 Mus muscu |
| C 400 | 43.6 | 2.9 | 150649 | 10 | AC102918 | 473 | 42.8 | 2.9 | 153258 | 2 | AC026206 | AC026206 Homo sapi |
| C 401 | 43.6 | 2.9 | 152711 | 9 | AP001178 | 474 | 42.8 | 2.9 | 167296 | 2 | AC141904 | AC141904 Rattus no |
| C 402 | 43.6 | 2.9 | 156080 | 2 | CR759833 | 475 | 42.8 | 2.9 | 169896 | 2 | AC101922 | AC101922 Mus muscu |
| C 403 | 43.6 | 2.9 | 165742 | 2 | AC020697 | 476 | 42.8 | 2.9 | 176609 | 10 | AC133992 | AC133992 Homo sapi |
| C 404 | 43.6 | 2.9 | 174469 | 9 | AC022882 | 477 | 42.8 | 2.9 | 176223 | 9 | AC034192 | AC034192 Homo sapi |
| C 405 | 43.6 | 2.9 | 178227 | 10 | AL831766 | 478 | 42.8 | 2.9 | 177176 | 2 | AC139877 | AC139877 Didelphis |
| C 406 | 43.6 | 2.9 | 178668 | 10 | AC131596 | 479 | 42.8 | 2.9 | 184836 | 2 | AC140360 | AC140360 Mus muscu |
| C 407 | 43.6 | 2.9 | 178779 | 2 | AC117442 | 480 | 42.8 | 2.9 | 185277 | 10 | AC098567 | AC098567 Genomic s |
| C 408 | 43.6 | 2.9 | 228405 | 2 | AC096406 | 481 | 42.8 | 2.9 | 186351 | 10 | AC117223 | AC117223 Mus muscu |
| C 409 | 43.6 | 2.9 | 230799 | 2 | AC098397 | 482 | 42.8 | 2.9 | 190554 | 10 | AC141874 | AC141874 Mus muscu |
| C 410 | 43.6 | 2.9 | 235924 | 10 | AC112938 | 483 | 42.8 | 2.9 | 193624 | 10 | AC131726 | AC131726 Mus muscu |
| C 411 | 43.6 | 2.9 | 271915 | 2 | AC096838 | 484 | 42.8 | 2.9 | 201413 | 2 | AC107868 | AC107868 Mus muscu |
| C 412 | 43.6 | 2.9 | 298982 | 2 | AC111908 | 485 | 42.8 | 2.9 | 203839 | 10 | AC129583 | AC129583 Mus muscu |
| C 413 | 43.6 | 2.9 | 344682 | 2 | AC096289 | 486 | 42.8 | 2.9 | 205206 | 2 | AC135913 | AC135913 Mus muscu |
| C 414 | 43.4 | 2.9 | 650 | 8 | AB050840 | 487 | 42.8 | 2.9 | 213673 | 10 | AC130218 | AC130218 Mus muscu |
| C 415 | 43.4 | 2.9 | 1084 | 6 | CO858783 | 488 | 42.8 | 2.9 | 215104 | 2 | AC107639 | AC107639 Mus muscu |
| C 416 | 43.4 | 2.9 | 1084 | 6 | CO858783 | 489 | 42.8 | 2.9 | 217293 | 10 | AC095958 | AC095958 Mus muscu |
| C 417 | 43.4 | 2.9 | 1145 | 10 | RATCAM | 490 | 42.8 | 2.9 | 226769 | 10 | AC113038 | AC113038 Mus muscu |
| C 418 | 43.4 | 2.9 | 1246 | 6 | BD269452 | 491 | 42.8 | 2.9 | 233323 | 2 | AC101871 | AC101871 Mus muscu |
| C 419 | 43.4 | 2.9 | 18034 | 6 | BD269452 | 492 | 42.8 | 2.9 | 233323 | 5 | AF187305 | AF187305 Mus muscu |
| C 420 | 43.4 | 2.9 | 18034 | 6 | BD269452 | 493 | 42.8 | 2.9 | 3672 | 1 | SF020634 | SF020634 |
| C 421 | 43.4 | 2.9 | 18034 | 6 | BD269452 | 494 | 42.8 | 2.9 | 10167 | 1 | SP080223 | SP080223 |
| C 422 | 43.4 | 2.9 | 176608 | 2 | AL807800 | 495 | 42.6 | 2.9 | 130345 | 2 | AC116710 | AC116710 Mus muscu |
| C 423 | 43.4 | 2.9 | 197761 | 2 | AC105321 | 496 | 42.6 | 2.9 | 150118 | 2 | AC101993 | AC101993 Mus muscu |
| C 424 | 43.4 | 2.9 | 204317 | 2 | AC103512 | 497 | 42.6 | 2.9 | 158958 | 9 | AC094014 | AC094014 Homo sapi |
| C 425 | 43.4 | 2.9 | 214377 | 10 | AC133511 | 498 | 42.6 | 2.9 | 161946 | 2 | AC119903 | AC119903 Mus muscu |
| C 426 | 43.4 | 2.9 | 227967 | 2 | AC094951 | 499 | 42.6 | 2.9 | 177771 | 2 | AC124010 | AC124010 Mus muscu |
| C 427 | 43.4 | 2.9 | 239847 | 2 | AC128434 | 500 | 42.6 | 2.9 | 182400 | 2 | AC107708 | AC107708 Mus muscu |
| C 428 | 43.2 | 2.9 | 447 | 6 | BD160956 | 501 | 42.6 | 2.9 | 196102 | 10 | AL732464 | AL732464 Mouse DNA |
| C 429 | 43.2 | 2.9 | 447 | 6 | BD160956 | 502 | 42.6 | 2.9 | 196806 | 10 | AC027184 | AC027184 Mus muscu |
| C 430 | 43.2 | 2.9 | 450 | 5 | CHKCALMA | 503 | 42.6 | 2.9 | 200426 | 2 | AC139759 | AC139759 Mus muscu |
| C 431 | 43.2 | 2.9 | 450 | 5 | CHKCALMA | 504 | 42.6 | 2.9 | 209428 | 10 | AC125948 | AC125948 Rattus no |
| C 432 | 43.2 | 2.9 | 450 | 12 | BT006855 | 505 | 42.6 | 2.9 | 217771 | 2 | AC109134 | AC109134 Rattus no |
| C 433 | 43.2 | 2.9 | 564 | 6 | AX887973 | 506 | 42.6 | 2.9 | 251079 | 2 | AC099134 | AC099134 Rattus no |
| C 434 | 43.2 | 2.9 | 564 | 6 | AX887973 | 507 | 42.6 | 2.9 | 354 | 8 | LEH14764 | LEH14764 |
| C 435 | 43.2 | 2.9 | 726 | 5 | BD027583 | 508 | 42.6 | 2.9 | 450 | 5 | CHKCM11 | CHKCM11 |
| C 436 | 43.2 | 2.9 | 1100 | 3 | AB003083 | 509 | 42.6 | 2.9 | 633 | 8 | AF085344 | AF085344 Pythium s |
| C 437 | 43.2 | 2.9 | 1123 | 5 | AF081672 | 510 | 42.6 | 2.9 | 13513 | 1 | AY423269 | AY423269 Chicken c |
| C 438 | 43.2 | 2.9 | 2908 | 8 | MZESUS1A | 511 | 42.6 | 2.9 | 62074 | 2 | AC101270 | AC101270 Streptomy |
| C 439 | 43.2 | 2.9 | 7341 | 8 | MZESUS1C | 512 | 42.6 | 2.9 | 80682 | 10 | AL953839 | AL953839 Mouse DNA |
| C 440 | 43.2 | 2.9 | 8648 | 8 | MZESUS1C | 513 | 42.6 | 2.9 | 80682 | 2 | AC151715 | AC151715 |
| C 441 | 43.2 | 2.9 | 75021 | 2 | AC040889 | 514 | 42.4 | 2.9 | 114337 | 10 | AC122019 | AC122019 Mus muscu |
| C 442 | 43.2 | 2.9 | 96360 | 10 | BX294441 | 515 | 42.4 | 2.9 | 132761 | 10 | AL772225 | AL772225 Mouse DNA |
| C 443 | 43.2 | 2.9 | 121869 | 10 | AL831739 | 516 | 42.4 | 2.9 | 133621 | 10 | AC135858 | AC135858 Mus muscu |
| C 444 | 43.2 | 2.9 | 157092 | 10 | AL805911 | 517 | 42.4 | 2.9 | 142903 | 10 | AC117253 | AC117253 Mus muscu |
| C 445 | 43.2 | 2.9 | 195294 | 10 | AC132248 | 518 | 42.4 | 2.9 | 145150 | 2 | AC119980 | AC119980 Mus muscu |
| C 446 | 43.2 | 2.9 | 197310 | 10 | AC099754 | 519 | 42.4 | 2.9 | 153994 | 10 | AC136081 | AC136081 Mus muscu |
| C 447 | 43.2 | 2.9 | 198320 | 10 | AL669814 | 520 | 42.4 | 2.9 | 155130 | 2 | AC147779 | AC147779 Mus muscu |
| C 448 | 43.2 | 2.9 | 238830 | 2 | AC102034 | 521 | 42.4 | 2.9 | 161408 | 5 | BX511269 | BX511269 Zebrafish |
| C 449 | 43.2 | 2.9 | 238908 | 2 | AC131583 | 522 | 42.4 | 2.9 | 184279 | 10 | AC140393 | AC140393 Mus muscu |
| C 450 | 43.2 | 2.9 | 262547 | 2 | AC123996 | 523 | 42.4 | 2.9 | | | | |
| C 451 | 43.2 | 2.9 | 266820 | 10 | AF312033 | 524 | 42.4 | 2.9 | | | | |
| C 452 | 43 | 2.9 | 5116 | 10 | MMU66858 | 525 | 42.4 | 2.9 | | | | |
| C 453 | 43 | 2.9 | 603772 | 2 | AC110005 | 526 | 42.4 | 2.9 | | | | |
| C 454 | 43 | 2.9 | 142133 | 2 | AC135014 | 527 | 42.4 | 2.9 | | | | |
| C 455 | 43 | 2.9 | 143681 | 9 | AC115934 | 528 | 42.4 | 2.9 | | | | |
| C 456 | 43 | 2.9 | 160269 | 9 | AC024230 | 529 | 42.4 | 2.9 | | | | |
| C 457 | 43 | 2.9 | 169004 | 2 | AC121682 | 530 | 42.4 | 2.9 | | | | |

| | | | | | | | | | | | | | |
|-----|------|-----|--------|----|-----------|----------------------------|-----|------|-----|--------|----|-----------|----------------------------|
| 531 | 42.4 | 2.9 | 187432 | 10 | AC117750 | AC117750 Mus muscu | 604 | 41.8 | 2.8 | 1505 | 8 | AB041712 | AB041712 Chara cor |
| 532 | 42.4 | 2.9 | 190734 | 10 | AC117784 | AC117784 Mus muscu | 605 | 41.8 | 2.8 | 1862 | 3 | AB044286 | AB044286 Chara cor |
| 533 | 42.4 | 2.9 | 191863 | 9 | AC010888 | AC010888 Homo sapi | 606 | 41.8 | 2.8 | 2359 | 3 | AF406767 | AF406767 Leishmani |
| 534 | 42.4 | 2.9 | 195273 | 10 | AC113548 | AC113548 Mus muscu | 607 | 41.8 | 2.8 | 2537 | 9 | AK094964 | AK094964 Homo sapi |
| 535 | 42.4 | 2.9 | 196468 | 10 | AC111065 | AC111065 Mus muscu | 608 | 41.8 | 2.8 | 74530 | 9 | AL606517 | AL606517 Human DNA |
| 536 | 42.4 | 2.9 | 201248 | 2 | AC116494 | AC116494 Mus muscu | 609 | 41.8 | 2.8 | 87684 | 4 | AY152828 | AY152828 Felis cat |
| 537 | 42.4 | 2.9 | 206352 | 2 | AC113923 | AC113923 Mus muscu | 610 | 41.8 | 2.8 | 105208 | 10 | AL671897 | AL671897 Mouse DNA |
| 538 | 42.4 | 2.9 | 220472 | 2 | AC147511 | AC147511 Mus muscu | 611 | 41.8 | 2.8 | 145837 | 10 | AL732527 | AL732527 Mouse DNA |
| 539 | 42.4 | 2.9 | 230629 | 2 | AC127332 | AC127332 Mus muscu | 612 | 41.8 | 2.8 | 154872 | 10 | AC122412 | AC122412 Mouse DNA |
| 540 | 42.2 | 2.8 | 779 | 8 | TAU48689 | TAU48689 Triticum ae | 613 | 41.8 | 2.8 | 165229 | 10 | AC109302 | AC109302 Mus muscu |
| 541 | 42.2 | 2.8 | 118080 | 2 | AL844550 | AL844550 Mouse DNA | 614 | 41.8 | 2.8 | 165229 | 10 | AC109302 | AC109302 Mus muscu |
| 542 | 42.2 | 2.8 | 140917 | 10 | AL929380 | AL929380 Mouse DNA | 615 | 41.8 | 2.8 | 169150 | 10 | AL732519 | AL732519 Mouse DNA |
| 543 | 42.2 | 2.8 | 157264 | 10 | AC132914 | AC132914 Mus muscu | 616 | 41.8 | 2.8 | 178754 | 2 | AC139446 | AC139446 Rattus no |
| 544 | 42.2 | 2.8 | 158321 | 8 | AP003626 | AP003626 Oryza sat | 617 | 41.8 | 2.8 | 183795 | 2 | AC116481 | AC116481 Mus muscu |
| 545 | 42.2 | 2.8 | 162556 | 10 | AL672228 | AL672228 Mouse DNA | 618 | 41.8 | 2.8 | 190390 | 10 | AC134400 | AC134400 Mus muscu |
| 546 | 42.2 | 2.8 | 163138 | 2 | AC135081 | AC135081 Mus muscu | 619 | 41.8 | 2.8 | 190996 | 2 | AC138084 | AC138084 Mus muscu |
| 547 | 42.2 | 2.8 | 163568 | 8 | AP003711 | AP003711 Oryza sat | 620 | 41.8 | 2.8 | 203794 | 2 | AC140930 | AC140930 Mus muscu |
| 548 | 42.2 | 2.8 | 174124 | 2 | AC102872 | AC102872 Mus muscu | 621 | 41.8 | 2.8 | 204165 | 10 | AC124717 | AC124717 Mus muscu |
| 549 | 42.2 | 2.8 | 181412 | 2 | AC120001 | AC120001 Mus muscu | 622 | 41.8 | 2.8 | 205030 | 9 | AL669911 | AL669911 Mouse DNA |
| 550 | 42.2 | 2.8 | 184677 | 10 | AC140257 | AC140257 Mus muscu | 623 | 41.8 | 2.8 | 206482 | 9 | AC091230 | AC091230 Homo sapi |
| 551 | 42.2 | 2.8 | 195978 | 10 | AC111099 | AC111099 Mus muscu | 624 | 41.8 | 2.8 | 211034 | 10 | AL731709 | AL731709 Mouse DNA |
| 552 | 42.2 | 2.8 | 202305 | 9 | AC114291 | AC114291 Homo sapi | 625 | 41.8 | 2.8 | 212365 | 2 | AC013350 | AC013350 Mus muscu |
| 553 | 42.2 | 2.8 | 213348 | 10 | AC098883 | AC098883 Mus muscu | 626 | 41.8 | 2.8 | 218817 | 2 | AC114704 | AC114704 Rattus no |
| 554 | 42.2 | 2.8 | 213848 | 2 | AC139346 | AC139346 Mus muscu | 627 | 41.8 | 2.8 | 221339 | 2 | AL604045 | AL604045 Mouse DNA |
| 555 | 42.2 | 2.8 | 227182 | 2 | AC112692 | AC112692 Mus muscu | 628 | 41.8 | 2.8 | 221642 | 10 | AC115978 | AC115978 Mus muscu |
| 556 | 42.2 | 2.8 | 232460 | 2 | AC103188 | AC103188 Rattus no | 629 | 41.8 | 2.8 | 236031 | 2 | AC105606 | AC105606 Rattus no |
| 557 | 42.2 | 2.8 | 243763 | 2 | AC126724 | AC126724 Rattus no | 630 | 41.8 | 2.8 | 238341 | 2 | AL773599 | AL773599 Mus muscu |
| 558 | 42.2 | 2.8 | 246940 | 2 | AC106561 | AC106561 Rattus no | 631 | 41.8 | 2.8 | 242619 | 2 | AC115464 | AC115464 Rattus no |
| 559 | 42.2 | 2.8 | 272459 | 2 | AC109059 | AC109059 Rattus no | 632 | 41.8 | 2.8 | 247196 | 2 | AC073822 | AC073822 Mus muscu |
| 560 | 42 | 2.8 | 556 | 11 | AF096544 | AF096544 Rattus no | 633 | 41.8 | 2.8 | 251966 | 2 | AC095883 | AC095883 Rattus no |
| 561 | 42 | 2.8 | 1110 | 9 | AF490905 | AF490905 Homo sapi | 634 | 41.8 | 2.8 | 255347 | 2 | AC112116 | AC112116 Rattus no |
| 562 | 42 | 2.8 | 7505 | 10 | AL645746 | AL645746 Mouse DNA | 635 | 41.8 | 2.8 | 255447 | 2 | AC096032 | AC096032 Rattus no |
| 563 | 42 | 2.8 | 1110 | 9 | AY566229 | AY566229 Homo sapi | 636 | 41.8 | 2.8 | 270435 | 2 | AC096252 | AC096252 Rattus no |
| 564 | 42 | 2.8 | 110000 | 2 | AC110363 | AC110363 Confimation (4 of | 637 | 41.8 | 2.8 | 309266 | 2 | AC106972 | AC106972 Rattus no |
| 565 | 42 | 2.8 | 110000 | 2 | AC113532 | AC113532 Confimation (2 of | 638 | 41.6 | 2.8 | 568 | 11 | H0075050 | H0075050 Human STS U |
| 566 | 42 | 2.8 | 110000 | 2 | AP006493 | AP006493 Confimation (6 of | 639 | 41.6 | 2.8 | 581 | 11 | BV048811 | BV048811 S212P6010 |
| 567 | 42 | 2.8 | 120868 | 2 | AC139379 | AC139379 Mus muscu | 640 | 41.6 | 2.8 | 748 | 8 | AB050839 | AB050839 Nicotiana |
| 568 | 42 | 2.8 | 136064 | 10 | AL928992 | AL928992 Mouse DNA | 641 | 41.6 | 2.8 | 807 | 2 | SC0318521 | SC0318521 Solanum c |
| 569 | 42 | 2.8 | 142565 | 10 | AL592545 | AL592545 Mouse DNA | 642 | 41.6 | 2.8 | 98392 | 8 | AL590620 | AL590620 Homo sapi |
| 570 | 42 | 2.8 | 153994 | 2 | AC136914 | AC136914 Mus muscu | 643 | 41.6 | 2.8 | 110000 | 2 | AC107636 | AC107636 Confimation (2 of |
| 571 | 42 | 2.8 | 155366 | 10 | AC102012 | AC102012 Mus muscu | 644 | 41.6 | 2.8 | 114007 | 9 | HS01185K9 | HS01185K9 Human DNA |
| 572 | 42 | 2.8 | 162282 | 2 | AC132879 | AC132879 Mus muscu | 645 | 41.6 | 2.8 | 152316 | 10 | AC007844 | AC007844 Mus muscu |
| 573 | 42 | 2.8 | 182672 | 10 | AC131332 | AC131332 Homo sapi | 646 | 41.6 | 2.8 | 157101 | 2 | AC102892 | AC102892 Mus muscu |
| 574 | 42 | 2.8 | 183179 | 2 | AL133212 | AL133212 Homo sapi | 647 | 41.6 | 2.8 | 157273 | 10 | BX293558 | BX293558 Mouse DNA |
| 575 | 42 | 2.8 | 183414 | 8 | CNS0809CF | AL732640 Oryza sat | 648 | 41.6 | 2.8 | 164277 | 10 | AL840625 | AL840625 Mouse DNA |
| 576 | 42 | 2.8 | 184037 | 10 | AC147369 | AC147369 Mus muscu | 649 | 41.6 | 2.8 | 170221 | 10 | AC127421 | AC127421 Mus muscu |
| 577 | 42 | 2.8 | 186486 | 10 | AC132459 | AC132459 Mus muscu | 650 | 41.6 | 2.8 | 171110 | 2 | AC119699 | AC119699 Rattus no |
| 578 | 42 | 2.8 | 186505 | 10 | AL772150 | AL772150 Mouse DNA | 651 | 41.6 | 2.8 | 172980 | 10 | AC126671 | AC126671 Mus muscu |
| 579 | 42 | 2.8 | 190119 | 10 | AC124441 | AC124441 Mus muscu | 652 | 41.6 | 2.8 | 173146 | 2 | AC112522 | AC112522 Mus muscu |
| 580 | 42 | 2.8 | 191301 | 2 | AC127820 | AC127820 Rattus no | 653 | 41.6 | 2.8 | 173643 | 10 | AC122782 | AC122782 Mus muscu |
| 581 | 42 | 2.8 | 191669 | 10 | AC118020 | AC118020 Mus muscu | 654 | 41.6 | 2.8 | 178135 | 2 | AC101738 | AC101738 Mus muscu |
| 582 | 42 | 2.8 | 191692 | 2 | AC022383 | AC022383 Mus muscu | 655 | 41.6 | 2.8 | 179481 | 2 | AC034100 | AC034100 Mus muscu |
| 583 | 42 | 2.8 | 199341 | 2 | AC113903 | AC113903 Rattus no | 656 | 41.6 | 2.8 | 187523 | 2 | AC102882 | AC102882 Mus muscu |
| 584 | 42 | 2.8 | 211743 | 2 | AC136147 | AC136147 Mus muscu | 657 | 41.6 | 2.8 | 188463 | 2 | AC101787 | AC101787 Mus muscu |
| 585 | 42 | 2.8 | 213462 | 2 | AC119365 | AC119365 Rattus no | 658 | 41.6 | 2.8 | 190519 | 2 | AC119186 | AC119186 Mus muscu |
| 586 | 42 | 2.8 | 217397 | 10 | AC123705 | AC123705 Mus muscu | 659 | 41.6 | 2.8 | 190679 | 2 | AC147747 | AC147747 Homo sapi |
| 587 | 42 | 2.8 | 219293 | 2 | AC141471 | AC141471 Mus muscu | 660 | 41.6 | 2.8 | 192561 | 10 | AL805943 | AL805943 Mouse DNA |
| 588 | 42 | 2.8 | 219393 | 2 | AC134216 | AC134216 Rattus no | 661 | 41.6 | 2.8 | 196274 | 2 | AC106841 | AC106841 Mus muscu |
| 589 | 42 | 2.8 | 226724 | 10 | AC125199 | AC125199 Mus muscu | 662 | 41.6 | 2.8 | 201114 | 10 | AL808132 | AL808132 Mouse DNA |
| 590 | 42 | 2.8 | 235956 | 2 | AC098638 | AC098638 Rattus no | 663 | 41.6 | 2.8 | 207182 | 2 | AC115795 | AC115795 Mus muscu |
| 591 | 42 | 2.8 | 247575 | 2 | AC133047 | AC133047 Rattus no | 664 | 41.6 | 2.8 | 210257 | 2 | AC135865 | AC135865 Rattus no |
| 592 | 42 | 2.8 | 248124 | 2 | AC096607 | AC096607 Rattus no | 665 | 41.6 | 2.8 | 21657 | 9 | AC123605 | AC123605 Mus muscu |
| 593 | 42 | 2.8 | 248132 | 2 | AC096927 | AC096927 Rattus no | 666 | 41.6 | 2.8 | 214702 | 9 | AC020689 | AC020689 Homo sapi |
| 594 | 42 | 2.8 | 255446 | 2 | AC095420 | AC095420 Rattus no | 667 | 41.6 | 2.8 | 216959 | 10 | AC116998 | AC116998 Homo sapi |
| 595 | 42 | 2.8 | 256476 | 10 | AC126940 | AC126940 Mus muscu | 668 | 41.6 | 2.8 | 231485 | 2 | AC098427 | AC098427 Mus muscu |
| 596 | 42 | 2.8 | 258798 | 2 | AC097761 | AC097761 Rattus no | 669 | 41.6 | 2.8 | 239114 | 2 | AC129936 | AC129936 Mus muscu |
| 597 | 42 | 2.8 | 325566 | 2 | AC125718 | AC125718 Rattus no | 670 | 41.6 | 2.8 | 239924 | 2 | AC111266 | AC111266 Rattus no |
| 598 | 42 | 2.8 | 325656 | 2 | AC120265 | AC120265 Rattus no | 671 | 41.6 | 2.8 | 264155 | 2 | AC099434 | AC099434 Rattus no |
| 599 | 41.8 | 2.8 | 580 | 5 | AF469957 | AF469957 Oncomyrnc | 672 | 41.6 | 2.8 | 271418 | 2 | AC113678 | AC113678 Rattus no |
| 600 | 41.8 | 2.8 | 1361 | 6 | C0858785 | C0858785 Sequence | 673 | 41.6 | 2.8 | 318435 | 2 | AC118697 | AC118697 Mus muscu |
| 601 | 41.8 | 2.8 | 1361 | 6 | AX305360 | AX305360 Sequence | 674 | 41.6 | 2.8 | 348953 | 2 | AC094554 | AC094554 Rattus no |
| 602 | 41.8 | 2.8 | 1361 | 10 | MMCALMOD | X61432 M.musculus | 675 | 41.4 | 2.8 | 468 | 6 | C0721078 | C0721078 Sequence |
| 603 | 41.8 | 2.8 | 1430 | 8 | AB041711 | AB041711 Chara cor | 676 | 41.4 | 2.8 | 627 | 11 | H0072290 | H0072290 Human STS U |

| | | | | | | | | | | | | | |
|-------|------|-----|--------|----|-------------|----------------------|-------|------|-----|--------|----|------------|----------------------|
| 677 | 41.4 | 2.8 | 2452 | 3 | TRBMRSG | K02944 Trypanosoma | 750 | 41.2 | 2.8 | 194401 | 2 | AC139951 | AC139951 Rattus no |
| C 678 | 41.4 | 2.8 | 42053 | 10 | CR626863 | CR626863 Mouse DNA | 751 | 41.2 | 2.8 | 197700 | 2 | AC102812 | AC102812 Mus muscu |
| C 679 | 41.4 | 2.8 | 54708 | 2 | AC132804 | AC132804 Homo sapi | C 752 | 41.2 | 2.8 | 197934 | 2 | AC117676 | AC117676 Mus muscu |
| C 680 | 41.4 | 2.8 | 68951 | 2 | AC100065 | AC100065 Mus muscu | C 753 | 41.2 | 2.8 | 200746 | 10 | AC117232 | AC117232 Mus muscu |
| C 681 | 41.4 | 2.8 | 99670 | 8 | AC123709 | AC123709 Mus muscu | C 754 | 41.2 | 2.8 | 204037 | 10 | AL566207 | AL566207 Mouse DNA |
| C 682 | 41.4 | 2.8 | 110000 | 10 | CR382133_11 | Continuation (12 o | C 755 | 41.2 | 2.8 | 205819 | 10 | AC115954 | AC115954 Mus muscu |
| C 683 | 41.4 | 2.8 | 132889 | 9 | AC007972 | AC007972 Homo sapi | C 756 | 41.2 | 2.8 | 205924 | 2 | AC138143 | AC138143 Mus muscu |
| C 684 | 41.4 | 2.8 | 138780 | 2 | AL356293 | AL356293 Homo sapi | C 757 | 41.2 | 2.8 | 206739 | 2 | AC113846 | AC113846 Rattus no |
| C 685 | 41.4 | 2.8 | 136268 | 10 | AC068496 | AC068496 Mus muscu | C 758 | 41.2 | 2.8 | 216347 | 10 | AL831741 | AL831741 Mouse DNA |
| C 686 | 41.4 | 2.8 | 139891 | 2 | AC090647 | AC090647 Genomic B | C 759 | 41.2 | 2.8 | 216323 | 2 | AC119507 | AC119507 Rattus no |
| C 687 | 41.4 | 2.8 | 140098 | 2 | AC024510 | AC024510 Homo sapi | C 760 | 41.2 | 2.8 | 217223 | 2 | AC093472 | AC093472 Mus muscu |
| C 688 | 41.4 | 2.8 | 142204 | 10 | EX927383 | EX927383 Mus muscu | C 761 | 41.2 | 2.8 | 218226 | 2 | AC126634 | AC126634 Rattus no |
| C 689 | 41.4 | 2.8 | 150645 | 10 | AC131774 | AC131774 Mus muscu | C 762 | 41.2 | 2.8 | 221782 | 2 | AC115156 | AC115156 Rattus no |
| C 690 | 41.4 | 2.8 | 168683 | 2 | AC147262 | AC147262 Mus muscu | C 763 | 41.2 | 2.8 | 222259 | 2 | AC110858 | AC110858 Rattus no |
| C 691 | 41.4 | 2.8 | 168683 | 2 | AC112923 | AC112923 Mus muscu | C 764 | 41.2 | 2.8 | 226637 | 2 | AC124813 | AC124813 Mus muscu |
| C 692 | 41.4 | 2.8 | 171820 | 10 | AC128550 | AC128550 Mus muscu | C 765 | 41.2 | 2.8 | 227759 | 2 | AC107446 | AC107446 Rattus no |
| C 693 | 41.4 | 2.8 | 183378 | 2 | AL607151 | AL607151 Mus muscu | C 766 | 41.2 | 2.8 | 232070 | 10 | AL808103 | AL808103 Mouse DNA |
| C 694 | 41.4 | 2.8 | 183518 | 10 | AC097366 | AC097366 Genomic B | C 767 | 41.2 | 2.8 | 233804 | 10 | AC130831 | AC130831 Mus muscu |
| C 695 | 41.4 | 2.8 | 184383 | 2 | AC099632 | AC099632 Mus muscu | C 768 | 41.2 | 2.8 | 234633 | 2 | AC111768 | AC111768 Rattus no |
| C 696 | 41.4 | 2.8 | 189115 | 2 | AC117766 | AC117766 Mus muscu | C 769 | 41.2 | 2.8 | 242744 | 2 | AC110204 | AC110204 Mus muscu |
| C 697 | 41.4 | 2.8 | 189115 | 10 | AL1772346 | AL1772346 Mouse DNA | C 770 | 41.2 | 2.8 | 245937 | 2 | AC133984 | AC133984 Rattus no |
| C 698 | 41.4 | 2.8 | 191132 | 2 | AC126895 | AC126895 Rattus no | C 771 | 41.2 | 2.8 | 247187 | 2 | AC094928 | AC094928 Rattus no |
| C 699 | 41.4 | 2.8 | 191132 | 2 | AC126895 | AC126895 Rattus no | C 772 | 41.2 | 2.8 | 248294 | 2 | AC097690 | AC097690 Rattus no |
| C 700 | 41.4 | 2.8 | 207763 | 10 | AC121279 | AC121279 Mus muscu | C 773 | 41.2 | 2.8 | 249086 | 2 | AC131856 | AC131856 Rattus no |
| C 701 | 41.4 | 2.8 | 209227 | 2 | AC140380 | AC140380 Mus muscu | C 774 | 41.2 | 2.8 | 251158 | 2 | AC117023 | AC117023 Rattus no |
| C 702 | 41.4 | 2.8 | 212472 | 2 | AC121077 | AC121077 Mus muscu | C 775 | 41.2 | 2.8 | 251173 | 2 | AC095202 | AC095202 Rattus no |
| C 703 | 41.4 | 2.8 | 212472 | 10 | AC1256029 | AC1256029 Mus muscu | C 776 | 41.2 | 2.8 | 256597 | 2 | AC109662 | AC109662 Rattus no |
| C 704 | 41.4 | 2.8 | 213482 | 10 | AC073883 | AC073883 Mus muscu | C 777 | 41.2 | 2.8 | 256687 | 2 | AC092362 | AC092362 Homo sapi |
| C 705 | 41.4 | 2.8 | 215228 | 2 | AC099586 | AC099586 Mus muscu | C 778 | 41.2 | 2.8 | 262608 | 2 | AC1092362 | AC1092362 Rattus no |
| C 706 | 41.4 | 2.8 | 220758 | 10 | AC117200 | AC117200 Mus muscu | C 779 | 41.2 | 2.8 | 271135 | 2 | AC105492 | AC105492 Rattus no |
| C 707 | 41.4 | 2.8 | 224056 | 2 | AC112832 | AC112832 Mus muscu | C 780 | 41.2 | 2.8 | 272030 | 2 | AC105482 | AC105482 Rattus no |
| C 708 | 41.4 | 2.8 | 225880 | 2 | AC131693 | AC131693 Mus muscu | C 781 | 41.2 | 2.8 | 291544 | 2 | AC128496 | AC128496 Rattus no |
| C 709 | 41.4 | 2.8 | 239423 | 2 | AC129279 | AC129279 Rattus no | C 782 | 41.2 | 2.8 | 297149 | 2 | AC097944 | AC097944 Rattus no |
| C 710 | 41.4 | 2.8 | 239423 | 2 | AC096602 | AC096602 Rattus no | C 783 | 41.2 | 2.8 | 309050 | 1 | SC0939117 | SC0939117 Streptomy |
| C 711 | 41.4 | 2.8 | 244529 | 2 | AC121112 | AC121112 Mus muscu | C 784 | 41.2 | 2.8 | 309050 | 1 | SSU90351 | SSU90351 Strongyloid |
| C 712 | 41.4 | 2.8 | 248760 | 2 | AC137456 | AC137456 Rattus no | C 785 | 41.2 | 2.8 | 749 | 8 | BT000036 | BT000036 Arabidops |
| C 713 | 41.4 | 2.8 | 253319 | 2 | AC094876 | AC094876 Rattus no | C 786 | 41.2 | 2.8 | 975 | 6 | AX507498 | AX507498 Sequence |
| C 714 | 41.4 | 2.8 | 254578 | 2 | AC109253 | AC109253 Mus muscu | C 787 | 41.2 | 2.8 | 975 | 6 | AX589929 | AX589929 Sequence |
| C 715 | 41.4 | 2.8 | 255871 | 2 | AC095418 | AC095418 Rattus no | C 788 | 41.2 | 2.8 | 975 | 6 | AX651961 | AX651961 Sequence |
| C 716 | 41.4 | 2.8 | 255871 | 2 | AC095418 | AC095418 Rattus no | C 789 | 41.2 | 2.8 | 1152 | 8 | AF424577 | AF424577 Arabidops |
| C 717 | 41.4 | 2.8 | 255946 | 2 | AC115114 | AC115114 Rattus no | C 790 | 41.2 | 2.8 | 1183 | 8 | AY120719 | AY120719 Arabidops |
| C 718 | 41.4 | 2.8 | 262917 | 2 | AC097239 | AC097239 Rattus no | C 791 | 41.2 | 2.8 | 1260 | 14 | PV1319028 | PV1319028 Suid heip |
| C 719 | 41.4 | 2.8 | 266099 | 2 | AC094795 | AC094795 Rattus no | C 792 | 41.2 | 2.8 | 51743 | 2 | AC100147 | AC100147 Pseudorab |
| C 720 | 41.4 | 2.8 | 284127 | 2 | AC128719 | AC128719 Rattus no | C 793 | 41.2 | 2.8 | 78291 | 2 | AC023216 | AC023216 Homo sapi |
| C 721 | 41.4 | 2.8 | 285425 | 2 | AC131435 | AC131435 Rattus no | C 794 | 41.2 | 2.8 | 110000 | 2 | AC151831_0 | AC151831 Mus muscu |
| C 722 | 41.2 | 2.8 | 447 | 6 | AX660884 | AX660884 Sequence | C 795 | 41.2 | 2.8 | 129663 | 2 | AC027081 | AC027081 Homo sapi |
| C 723 | 41.2 | 2.8 | 450 | 3 | BLRNC | Y09880 B. lanceolat | C 796 | 41.2 | 2.8 | 132457 | 2 | AC102180 | AC102180 Mus muscu |
| C 724 | 41.2 | 2.8 | 480 | 8 | AF031482 | AF031482 Zea mays | C 797 | 41.2 | 2.8 | 134805 | 10 | AC099998 | AC099998 Mus muscu |
| C 725 | 41.2 | 2.8 | 616 | 3 | LTCAMA | X80231 L. tarentolia | C 798 | 41.2 | 2.8 | 135697 | 10 | AC133934 | AC133934 Mus muscu |
| C 726 | 41.2 | 2.8 | 819 | 8 | PPCAMPROT | X90560 Physcomitre | C 799 | 41.2 | 2.8 | 136809 | 10 | AL683892 | AL683892 Mouse DNA |
| C 727 | 41.2 | 2.8 | 942 | 8 | ZMCAM1 | X77396 Z. mays Cam1 | C 800 | 41.2 | 2.8 | 149871 | 10 | AL928991 | AL928991 Mouse DNA |
| C 728 | 41.2 | 2.8 | 1353 | 3 | AB003081 | AB003081 Branchios | C 801 | 41.2 | 2.8 | 166977 | 9 | AC007198 | AC007198 Homo sapi |
| C 729 | 41.2 | 2.8 | 1375 | 3 | AB003082 | AB003082 Branchios | C 802 | 41.2 | 2.8 | 168794 | 10 | AC134569 | AC134569 Mus muscu |
| C 730 | 41.2 | 2.8 | 1405 | 3 | BF9NAC | Y09863 B. floridiae | C 803 | 41.2 | 2.8 | 169687 | 9 | AC103871 | AC103871 Homo sapi |
| C 731 | 41.2 | 2.8 | 42262 | 5 | AL662837 | AL662837 Human DNA | C 804 | 41.2 | 2.8 | 174533 | 2 | AC073718 | AC073718 Mus muscu |
| C 732 | 41.2 | 2.8 | 113421 | 5 | BX284637 | BX284637 Zebrafish | C 805 | 41.2 | 2.8 | 181088 | 2 | AC102356 | AC102356 Mus muscu |
| C 733 | 41.2 | 2.8 | 149407 | 10 | AL671984 | AL671984 Mouse DNA | C 806 | 41.2 | 2.8 | 181467 | 10 | AL844586 | AL844586 Mouse DNA |
| C 734 | 41.2 | 2.8 | 149407 | 10 | AL671984 | AL671984 Mouse DNA | C 807 | 41.2 | 2.8 | 187930 | 2 | AC127565 | AC127565 Mus muscu |
| C 735 | 41.2 | 2.8 | 150222 | 10 | AL645319 | AL645319 Mouse DNA | C 808 | 41.2 | 2.8 | 191020 | 2 | AC090758 | AC090758 Homo sapi |
| C 736 | 41.2 | 2.8 | 152462 | 10 | AC131998 | AC131998 Mus muscu | C 809 | 41.2 | 2.8 | 193105 | 10 | AC107236 | AC107236 Mus muscu |
| C 737 | 41.2 | 2.8 | 159330 | 10 | AC118047 | AC118047 Mus muscu | C 810 | 41.2 | 2.8 | 195294 | 2 | AC051623 | AC051623 Mus muscu |
| C 738 | 41.2 | 2.8 | 163309 | 2 | AC132361 | AC132361 Mus muscu | C 811 | 41.2 | 2.8 | 196557 | 10 | AC131742 | AC131742 Mus muscu |
| C 739 | 41.2 | 2.8 | 163379 | 10 | AC140394 | AC140394 Mus muscu | C 812 | 41.2 | 2.8 | 197909 | 2 | AL928879 | AL928879 Mouse DNA |
| C 740 | 41.2 | 2.8 | 164223 | 2 | AC127176 | AC127176 Rattus no | C 813 | 41.2 | 2.8 | 200824 | 2 | AC015725 | AC015725 Mus muscu |
| C 741 | 41.2 | 2.8 | 164885 | 2 | AC132365 | AC132365 Mus muscu | C 814 | 41.2 | 2.8 | 201267 | 10 | AC073786 | AC073786 Mus muscu |
| C 742 | 41.2 | 2.8 | 168786 | 9 | AC104864 | AC104864 Homo sapi | C 815 | 41.2 | 2.8 | 202804 | 10 | AC021630 | AC021630 Mus muscu |
| C 743 | 41.2 | 2.8 | 172837 | 9 | AL450304 | AL450304 Human DNA | C 816 | 41.2 | 2.8 | 202807 | 10 | AC021063 | AC021063 Mus muscu |
| C 744 | 41.2 | 2.8 | 179333 | 2 | AC117658 | AC117658 Mus muscu | C 817 | 41.2 | 2.8 | 204935 | 2 | AC123793 | AC123793 Mus muscu |
| C 745 | 41.2 | 2.8 | 182061 | 10 | AC107869 | AC107869 Mus muscu | C 818 | 41.2 | 2.8 | 207949 | 2 | AC131720 | AC131720 Mus muscu |
| C 746 | 41.2 | 2.8 | 187977 | 10 | AL672229 | AL672229 Mouse DNA | C 819 | 41.2 | 2.8 | 208738 | 10 | AC130528 | AC130528 Mus muscu |
| C 747 | 41.2 | 2.8 | 188255 | 2 | AC124990 | AC124990 Mus muscu | C 820 | 41.2 | 2.8 | 208738 | 10 | AC130528 | AC130528 Mus muscu |
| C 748 | 41.2 | 2.8 | 188853 | 10 | AC102105 | AC102105 Mus muscu | C 821 | 41.2 | 2.8 | 208738 | 10 | AC130528 | AC130528 Mus muscu |
| C 749 | 41.2 | 2.8 | 191721 | 10 | AC101883 | AC101883 Mus muscu | C 822 | 41.2 | 2.8 | 208738 | 10 | AC130528 | AC130528 Mus muscu |

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|-----|------|-----|--------|----|-----------|---------------------|-----|------|-----|--------|----|-----------|----------------------|
| 823 | 41 | 2.8 | 209523 | 10 | AC084386 | AC084386 Mus muscu | 896 | 40.8 | 2.7 | 234448 | 10 | AC122202 | AC122202 Mus muscu |
| 824 | 41 | 2.8 | 210688 | 10 | AC127371 | AC127371 Mus muscu | 897 | 40.8 | 2.7 | 235509 | 10 | AC091523 | AC091523 Mus muscu |
| 825 | 41 | 2.8 | 216860 | 10 | AC134793 | AC134793 Mus muscu | 898 | 40.8 | 2.7 | 244042 | 2 | AC103004 | AC103004 Rattus no |
| 826 | 41 | 2.8 | 218815 | 10 | AL807384 | AL807384 Mouse DNA | 899 | 40.8 | 2.7 | 244759 | 2 | AC098158 | AC098158 Rattus no |
| 827 | 41 | 2.8 | 225196 | 2 | AC138621 | AC138621 Mus muscu | 900 | 40.8 | 2.7 | 246557 | 2 | AC106539 | AC106539 Rattus no |
| 828 | 41 | 2.8 | 228400 | 10 | AC131711 | AC131711 Mus muscu | 901 | 40.8 | 2.7 | 251814 | 10 | AL591882 | AL591882 Mouse DNA |
| 829 | 41 | 2.8 | 229494 | 10 | AL627328 | AL627328 Mouse DNA | 902 | 40.8 | 2.7 | 252645 | 2 | AC130522 | AC130522 Rattus no |
| 830 | 41 | 2.8 | 235915 | 10 | AC129606 | AC129606 Mus muscu | 903 | 40.8 | 2.7 | 253645 | 2 | AC137382 | AC137382 Rattus no |
| 831 | 41 | 2.8 | 240534 | 2 | AC102528 | AC102528 Mus muscu | 904 | 40.8 | 2.7 | 253945 | 2 | AC119776 | AC119776 Rattus no |
| 832 | 41 | 2.8 | 251814 | 10 | AL591882 | AL591882 Mouse DNA | 905 | 40.8 | 2.7 | 258088 | 2 | AC073766 | AC073766 Mus muscu |
| 833 | 41 | 2.8 | 272588 | 2 | AC109673 | AC109673 Rattus no | 906 | 40.8 | 2.7 | 259834 | 2 | AC128503 | AC128503 Rattus no |
| 834 | 41 | 2.8 | 278111 | 2 | AC148992 | AC148992 Mus muscu | 907 | 40.8 | 2.7 | 264127 | 2 | AC102974 | AC102974 Rattus no |
| 835 | 41 | 2.8 | 286588 | 2 | AC106454 | AC106454 Rattus no | 908 | 40.8 | 2.7 | 268510 | 2 | AC095840 | AC095840 Rattus no |
| 836 | 41 | 2.8 | 289531 | 2 | AC113695 | AC113695 Rattus no | 909 | 40.8 | 2.7 | 272147 | 2 | AC095648 | AC095648 Rattus no |
| 837 | 41 | 2.8 | 300574 | 2 | AC097618 | AC097618 Rattus no | 910 | 40.6 | 2.7 | 447 | 6 | EO2314 | EO2314 DNA encodin |
| 838 | 41 | 2.8 | 314521 | 2 | AC126972 | AC126972 Rattus no | 911 | 40.6 | 2.7 | 796 | 8 | TAU4668 | TAU4668 Triticum ae |
| 839 | 40.8 | 2.7 | 7405 | 8 | BP0ALMGEN | X89890 B.pilosa mr | 912 | 40.6 | 2.7 | 816 | 8 | TAU48242 | TAU48242 Triticum ae |
| 840 | 40.8 | 2.7 | 7608 | 8 | AK062496 | AK062496 Oryza sat | 913 | 40.6 | 2.7 | 1358 | 8 | PHTCALPIA | MB3535 P.infestans |
| 841 | 40.8 | 2.7 | 1090 | 5 | BC041530 | BC041530 Xenopus l | 914 | 40.6 | 2.7 | 1362 | 12 | AB178711 | AB178711 Synthetic |
| 842 | 40.8 | 2.7 | 1378 | 5 | AY235104 | AY235104 Meleagris | 915 | 40.6 | 2.7 | 1962 | 12 | AB178712 | AB178712 Synthetic |
| 843 | 40.8 | 2.7 | 42204 | 2 | AC099977 | AC099977 Mus muscu | 916 | 40.6 | 2.7 | 1962 | 12 | AB178713 | AB178713 Synthetic |
| 844 | 40.8 | 2.7 | 54536 | 8 | AH151534 | AH151534 Antitritin | 917 | 40.6 | 2.7 | 2076 | 12 | AB178714 | AB178714 Synthetic |
| 845 | 40.8 | 2.7 | 61518 | 2 | AC133877 | AC133877 Mus muscu | 918 | 40.6 | 2.7 | 61310 | 10 | AL691462 | AL691462 Mouse DNA |
| 846 | 40.8 | 2.7 | 79284 | 2 | EX927314 | EX927314 Danio rer | 919 | 40.6 | 2.7 | 77710 | 10 | AL844552 | AL844552 Mouse DNA |
| 847 | 40.8 | 2.7 | 84664 | 10 | BX005298 | BX005298 Mouse DNA | 920 | 40.6 | 2.7 | 81270 | 10 | EX679673 | EX679673 Mouse DNA |
| 848 | 40.8 | 2.7 | 87478 | 2 | AC139860 | AC139860 Mus muscu | 921 | 40.6 | 2.7 | 101335 | 10 | AL928882 | AL928882 Mouse DNA |
| 849 | 40.8 | 2.7 | 110000 | 2 | AC098192 | AC098192 Rattus no | 922 | 40.6 | 2.7 | 110000 | 2 | AC103072 | AC103072 Rattus no |
| 850 | 40.8 | 2.7 | 118604 | 10 | AL714010 | AL714010 Mouse DNA | 923 | 40.6 | 2.7 | 115932 | 2 | AC011446 | AC011446 Homo sapi |
| 851 | 40.8 | 2.7 | 134073 | 10 | AC110734 | AC110734 Mus muscu | 924 | 40.6 | 2.7 | 133633 | 10 | AL928857 | AL928857 Mouse DNA |
| 852 | 40.8 | 2.7 | 143702 | 9 | AC091940 | AC091940 Homo sapi | 925 | 40.6 | 2.7 | 149358 | 10 | AC087251 | AC087251 Rattus no |
| 853 | 40.8 | 2.7 | 151259 | 2 | AP002019 | AP002019 Homo sapi | 926 | 40.6 | 2.7 | 152651 | 2 | AC015556 | AC015556 Homo sapi |
| 854 | 40.8 | 2.7 | 153791 | 10 | AC141876 | AC141876 Mus muscu | 927 | 40.6 | 2.7 | 153520 | 8 | AP005727 | AP005727 Oryza sat |
| 855 | 40.8 | 2.7 | 157702 | 2 | AC119629 | AC119629 Rattus no | 928 | 40.6 | 2.7 | 154002 | 10 | AL662902 | AL662902 Mouse DNA |
| 856 | 40.8 | 2.7 | 158245 | 10 | AL805895 | AL805895 Mouse DNA | 929 | 40.6 | 2.7 | 162394 | 10 | AC114555 | AC114555 Mus muscu |
| 857 | 40.8 | 2.7 | 159605 | 2 | AC120405 | AC120405 Mus muscu | 930 | 40.6 | 2.7 | 165818 | 10 | AC121941 | AC121941 Mus muscu |
| 858 | 40.8 | 2.7 | 168358 | 2 | AC020857 | AC020857 Mus muscu | 931 | 40.6 | 2.7 | 168030 | 2 | AC091462 | AC091462 Mus muscu |
| 859 | 40.8 | 2.7 | 172399 | 10 | AC126679 | AC126679 Mus muscu | 932 | 40.6 | 2.7 | 171142 | 10 | AC111378 | AC111378 Rattus no |
| 860 | 40.8 | 2.7 | 173460 | 10 | AC137154 | AC137154 Mus muscu | 933 | 40.6 | 2.7 | 175616 | 10 | AC109307 | AC109307 Mus muscu |
| 861 | 40.8 | 2.7 | 176375 | 10 | AL808124 | AL808124 Mouse DNA | 934 | 40.6 | 2.7 | 176948 | 10 | AC084387 | AC084387 Mus muscu |
| 862 | 40.8 | 2.7 | 178256 | 10 | AC127264 | AC127264 Mus muscu | 935 | 40.6 | 2.7 | 178191 | 2 | AC113321 | AC113321 Mus muscu |
| 863 | 40.8 | 2.7 | 178988 | 10 | AC126679 | AC126679 Mus muscu | 936 | 40.6 | 2.7 | 178988 | 2 | AC107687 | AC107687 Mus muscu |
| 864 | 40.8 | 2.7 | 179460 | 10 | AC137154 | AC137154 Mus muscu | 937 | 40.6 | 2.7 | 183877 | 10 | EX649561 | EX649561 Mouse DNA |
| 865 | 40.8 | 2.7 | 180668 | 2 | AC020857 | AC020857 Mus muscu | 938 | 40.6 | 2.7 | 195082 | 10 | AC140245 | AC140245 Mus muscu |
| 866 | 40.8 | 2.7 | 181029 | 10 | AC140183 | AC140183 Mus muscu | 939 | 40.6 | 2.7 | 195555 | 10 | AC121603 | AC121603 Mus muscu |
| 867 | 40.8 | 2.7 | 184106 | 2 | AC116277 | AC116277 Rattus no | 940 | 40.6 | 2.7 | 198030 | 10 | AC124585 | AC124585 Mus muscu |
| 868 | 40.8 | 2.7 | 184607 | 10 | EX465196 | EX465196 Mouse DNA | 941 | 40.6 | 2.7 | 199872 | 2 | AC121012 | AC121012 Rattus no |
| 869 | 40.8 | 2.7 | 187880 | 2 | AC114669 | AC114669 Mus muscu | 942 | 40.6 | 2.7 | 200102 | 5 | AC145955 | AC145955 Gallus ga |
| 870 | 40.8 | 2.7 | 188575 | 10 | AC107758 | AC107758 Mus muscu | 943 | 40.6 | 2.7 | 202788 | 2 | AC136457 | AC136457 Mus muscu |
| 871 | 40.8 | 2.7 | 192550 | 2 | AC025584 | AC025584 Mus muscu | 944 | 40.6 | 2.7 | 205925 | 9 | AC009711 | AC009711 Homo sapi |
| 872 | 40.8 | 2.7 | 193004 | 10 | AL591177 | AL591177 Mouse DNA | 945 | 40.6 | 2.7 | 206182 | 10 | AC107720 | AC107720 Mus muscu |
| 873 | 40.8 | 2.7 | 194194 | 2 | AC103378 | AC103378 Mus muscu | 946 | 40.6 | 2.7 | 218291 | 10 | AC146610 | AC146610 Mus muscu |
| 874 | 40.8 | 2.7 | 197132 | 2 | AC144519 | AC144519 Mus muscu | 947 | 40.6 | 2.7 | 221455 | 10 | AL606831 | AL606831 Mouse DNA |
| 875 | 40.8 | 2.7 | 198784 | 2 | AC091521 | AC091521 Mus muscu | 948 | 40.6 | 2.7 | 225159 | 10 | AC135086 | AC135086 Mus muscu |
| 876 | 40.8 | 2.7 | 200923 | 9 | AC091928 | AC091928 Homo sapi | 949 | 40.6 | 2.7 | 231530 | 2 | AC120878 | AC120878 Mus muscu |
| 877 | 40.8 | 2.7 | 201275 | 10 | AC102613 | AC102613 Mus muscu | 950 | 40.6 | 2.7 | 236694 | 10 | AC093467 | AC093467 Mus muscu |
| 878 | 40.8 | 2.7 | 202444 | 10 | AC098705 | AC098705 Mus muscu | 951 | 40.6 | 2.7 | 237284 | 2 | AC097207 | AC097207 Rattus no |
| 879 | 40.8 | 2.7 | 203805 | 10 | AC055817 | AC055817 Mus muscu | 952 | 40.6 | 2.7 | 245617 | 2 | AC095526 | AC095526 Rattus no |
| 880 | 40.8 | 2.7 | 205508 | 10 | AC079243 | AC079243 Mus muscu | 953 | 40.6 | 2.7 | 248140 | 2 | EX901898 | EX901898 Danio rer |
| 881 | 40.8 | 2.7 | 208903 | 2 | AC128820 | AC128820 Rattus no | 954 | 40.6 | 2.7 | 250759 | 2 | AC115228 | AC115228 Rattus no |
| 882 | 40.8 | 2.7 | 214035 | 2 | AC148503 | AC148503 Callithr | 955 | 40.4 | 2.7 | 2240 | 6 | AX834071 | AX834071 Sequence |
| 883 | 40.8 | 2.7 | 214974 | 10 | AC118630 | AC118630 Mus muscu | 956 | 40.4 | 2.7 | 2240 | 6 | AX096294 | AX096294 Homo sapi |
| 884 | 40.8 | 2.7 | 215062 | 2 | AC123354 | AC123354 Rattus no | 957 | 40.4 | 2.7 | 2284 | 6 | COB42342 | COB42342 Sequence |
| 885 | 40.8 | 2.7 | 215882 | 2 | AC099288 | AC099288 Rattus no | 958 | 40.4 | 2.7 | 2284 | 3 | AK128821 | AK128821 Homo sapi |
| 886 | 40.8 | 2.7 | 216882 | 2 | AC132716 | AC132716 Rattus no | 959 | 40.4 | 2.7 | 2632 | 3 | AY568293 | AY568293 Crithidia |
| 887 | 40.8 | 2.7 | 218468 | 2 | AC123108 | AC123108 Rattus no | 960 | 40.4 | 2.7 | 7722 | 1 | AL133394 | AL133394 Homo sapi |
| 888 | 40.8 | 2.7 | 220114 | 10 | AC115804 | AC115804 Mus muscu | 961 | 40.4 | 2.7 | 11677 | 1 | AE012391 | AE012391 Xanthomon |
| 889 | 40.8 | 2.7 | 220848 | 2 | AC091579 | AC091579 Homo sapi | 962 | 40.4 | 2.7 | 110000 | 2 | AC097101 | AC097101 Sequence |
| 890 | 40.8 | 2.7 | 222845 | 10 | AC100491 | AC100491 Mus muscu | 963 | 40.4 | 2.7 | 110000 | 2 | AC108668 | AC108668 Rattus no |
| 891 | 40.8 | 2.7 | 224735 | 2 | AC132661 | AC132661 Rattus no | 964 | 40.4 | 2.7 | 110000 | 2 | AC131464 | AC131464_4 |
| 892 | 40.8 | 2.7 | 226642 | 2 | AC122971 | AC122971 Rattus no | 965 | 40.4 | 2.7 | 110000 | 8 | CR386130 | CR386130_28 |
| 893 | 40.8 | 2.7 | 229220 | 10 | AC091519 | AC091519 Mus muscu | 966 | 40.4 | 2.7 | 137571 | 2 | AC118969 | AC118969 Rattus no |
| 894 | 40.8 | 2.7 | 233132 | 2 | AC118308 | AC118308 Rattus no | 967 | 40.4 | 2.7 | 145678 | 2 | AC118969 | AC118969 Rattus no |
| 895 | 40.8 | 2.7 | 233519 | 2 | AC098446 | AC098446 Rattus no | 968 | 40.4 | 2.7 | 154608 | 10 | EX664619 | EX664619 Mouse DNA |

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|------|------|-----|--------|----|------------|---------------------|------|------|-----|--------|----|------------|---------------------|
| 969 | 40.4 | 2.7 | 157159 | 2 | AC026279 | AC026279 Homo sapi | 1042 | 40.2 | 2.7 | 176104 | 2 | AC143751 | AC143751 Macaca mu |
| 970 | 40.4 | 2.7 | 161461 | 10 | AC124355 | AC124355 Mus muscu | 1043 | 40.2 | 2.7 | 176184 | 2 | AC119918 | AC119918 Mus muscu |
| 971 | 40.4 | 2.7 | 163773 | 10 | AC125430 | AC125430 Mus muscu | 1044 | 40.2 | 2.7 | 177152 | 2 | AC021115 | AC021115 Homo sapi |
| 972 | 40.4 | 2.7 | 169834 | 10 | AC124430 | AC124430 Mus muscu | 1045 | 40.2 | 2.7 | 177770 | 9 | AC110027 | AC110027 Homo sapi |
| 973 | 40.4 | 2.7 | 169865 | 2 | AC125341 | AC125341 Mus muscu | 1046 | 40.2 | 2.7 | 178137 | 9 | AC011302 | AC011302 Homo sapi |
| 974 | 40.4 | 2.7 | 174025 | 9 | AC073388 | AC073388 Homo sapi | 1047 | 40.2 | 2.7 | 179254 | 9 | AC134306 | AC134306 Homo sapi |
| 975 | 40.4 | 2.7 | 175583 | 9 | AL590502 | AL590502 Human DNA | 1048 | 40.2 | 2.7 | 181413 | 9 | AC080032 | AC080032 Homo sapi |
| 976 | 40.4 | 2.7 | 177779 | 2 | AC116870 | AC116870 Mus muscu | 1049 | 40.2 | 2.7 | 181851 | 10 | AC102413 | AC102413 Homo sapi |
| 977 | 40.4 | 2.7 | 183797 | 2 | AC022400 | AC022400 Homo sapi | 1050 | 40.2 | 2.7 | 185121 | 2 | AC149619 | AC149619 Papio anu |
| 978 | 40.4 | 2.7 | 185867 | 10 | AL606744 | AL606744 Mouse DNA | 1051 | 40.2 | 2.7 | 189782 | 2 | AC117808 | AC117808 Mus muscu |
| 979 | 40.4 | 2.7 | 185889 | 2 | AC023000 | AC023000 Homo sapi | 1052 | 40.2 | 2.7 | 190904 | 2 | AC138081 | AC138081 Homo sapi |
| 980 | 40.4 | 2.7 | 188201 | 10 | AC122303 | AC122303 Mus muscu | 1053 | 40.2 | 2.7 | 194176 | 2 | AC132155 | AC132155 Homo sapi |
| 981 | 40.4 | 2.7 | 190462 | 9 | AC092535 | AC092535 Homo sapi | 1054 | 40.2 | 2.7 | 199227 | 2 | AC110876 | AC110876 Mus muscu |
| 982 | 40.4 | 2.7 | 192717 | 10 | AC121291 | AC121291 Mus muscu | 1055 | 40.2 | 2.7 | 201126 | 10 | AC138318 | AC138318 Homo sapi |
| 983 | 40.4 | 2.7 | 194715 | 9 | AC078898 | AC078898 Homo sapi | 1056 | 40.2 | 2.7 | 203668 | 2 | AC084411 | AC084411 Mus muscu |
| 984 | 40.4 | 2.7 | 197176 | 2 | AC022763 | AC022763 Homo sapi | 1057 | 40.2 | 2.7 | 204205 | 10 | AL669929 | AL669929 Mouse DNA |
| 985 | 40.4 | 2.7 | 198218 | 2 | AC037447 | AC037447 Homo sapi | 1058 | 40.2 | 2.7 | 204533 | 9 | AC116994 | AC116994 Mus muscu |
| 986 | 40.4 | 2.7 | 200858 | 10 | AC118255 | AC118255 Mus muscu | 1059 | 40.2 | 2.7 | 207366 | 2 | AC090001 | AC090001 Homo sapi |
| 987 | 40.4 | 2.7 | 203180 | 10 | AC145307 | AC145307 Mus muscu | 1060 | 40.2 | 2.7 | 210291 | 10 | AC129593 | AC129593 Homo sapi |
| 988 | 40.4 | 2.7 | 203669 | 2 | AC113929 | AC113929 Homo sapi | 1061 | 40.2 | 2.7 | 210849 | 9 | AC104209 | AC104209 Homo sapi |
| 989 | 40.4 | 2.7 | 203720 | 2 | AC093861 | AC093861 Homo sapi | 1062 | 40.2 | 2.7 | 212373 | 10 | AL606927 | AL606927 Mouse DNA |
| 990 | 40.4 | 2.7 | 207120 | 2 | AL844520 | AL844520 Homo sapi | 1063 | 40.2 | 2.7 | 215129 | 2 | AC131861 | AC131861 Rattus no |
| 991 | 40.4 | 2.7 | 208432 | 10 | AC114411 | AC114411 Mus muscu | 1064 | 40.2 | 2.7 | 215390 | 10 | AL672089 | AL672089 Mus muscu |
| 992 | 40.4 | 2.7 | 209336 | 10 | AC108840 | AC108840 Mus muscu | 1065 | 40.2 | 2.7 | 215676 | 2 | AC131299 | AC131299 Homo sapi |
| 993 | 40.4 | 2.7 | 210188 | 2 | AC124611 | AC124611 Mus muscu | 1066 | 40.2 | 2.7 | 221792 | 2 | AC112344 | AC112344 Rattus no |
| 994 | 40.4 | 2.7 | 213660 | 2 | AC073659 | AC073659 Mus muscu | 1067 | 40.2 | 2.7 | 225600 | 10 | AC115766 | AC115766 Homo sapi |
| 995 | 40.4 | 2.7 | 215860 | 2 | AC115801 | AC115801 Mus muscu | 1068 | 40.2 | 2.7 | 227696 | 2 | AC112936 | AC112936 Mus muscu |
| 996 | 40.4 | 2.7 | 216800 | 10 | AL589744 | AL589744 Mouse DNA | 1069 | 40.2 | 2.7 | 232409 | 10 | AL772187 | AL772187 Mouse DNA |
| 997 | 40.4 | 2.7 | 220638 | 10 | AL645723 | AL645723 Mouse DNA | 1070 | 40.2 | 2.7 | 233573 | 2 | AC098491 | AC098491 Rattus no |
| 998 | 40.4 | 2.7 | 221526 | 10 | AC117668 | AC117668 Mus muscu | 1071 | 40.2 | 2.7 | 237732 | 2 | AC096491 | AC096491 Rattus no |
| 999 | 40.4 | 2.7 | 223366 | 10 | AC023174 | AC023174 Mus muscu | 1072 | 40.2 | 2.7 | 240692 | 2 | AC111246 | AC111246 Rattus no |
| 1000 | 40.4 | 2.7 | 226373 | 2 | AC119821 | AC119821 Mus muscu | 1073 | 40.2 | 2.7 | 252366 | 2 | AC096178 | AC096178 Rattus no |
| 1001 | 40.4 | 2.7 | 229658 | 2 | AC096408 | AC096408 Rattus no | 1074 | 40.2 | 2.7 | 260795 | 2 | AC132869 | AC132869 Mus muscu |
| 1002 | 40.4 | 2.7 | 237475 | 2 | AC117027 | AC117027 Rattus no | 1075 | 40.2 | 2.7 | 266770 | 2 | AC130136 | AC130136 Rattus no |
| 1003 | 40.4 | 2.7 | 240822 | 2 | AC095369 | AC095369 Rattus no | 1076 | 40.2 | 2.7 | 267438 | 2 | AC087561 | AC087561 Rattus no |
| 1004 | 40.4 | 2.7 | 243589 | 2 | AC111432 | AC111432 Rattus no | 1077 | 40.2 | 2.7 | 272628 | 2 | AC113669 | AC113669 Rattus no |
| 1005 | 40.4 | 2.7 | 248550 | 1 | SC093120 | SC093120 Streptomy | 1078 | 40.2 | 2.7 | 282163 | 2 | AC113669 | AC113669 Rattus no |
| 1006 | 40.4 | 2.7 | 249638 | 2 | AC107177 | AC107177 Rattus no | 1079 | 40.2 | 2.7 | 285591 | 2 | AC123095 | AC123095 Rattus no |
| 1007 | 40.4 | 2.7 | 263658 | 2 | AC126697 | AC126697 Rattus no | 1080 | 40.2 | 2.7 | 290433 | 1 | AE016782 | AE016782 Pseudomon |
| 1008 | 40.4 | 2.7 | 272384 | 2 | AC125722 | AC125722 Rattus no | 1081 | 40.2 | 2.7 | 300620 | 2 | SC093912 | SC093912 Streptomy |
| 1009 | 40.4 | 2.7 | 277285 | 2 | AC110434 | AC110434 Rattus no | 1082 | 40.2 | 2.7 | 300800 | 2 | AC106099 | AC106099 Rattus no |
| 1010 | 40.4 | 2.7 | 301833 | 2 | AC112629 | AC112629 Rattus no | 1083 | 40.2 | 2.7 | 314959 | 2 | AC108045 | AC108045 Rattus no |
| 1011 | 40.4 | 2.7 | 315176 | 2 | AC078956 | AC078956 Homo sapi | 1084 | 40.2 | 2.7 | 340972 | 2 | AC109045 | AC109045 Rattus no |
| 1012 | 40.4 | 2.7 | 320381 | 2 | AC126143 | AC126143 Rattus no | 1085 | 40.2 | 2.7 | 3434 | 6 | CQ727832 | CQ727832 Sequence |
| 1013 | 40.4 | 2.7 | 331543 | 2 | AC111236 | AC111236 Rattus no | 1086 | 40.2 | 2.7 | 334 | 8 | LE14765 | LE14765 Lycopersico |
| 1014 | 40.2 | 2.7 | 654 | 6 | E02315 | E02315 DNA encodin | 1087 | 40.2 | 2.7 | 447 | 8 | BD174656 | BD174656 Fluoresce |
| 1015 | 40.2 | 2.7 | 654 | 6 | AX401676 | AX401676 Sequence | 1088 | 40.2 | 2.7 | 1278 | 6 | AX514969 | AX514969 Sequence |
| 1016 | 40.2 | 2.7 | 1446 | 6 | AX164174 | AX164174 Sequence | 1089 | 40.2 | 2.7 | 1278 | 6 | AX514969 | AX514969 Sequence |
| 1017 | 40.2 | 2.7 | 1446 | 10 | RNRCM1 | RNRCM1 | 1090 | 40.2 | 2.7 | 1278 | 6 | AX514969 | AX514969 Sequence |
| 1018 | 40.2 | 2.7 | 3513 | 10 | AF178845 | AF178845 Rattus no | 1091 | 40.2 | 2.7 | 4732 | 9 | SHDNAROLA | SHDNAROLA |
| 1019 | 40.2 | 2.7 | 4021 | 10 | BC054805 | BC054805 Mus muscu | 1092 | 40.2 | 2.7 | 47198 | 2 | AC090252 | AC090252 Homo sapi |
| 1020 | 40.2 | 2.7 | 4229 | 8 | AK120277 | AK120277 Rattus no | 1093 | 40.2 | 2.7 | 79560 | 9 | AL591471 | AL591471 Human DNA |
| 1021 | 40.2 | 2.7 | 104563 | 9 | AL442065 | AL442065 Human DNA | 1094 | 40.2 | 2.7 | 87140 | 9 | AL669942 | AL669942 Human DNA |
| 1022 | 40.2 | 2.7 | 105608 | 2 | AC116396 | AC116396 Mus muscu | 1095 | 40.2 | 2.7 | 105928 | 9 | BX664727 | BX664727 Human DNA |
| 1023 | 40.2 | 2.7 | 112171 | 10 | AF162137-1 | AF162137-1 | 1096 | 40.2 | 2.7 | 107579 | 9 | AC114962 | AC114962 Homo sapi |
| 1024 | 40.2 | 2.7 | 112171 | 8 | AP003930 | AP003930 Oryza sat | 1097 | 40.2 | 2.7 | 110000 | 2 | AC094437-2 | AC094437-2 |
| 1025 | 40.2 | 2.7 | 125217 | 8 | AP003930 | AP003930 Oryza sat | 1098 | 40.2 | 2.7 | 111000 | 2 | AL360016-2 | AL360016-2 |
| 1026 | 40.2 | 2.7 | 130654 | 2 | HS1007616 | HS1007616 Human DNA | 1099 | 40.2 | 2.7 | 111183 | 9 | AC080850 | AC080850 Homo sapi |
| 1027 | 40.2 | 2.7 | 137127 | 2 | AC113343 | AC113343 Homo sapi | 1100 | 40.2 | 2.7 | 127405 | 10 | AL645599 | AL645599 Mouse DNA |
| 1028 | 40.2 | 2.7 | 144131 | 10 | AC110822 | AC110822 Mus muscu | 1101 | 40.2 | 2.7 | 133753 | 9 | AC131180 | AC131180 Homo sapi |
| 1029 | 40.2 | 2.7 | 152876 | 2 | AC099488 | AC099488 Homo sapi | 1102 | 40.2 | 2.7 | 133910 | 10 | AL929253 | AL929253 Sorex ara |
| 1030 | 40.2 | 2.7 | 153754 | 9 | BS000598 | BS000598 Pan trogl | 1103 | 40.2 | 2.7 | 134736 | 2 | AC151493 | AC151493 Mus muscu |
| 1031 | 40.2 | 2.7 | 153967 | 2 | AC132224 | AC132224 Mus muscu | 1104 | 40.2 | 2.7 | 140817 | 10 | AC127231 | AC127231 Mus muscu |
| 1032 | 40.2 | 2.7 | 158009 | 10 | AL837508 | AL837508 Mouse DNA | 1105 | 40.2 | 2.7 | 142178 | 10 | AL603705 | AL603705 Homo sapi |
| 1033 | 40.2 | 2.7 | 163444 | 2 | AC025866 | AC025866 Homo sapi | 1106 | 40.2 | 2.7 | 143650 | 10 | AL928862 | AL928862 Mouse DNA |
| 1034 | 40.2 | 2.7 | 163780 | 2 | AC146215 | AC146215 Pan trogl | 1107 | 40.2 | 2.7 | 148251 | 9 | AC083867 | AC083867 Homo sapi |
| 1035 | 40.2 | 2.7 | 163914 | 9 | AC098487 | AC098487 Homo sapi | 1108 | 40.2 | 2.7 | 148996 | 9 | AC102953 | AC102953 Homo sapi |
| 1036 | 40.2 | 2.7 | 168027 | 9 | AC147337 | AC147337 Pan trogl | 1109 | 40.2 | 2.7 | 151398 | 10 | BX649549 | BX649549 Mouse DNA |
| 1037 | 40.2 | 2.7 | 168364 | 10 | AC116507 | AC116507 Mus muscu | 1110 | 40.2 | 2.7 | 158419 | 10 | AC137901 | AC137901 Homo sapi |
| 1038 | 40.2 | 2.7 | 168605 | 2 | AC022477 | AC022477 Homo sapi | 1111 | 40.2 | 2.7 | 158419 | 10 | AL929117 | AL929117 Mouse DNA |
| 1039 | 40.2 | 2.7 | 169342 | 2 | AL136991 | AL136991 Human DNA | 1112 | 40.2 | 2.7 | 161940 | 10 | AL929117 | AL929117 Mouse DNA |
| 1040 | 40.2 | 2.7 | 172116 | 2 | AC087100 | AC087100 Mus muscu | 1113 | 40.2 | 2.7 | 163776 | 2 | AC109289 | AC109289 Mus muscu |
| 1041 | 40.2 | 2.7 | 173169 | 9 | AC068538 | AC068538 Homo sapi | 1114 | 40.2 | 2.7 | 164256 | 2 | AC134725 | AC134725 Rattus no |

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|------|----|-----|--------|----|------------------------------|------|------|-----|--------|----|-------------|
| 1115 | 40 | 2.7 | 164795 | 9 | AP002518 Homo sapi | 1188 | 39.8 | 2.7 | 634 | 8 | AK104031 |
| 1116 | 40 | 2.7 | 166743 | 2 | AC140242 Mus muscu | 1189 | 39.8 | 2.7 | 681 | 6 | AX899104 |
| 1117 | 40 | 2.7 | 166826 | 3 | AL445670 Human DNA | 1190 | 39.8 | 2.7 | 681 | 6 | BD034637 |
| 1118 | 40 | 2.7 | 166976 | 8 | AP001539 Oryza sat | 1191 | 39.8 | 2.7 | 731 | 8 | AK071852 |
| 1119 | 40 | 2.7 | 169442 | 10 | AC124545 Mus muscu | 1192 | 39.8 | 2.7 | 798 | 8 | AX652177 |
| 1120 | 40 | 2.7 | 170540 | 2 | AC133333 Mus muscu | 1193 | 39.8 | 2.7 | 813 | 6 | AF441191 |
| 1121 | 40 | 2.7 | 172539 | 2 | AC110523 Mus muscu | 1194 | 39.8 | 2.7 | 970 | 5 | AF180890 |
| 1122 | 40 | 2.7 | 173136 | 10 | AC103380 Mus muscu | 1195 | 39.8 | 2.7 | 1139 | 10 | RNMR1CB |
| 1123 | 40 | 2.7 | 174241 | 9 | AC018634 Human Chr | 1196 | 39.8 | 2.7 | 1248 | 6 | AX653136 |
| 1124 | 40 | 2.7 | 174613 | 2 | AC012522 Homo sapi | 1197 | 39.8 | 2.7 | 1491 | 5 | BC064284 |
| 1125 | 40 | 2.7 | 176001 | 2 | AC118688 Mus muscu | 1198 | 39.8 | 2.7 | 1635 | 3 | AK112671 |
| 1126 | 40 | 2.7 | 176616 | 2 | AC150016 Homo sapi | 1199 | 39.8 | 2.7 | 2022 | 9 | AF105372 |
| 1127 | 40 | 2.7 | 177191 | 9 | AC145146 Papio anu | 1200 | 39.8 | 2.7 | 2312 | 9 | AB047906 |
| 1128 | 40 | 2.7 | 177630 | 2 | AC087156 Mus muscu | 1201 | 39.8 | 2.7 | 3612 | 10 | MMCOLA4 |
| 1129 | 40 | 2.7 | 177830 | 2 | AC123821 Mus muscu | 1202 | 39.8 | 2.7 | 6512 | 6 | AX306181 |
| 1130 | 40 | 2.7 | 179299 | 10 | AC132295 Mus muscu | 1203 | 39.8 | 2.7 | 6512 | 10 | MUSCOLA4A |
| 1131 | 40 | 2.7 | 182517 | 2 | AC149571 Rhinoloph | 1204 | 39.8 | 2.7 | 6522 | 10 | BC072650 |
| 1132 | 40 | 2.7 | 184536 | 2 | AC068682 Homo sapi | 1205 | 39.8 | 2.7 | 13697 | 9 | AP001475 |
| 1133 | 40 | 2.7 | 186265 | 9 | AC123644 Homo sapi | 1206 | 39.8 | 2.7 | 79560 | 9 | AL591471 |
| 1134 | 40 | 2.7 | 186713 | 2 | AC123644 Mus muscu | 1207 | 39.8 | 2.7 | 105929 | 9 | BX664727 |
| 1135 | 40 | 2.7 | 188616 | 10 | AC123795 Mus muscu | 1208 | 39.8 | 2.7 | 106214 | 8 | AP003818 |
| 1136 | 40 | 2.7 | 188889 | 10 | AC122381 Mus muscu | 1209 | 39.8 | 2.7 | 110000 | 1 | BX571966_30 |
| 1137 | 40 | 2.7 | 190557 | 2 | AC130064 Ratcus no | 1210 | 39.8 | 2.7 | 110000 | 2 | AC094428_0 |
| 1138 | 40 | 2.7 | 190654 | 2 | AC018949 Homo sapi | 1211 | 39.8 | 2.7 | 110000 | 2 | AC130964_1 |
| 1139 | 40 | 2.7 | 190680 | 9 | AC147575 Homo sapi | 1212 | 39.8 | 2.7 | 112597 | 9 | HS82110 |
| 1140 | 40 | 2.7 | 191965 | 9 | CNS057DG Human chr | 1213 | 39.8 | 2.7 | 130805 | 9 | AC118283 |
| 1141 | 40 | 2.7 | 191965 | 10 | AC122274 Mus muscu | 1214 | 39.8 | 2.7 | 130973 | 8 | AP003813 |
| 1142 | 40 | 2.7 | 192135 | 2 | AC119581 Ratcus no | 1215 | 39.8 | 2.7 | 133289 | 9 | AC012317 |
| 1143 | 40 | 2.7 | 194209 | 2 | AC147745 Homo sapi | 1216 | 39.8 | 2.7 | 140367 | 10 | AL7732439 |
| 1144 | 40 | 2.7 | 194476 | 2 | AC147745 Homo sapi | 1217 | 39.8 | 2.7 | 145972 | 10 | AC145608 |
| 1145 | 40 | 2.7 | 195226 | 2 | AC141305 Homo sapi | 1218 | 39.8 | 2.7 | 149791 | 2 | CR848007 |
| 1146 | 40 | 2.7 | 195226 | 2 | AC139199 Mus muscu | 1219 | 39.8 | 2.7 | 152564 | 10 | AC127549 |
| 1147 | 40 | 2.7 | 196026 | 2 | AC124730 Mus muscu | 1220 | 39.8 | 2.7 | 153416 | 9 | AL160286 |
| 1148 | 40 | 2.7 | 196026 | 10 | AL928812 Mouse DNA | 1221 | 39.8 | 2.7 | 156398 | 10 | AL929020 |
| 1149 | 40 | 2.7 | 199019 | 10 | AC078911 Mus muscu | 1222 | 39.8 | 2.7 | 160321 | 10 | AL772321 |
| 1150 | 40 | 2.7 | 200329 | 2 | AC116131 Ratcus no | 1223 | 39.8 | 2.7 | 163632 | 2 | AC121960 |
| 1151 | 40 | 2.7 | 200329 | 2 | AC116131 Ratcus no | 1224 | 39.8 | 2.7 | 163632 | 10 | AL591441 |
| 1152 | 40 | 2.7 | 203786 | 2 | AC139809 Homo sapi | 1225 | 39.8 | 2.7 | 162441 | 9 | AL591441 |
| 1153 | 40 | 2.7 | 203865 | 10 | EX088573 Mouse DNA | 1226 | 39.8 | 2.7 | 162681 | 10 | AC122059 |
| 1154 | 40 | 2.7 | 206973 | 10 | AC149059 Mus muscu | 1227 | 39.8 | 2.7 | 163368 | 2 | AC120421 |
| 1155 | 40 | 2.7 | 208885 | 2 | AC101703 Mus muscu | 1228 | 39.8 | 2.7 | 164926 | 2 | AC124922 |
| 1156 | 40 | 2.7 | 209688 | 2 | AC139829 Homo sapi | 1229 | 39.8 | 2.7 | 165901 | 4 | AC095021 |
| 1157 | 40 | 2.7 | 211763 | 2 | AC123558 Mus muscu | 1230 | 39.8 | 2.7 | 165932 | 10 | AC102196 |
| 1158 | 40 | 2.7 | 215524 | 10 | AL603913 Mouse DNA | 1231 | 39.8 | 2.7 | 166801 | 10 | AC132948 |
| 1159 | 40 | 2.7 | 221389 | 2 | AC112122 Ratcus no | 1232 | 39.8 | 2.7 | 167869 | 10 | AC126437 |
| 1160 | 40 | 2.7 | 221803 | 2 | AC106977 Ratcus no | 1233 | 39.8 | 2.7 | 167869 | 2 | AC119920 |
| 1161 | 40 | 2.7 | 222825 | 2 | AC094945 Ratcus no | 1234 | 39.8 | 2.7 | 171267 | 2 | AC145538 |
| 1162 | 40 | 2.7 | 224522 | 2 | AC129172 Ratcus no | 1235 | 39.8 | 2.7 | 171749 | 2 | AC110195 |
| 1163 | 40 | 2.7 | 224760 | 10 | AC124543 Mus muscu | 1236 | 39.8 | 2.7 | 173534 | 9 | AC007920 |
| 1164 | 40 | 2.7 | 231371 | 2 | AC118527 Ratcus no | 1237 | 39.8 | 2.7 | 175639 | 10 | AC133515 |
| 1165 | 40 | 2.7 | 231530 | 2 | AC120878 Mus muscu | 1238 | 39.8 | 2.7 | 176959 | 9 | AC026402 |
| 1166 | 40 | 2.7 | 231593 | 10 | AC140433 Mus muscu | 1239 | 39.8 | 2.7 | 178361 | 10 | AL645471 |
| 1167 | 40 | 2.7 | 232410 | 2 | AC094535 Ratcus no | 1240 | 39.8 | 2.7 | 178367 | 9 | AC006115 |
| 1168 | 40 | 2.7 | 234139 | 2 | AC094725 Ratcus no | 1241 | 39.8 | 2.7 | 178410 | 2 | AC145190 |
| 1169 | 40 | 2.7 | 238937 | 2 | AC094926 Ratcus no | 1242 | 39.8 | 2.7 | 180498 | 9 | AL513478 |
| 1170 | 40 | 2.7 | 239441 | 2 | AC128882 Ratcus no | 1243 | 39.8 | 2.7 | 182366 | 10 | AC124481 |
| 1171 | 40 | 2.7 | 241781 | 2 | AC122087 Ratcus no | 1244 | 39.8 | 2.7 | 183479 | 9 | AC017014 |
| 1172 | 40 | 2.7 | 244645 | 2 | AC120348 Mus muscu | 1245 | 39.8 | 2.7 | 183479 | 2 | AC114907 |
| 1173 | 40 | 2.7 | 248640 | 2 | AC107343 Ratcus no | 1246 | 39.8 | 2.7 | 184748 | 9 | AC124915 |
| 1174 | 40 | 2.7 | 248943 | 2 | AC106543 Ratcus no | 1247 | 39.8 | 2.7 | 184237 | 2 | AC108418 |
| 1175 | 40 | 2.7 | 253093 | 2 | AC104053 Ratcus no | 1248 | 39.8 | 2.7 | 184736 | 10 | AL808128 |
| 1176 | 40 | 2.7 | 254973 | 2 | AC127437 Ratcus no | 1249 | 39.8 | 2.7 | 187651 | 8 | AC129718 |
| 1177 | 40 | 2.7 | 255090 | 2 | AC098534 Ratcus no | 1250 | 39.8 | 2.7 | 189335 | 10 | AC112945 |
| 1178 | 40 | 2.7 | 255749 | 2 | AC148018 Mus muscu | 1251 | 39.8 | 2.7 | 190338 | 2 | AC131109 |
| 1179 | 40 | 2.7 | 263936 | 10 | AC094412 Ratcus no | 1252 | 39.8 | 2.7 | 190654 | 2 | AC018949 |
| 1180 | 40 | 2.7 | 264425 | 2 | AC019028 Mus muscu | 1253 | 39.8 | 2.7 | 193773 | 2 | AC133652 |
| 1181 | 40 | 2.7 | 286117 | 2 | AC112951 Ratcus no | 1254 | 39.8 | 2.7 | 197741 | 10 | AC113938 |
| 1182 | 40 | 2.7 | 286117 | 2 | AC115390 Ratcus no | 1255 | 39.8 | 2.7 | 199215 | 10 | AC146609 |
| 1183 | 40 | 2.7 | 292128 | 2 | AC151412 Mus muscu | 1256 | 39.8 | 2.7 | 201218 | 9 | AC104445 |
| 1184 | 40 | 2.7 | 302564 | 2 | AC105608 Ratcus no | 1257 | 39.8 | 2.7 | 203301 | 2 | AC147067 |
| 1185 | 40 | 2.7 | 303091 | 2 | AC084799 Mus muscu | 1258 | 39.8 | 2.7 | 205129 | 2 | AC148031 |
| 1186 | 40 | 2.7 | 450 | 8 | OSCALMODU Z1827 O.sativa ge | 1259 | 39.8 | 2.7 | 206377 | 10 | AC126689 |
| 1187 | 40 | 2.7 | 450 | 8 | RICALMODU L18913 Oryza sativ | 1260 | 39.8 | 2.7 | 207841 | 2 | AC072019 |

| | | | | | | | | | | | | | |
|-------|------|-----|--------|----|----------|----------------------|-------|------|-----|--------|----|----------|--------------------|
| c1261 | 39.8 | 2.7 | 209178 | 10 | AC120425 | AC120425 Mus muscu | 1334 | 39.6 | 2.7 | 161274 | 2 | AC139613 | AC139613 Rattus no |
| c1262 | 39.8 | 2.7 | 211869 | 2 | AC144687 | AC144687 Rattus no | c1335 | 39.6 | 2.7 | 164571 | 10 | AL929003 | AL929003 Mus muscu |
| c1263 | 39.8 | 2.7 | 212557 | 2 | AC120134 | AC120134 Mus muscu | c1336 | 39.6 | 2.7 | 165390 | 2 | AC093185 | AC093185 Mus muscu |
| c1264 | 39.8 | 2.7 | 214619 | 10 | AC122267 | AC122267 Mus muscu | c1337 | 39.6 | 2.7 | 165700 | 10 | AL833781 | AL833781 Mus muscu |
| c1265 | 39.8 | 2.7 | 214690 | 2 | AC083889 | AC083889 Mus muscu | c1338 | 39.6 | 2.7 | 170573 | 2 | AC138890 | AC138890 Mus muscu |
| c1266 | 39.8 | 2.7 | 215455 | 10 | AC122845 | AC122845 Mus muscu | c1339 | 39.6 | 2.7 | 173967 | 2 | AC122093 | AC122093 Rattus no |
| c1267 | 39.8 | 2.7 | 215505 | 10 | AL844166 | AL844166 Mouse DNA | c1340 | 39.6 | 2.7 | 177390 | 10 | AC136923 | AC136923 Mus muscu |
| c1268 | 39.8 | 2.7 | 218552 | 10 | AC118607 | AC118607 Mus muscu | c1341 | 39.6 | 2.7 | 177631 | 10 | AC101968 | AC101968 Mus muscu |
| c1269 | 39.8 | 2.7 | 219559 | 10 | AC087329 | AC087329 Mus muscu | c1342 | 39.6 | 2.7 | 178897 | 2 | AC115715 | AC115715 Mus muscu |
| c1270 | 39.8 | 2.7 | 222046 | 10 | AL772291 | AL772291 Mouse DNA | c1343 | 39.6 | 2.7 | 179064 | 10 | AC129081 | AC129081 Mus muscu |
| c1271 | 39.8 | 2.7 | 223730 | 2 | AC140553 | AC140553 Mus muscu | c1344 | 39.6 | 2.7 | 179246 | 9 | AC114877 | AC114877 Homo sapi |
| c1272 | 39.8 | 2.7 | 226374 | 2 | AC123609 | AC123609 Mus muscu | c1345 | 39.6 | 2.7 | 181602 | 10 | AL935168 | AL935168 Mus muscu |
| c1273 | 39.8 | 2.7 | 227736 | 2 | AC109946 | AC109946 Rattus no | c1346 | 39.6 | 2.7 | 182019 | 9 | AC007077 | AC007077 Homo sapi |
| c1274 | 39.8 | 2.7 | 228428 | 2 | AL596456 | AL596456 Mouse DNA | c1347 | 39.6 | 2.7 | 182387 | 10 | AC024950 | AC024950 Mus muscu |
| c1275 | 39.8 | 2.7 | 228727 | 2 | AC116415 | AC116415 Mus muscu | c1348 | 39.6 | 2.7 | 183428 | 10 | AC124389 | AC124389 Mus muscu |
| c1276 | 39.8 | 2.7 | 232321 | 2 | AC107824 | AC107824 Mus muscu | c1349 | 39.6 | 2.7 | 184256 | 10 | AL929163 | AL929163 Mouse DNA |
| c1277 | 39.8 | 2.7 | 235349 | 2 | AC101894 | AC101894 Mus muscu | c1350 | 39.6 | 2.7 | 185819 | 2 | AC108425 | AC108425 Mus muscu |
| c1278 | 39.8 | 2.7 | 235574 | 10 | AC133889 | AC133889 Mus muscu | c1351 | 39.6 | 2.7 | 187005 | 10 | AC124470 | AC124470 Mus muscu |
| c1279 | 39.8 | 2.7 | 242105 | 2 | AC133381 | AC133381 Mus muscu | c1352 | 39.6 | 2.7 | 187278 | 2 | AC044806 | AC044806 Mus muscu |
| c1280 | 39.8 | 2.7 | 251933 | 2 | AC133356 | AC133356 Rattus no | c1353 | 39.6 | 2.7 | 188796 | 2 | AC112321 | AC112321 Mus muscu |
| c1281 | 39.8 | 2.7 | 256754 | 10 | AC101559 | AC101559 Mus muscu | c1354 | 39.6 | 2.7 | 189295 | 2 | AC148110 | AC148110 Mus muscu |
| c1282 | 39.8 | 2.7 | 256754 | 2 | AC109139 | AC109139 Mus muscu | c1355 | 39.6 | 2.7 | 189315 | 9 | AC098848 | AC098848 Homo sapi |
| c1283 | 39.8 | 2.7 | 263937 | 2 | AC129555 | AC129555 Mus muscu | c1356 | 39.6 | 2.7 | 189774 | 10 | AC098709 | AC098709 Mus muscu |
| c1284 | 39.8 | 2.7 | 265566 | 2 | AC123187 | AC123187 Rattus no | c1357 | 39.6 | 2.7 | 190089 | 10 | AC133092 | AC133092 Mus muscu |
| c1285 | 39.8 | 2.7 | 270418 | 1 | AE017303 | AE017303 Thermanus t | c1358 | 39.6 | 2.7 | 191111 | 9 | AC006080 | AC006080 Homo sapi |
| c1286 | 39.8 | 2.7 | 275204 | 2 | AC104224 | AC104224 Mus muscu | c1359 | 39.6 | 2.7 | 191140 | 2 | AC102770 | AC102770 Mus muscu |
| c1287 | 39.8 | 2.7 | 282610 | 2 | AC096244 | AC096244 Rattus no | c1360 | 39.6 | 2.7 | 191635 | 10 | AL831710 | AL831710 Mouse DNA |
| c1288 | 39.8 | 2.7 | 340000 | 9 | AE001759 | AE001759 Homo sapi | c1361 | 39.6 | 2.7 | 192452 | 2 | AC118247 | AC118247 Mus muscu |
| c1289 | 39.6 | 2.7 | 435 | 8 | BT011896 | BT011896 Arabidops | c1362 | 39.6 | 2.7 | 192806 | 10 | AC132442 | AC132442 Mus muscu |
| c1290 | 39.6 | 2.7 | 447 | 8 | DMCAMR | DMCAMR | c1363 | 39.6 | 2.7 | 196868 | 2 | AC110242 | AC110242 Mus muscu |
| c1291 | 39.6 | 2.7 | 462 | 6 | IO9061 | IO9061 Sequence 42 | c1364 | 39.6 | 2.7 | 202881 | 2 | AC115947 | AC115947 Mus muscu |
| c1292 | 39.6 | 2.7 | 495 | 8 | AF292108 | AF292108 Rattus av | c1365 | 39.6 | 2.7 | 202920 | 10 | AL929441 | AL929441 Mus muscu |
| c1293 | 39.6 | 2.7 | 507 | 11 | BC004977 | BC004977 S208P6884 | c1366 | 39.6 | 2.7 | 203356 | 2 | AC123635 | AC123635 Mus muscu |
| c1294 | 39.6 | 2.7 | 524 | 8 | FSQAMR1 | X97612 F. sylvatica | c1367 | 39.6 | 2.7 | 206919 | 2 | AC142127 | AC142127 Rattus no |
| c1295 | 39.6 | 2.7 | 533 | 8 | AF150059 | AF150059 Braeafrica | c1368 | 39.6 | 2.7 | 207400 | 2 | AC109082 | AC109082 Mus muscu |
| c1296 | 39.6 | 2.7 | 533 | 8 | AX660639 | AX660639 Sequence | c1369 | 39.6 | 2.7 | 207763 | 10 | AC121279 | AC121279 Mus muscu |
| c1297 | 39.6 | 2.7 | 709 | 6 | CO599700 | CO599700 Sequence | c1370 | 39.6 | 2.7 | 210029 | 2 | AC122888 | AC122888 Mus muscu |
| c1298 | 39.6 | 2.7 | 837 | 6 | BT003282 | BT003282 Drosophila | c1371 | 39.6 | 2.7 | 212456 | 10 | AC118007 | AC118007 Mus muscu |
| c1299 | 39.6 | 2.7 | 846 | 8 | AF295637 | AF295637 Elaeis gu | c1372 | 39.6 | 2.7 | 216211 | 2 | AC091315 | AC091315 Mus muscu |
| c1300 | 39.6 | 2.7 | 858 | 3 | BT133837 | BT133837 Branchios | c1373 | 39.6 | 2.7 | 217606 | 10 | AC113176 | AC113176 Mus muscu |
| c1301 | 39.6 | 2.7 | 995 | 3 | CO590661 | CO590661 Sequence | c1374 | 39.6 | 2.7 | 217999 | 10 | AC133835 | AC133835 Mus muscu |
| c1302 | 39.6 | 2.7 | 1011 | 6 | CO856061 | CO856061 Sequence | c1375 | 39.6 | 2.7 | 222896 | 2 | AC119773 | AC119773 Rattus no |
| c1303 | 39.6 | 2.7 | 1049 | 3 | CO599694 | CO599694 Sequence | c1376 | 39.6 | 2.7 | 223669 | 2 | AC097813 | AC097813 Rattus no |
| c1304 | 39.6 | 2.7 | 1357 | 3 | AY118890 | AY118890 Drosophila | c1377 | 39.6 | 2.7 | 224723 | 2 | AC106982 | AC106982 Rattus no |
| c1305 | 39.6 | 2.7 | 1412 | 3 | AY269783 | AY269783 Branchios | c1378 | 39.6 | 2.7 | 225631 | 2 | AC097992 | AC097992 Rattus no |
| c1306 | 39.6 | 2.7 | 1434 | 6 | AX653002 | AX653002 Sequence | c1379 | 39.6 | 2.7 | 228380 | 2 | AC079636 | AC079636 Mus muscu |
| c1307 | 39.6 | 2.7 | 1928 | 8 | AK103307 | AK103307 Oryza sat | c1380 | 39.6 | 2.7 | 230614 | 10 | AL626772 | AL626772 Mouse DNA |
| c1308 | 39.6 | 2.7 | 3001 | 6 | AX344924 | AX344924 Sequence | c1381 | 39.6 | 2.7 | 230674 | 10 | AL731732 | AL731732 Mouse DNA |
| c1309 | 39.6 | 2.7 | 3763 | 5 | PMU19361 | PMU19361 Petromyzon | c1382 | 39.6 | 2.7 | 232631 | 2 | AC114346 | AC114346 Rattus no |
| c1310 | 39.6 | 2.7 | 4505 | 9 | AK024485 | AK024485 Homo sapi | c1383 | 39.6 | 2.7 | 233852 | 2 | AC108549 | AC108549 Mus muscu |
| c1311 | 39.6 | 2.7 | 6120 | 6 | AX323826 | AX323826 Sequence | c1384 | 39.6 | 2.7 | 234724 | 10 | AL683854 | AL683854 Mouse DNA |
| c1312 | 39.6 | 2.7 | 6120 | 6 | AX344895 | AX344895 Sequence | c1385 | 39.6 | 2.7 | 237929 | 2 | AC096103 | AC096103 Rattus no |
| c1313 | 39.6 | 2.7 | 73488 | 2 | AC133822 | AC133822 Mus muscu | c1386 | 39.6 | 2.7 | 237945 | 10 | AC117994 | AC117994 Mus muscu |
| c1314 | 39.6 | 2.7 | 92882 | 9 | AL355815 | AL355815 Human DNA | c1387 | 39.6 | 2.7 | 239595 | 2 | AC124937 | AC124937 Rattus no |
| c1315 | 39.6 | 2.7 | 110000 | 1 | AP006618 | AP006618 Human DNA | c1388 | 39.6 | 2.7 | 242465 | 2 | AC128332 | AC128332 Rattus no |
| c1316 | 39.6 | 2.7 | 110000 | 2 | AC120236 | Continuation (60 of | c1389 | 39.6 | 2.7 | 244377 | 2 | AC110661 | AC110661 Rattus no |
| c1317 | 39.6 | 2.7 | 110000 | 2 | AC120752 | Continuation (2 of | c1390 | 39.6 | 2.7 | 246377 | 2 | AC127975 | AC127975 Rattus no |
| c1318 | 39.6 | 2.7 | 125116 | 10 | AC148086 | AC148086 Mus muscu | c1391 | 39.6 | 2.7 | 252488 | 2 | AC116792 | AC116792 Mus muscu |
| c1319 | 39.6 | 2.7 | 125419 | 2 | AC026260 | AC026260 Homo sapi | c1392 | 39.6 | 2.7 | 254669 | 2 | AC103340 | AC103340 Rattus no |
| c1320 | 39.6 | 2.7 | 129016 | 2 | AC130257 | AC130257 Rattus no | c1393 | 39.6 | 2.7 | 260820 | 2 | AC119137 | AC119137 Mus muscu |
| c1321 | 39.6 | 2.7 | 129950 | 9 | AL356952 | AL356952 Human DNA | c1394 | 39.6 | 2.7 | 264029 | 2 | AC104225 | AC104225 Mus muscu |
| c1322 | 39.6 | 2.7 | 131682 | 9 | AL672277 | AL672277 Human DNA | c1395 | 39.6 | 2.7 | 264291 | 2 | AC094902 | AC094902 Rattus no |
| c1323 | 39.6 | 2.7 | 139973 | 2 | AC135372 | AC135372 Rattus no | c1396 | 39.6 | 2.7 | 266305 | 2 | AC097701 | AC097701 Rattus no |
| c1324 | 39.6 | 2.7 | 141025 | 2 | AC123528 | AC123528 Oryza sat | c1397 | 39.6 | 2.7 | 269607 | 2 | AC096303 | AC096303 Rattus no |
| c1325 | 39.6 | 2.7 | 147559 | 10 | AC117702 | AC117702 Mus muscu | c1398 | 39.6 | 2.7 | 334269 | 2 | AC126726 | AC126726 Rattus no |
| c1326 | 39.6 | 2.7 | 149576 | 2 | AC118368 | AC118368 Rattus no | c1399 | 39.6 | 2.7 | 349980 | 6 | AX344557 | AX344557 Sequence |
| c1327 | 39.6 | 2.7 | 150121 | 10 | AC114925 | AC114925 Mus muscu | c1400 | 39.6 | 2.7 | 349980 | 6 | AX344558 | AX344558 Sequence |
| c1328 | 39.6 | 2.7 | 151365 | 10 | AL591426 | AL591426 Mouse DNA | c1401 | 39.6 | 2.7 | 450 | 11 | G47340 | G47340 Zea |
| c1329 | 39.6 | 2.7 | 153420 | 9 | AL591426 | AL591426 Mouse DNA | c1402 | 39.4 | 2.7 | 559 | 8 | NEUCMDLN | NEUCMDLN Mus muscu |
| c1330 | 39.6 | 2.7 | 154288 | 9 | AL513164 | AL513164 Human DNA | c1403 | 39.4 | 2.7 | 576 | 11 | BY004237 | BY004237 Rattus no |
| c1331 | 39.6 | 2.7 | 158111 | 2 | AC121548 | AC121548 Mus muscu | c1404 | 39.4 | 2.7 | 640 | 4 | RABTNC | RABTNC Rattus no |
| c1332 | 39.6 | 2.7 | 160241 | 9 | HS88517 | HS88517 Human DNA | c1405 | 39.4 | 2.7 | 706 | 11 | BY067038 | BY067038 Rattus no |
| c1333 | 39.6 | 2.7 | 160688 | 10 | AC118731 | AC118731 Mus muscu | c1406 | 39.4 | 2.7 | 820 | 8 | NCALMOE | NCALMOE Rattus no |

| | | | | | | |
|------|------|-----|--------|----|-----------|---------------------|
| 1407 | 39.4 | 2.7 | 1276 | 0 | BC003839 | BC003839 Mus muscu |
| 1408 | 39.4 | 2.7 | 2134 | 1 | SOEXCH1 | XI1080 S. olivaceov |
| 1409 | 39.4 | 2.7 | 2134 | 1 | RNCAM113 | XI1835 R. norvegicu |
| 1410 | 39.4 | 2.7 | 2192 | 10 | BC005427 | BC005427 Mus muscu |
| 1411 | 39.4 | 2.7 | 3396 | 6 | AX305818 | AX305818 Sequence |
| 1412 | 39.4 | 2.7 | 3396 | 6 | MMU35623 | U35623 Mus musculi |
| 1413 | 39.4 | 2.7 | 3464 | 10 | BC021638 | BC021638 Mus muscu |
| 1414 | 39.4 | 2.7 | 10172 | 10 | AF083064 | AF083064 Mus muscu |
| 1415 | 39.4 | 2.7 | 20450 | 6 | AX695896 | AX695896 Sequence |
| 1416 | 39.4 | 2.7 | 37820 | 2 | AL928652 | AL928652 Mouse DNA |
| 1417 | 39.4 | 2.7 | 57510 | 2 | AC104263 | AC104263 Homo sapi |
| 1418 | 39.4 | 2.7 | 60396 | 2 | AC104378 | AC104378 Homo sapi |
| 1419 | 39.4 | 2.7 | 89944 | 9 | AC093127 | AC093127 Papio anu |
| 1420 | 39.4 | 2.7 | 91927 | 9 | AC004771 | AC004771 Homo sapi |
| 1421 | 39.4 | 2.7 | 110000 | 2 | AC068782 | Continuatiom (3 of |
| 1422 | 39.4 | 2.7 | 112769 | 2 | HSJ635E18 | AL109811 Human DNA |
| 1423 | 39.4 | 2.7 | 115498 | 9 | BX664701 | BX664701 Homo sapi |
| 1424 | 39.4 | 2.7 | 118499 | 9 | AL390722 | AL390722 Human DNA |
| 1425 | 39.4 | 2.7 | 120333 | 10 | AL844224 | AL844224 Mouse DNA |
| 1426 | 39.4 | 2.7 | 127955 | 2 | AL139907 | AL139907 Rattus no |
| 1427 | 39.4 | 2.7 | 129719 | 9 | AL358113 | AL358113 Human DNA |
| 1428 | 39.4 | 2.7 | 135772 | 10 | AC122478 | AC122478 Mus muscu |
| 1429 | 39.4 | 2.7 | 136483 | 10 | AL672162 | AL672162 Mouse DNA |
| 1430 | 39.4 | 2.7 | 142275 | 2 | AC141996 | AC141996 Rattus no |
| 1431 | 39.4 | 2.7 | 144643 | 2 | AC148749 | AC148749 Sorex ara |
| 1432 | 39.4 | 2.7 | 144988 | 2 | AC101022 | AC101022 Mus muscu |
| 1433 | 39.4 | 2.7 | 146713 | 8 | AP005002 | AP005002 Oryza sat |
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| 1435 | 39.4 | 2.7 | 147431 | 10 | AL591936 | AL591936 Mouse DNA |
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| 1438 | 39.4 | 2.7 | 157015 | 2 | AP001365 | AP001365 Homo sapi |
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| 1440 | 39.4 | 2.7 | 158458 | 9 | AC091495 | AC091495 Homo sapi |
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| 1442 | 39.4 | 2.7 | 161964 | 2 | AC111055 | AC111055 Mus muscu |
| 1443 | 39.4 | 2.7 | 162267 | 2 | AC116499 | AC116499 Mus muscu |
| 1444 | 39.4 | 2.7 | 164681 | 9 | AC011850 | AC011850 Homo sapi |
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| 1446 | 39.4 | 2.7 | 165255 | 2 | AC113590 | AC113590 Mus muscu |
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| 1448 | 39.4 | 2.7 | 171135 | 9 | AC093895 | AC093895 Homo sapi |
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| 1451 | 39.4 | 2.7 | 173892 | 2 | AC149015 | AC149015 Papio anu |
| 1452 | 39.4 | 2.7 | 175999 | 2 | AC150030 | AC150030 Sorex ara |
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| 1454 | 39.4 | 2.7 | 176338 | 10 | AC131786 | AC131786 Mus muscu |
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| 1463 | 39.4 | 2.7 | 187665 | 10 | AL772301 | AL772301 Mouse DNA |
| 1464 | 39.4 | 2.7 | 189315 | 10 | AL606508 | AL606508 Mouse DNA |
| 1465 | 39.4 | 2.7 | 190173 | 10 | AC110573 | AC110573 Mus muscu |
| 1466 | 39.4 | 2.7 | 190549 | 10 | AL591512 | AL591512 Mouse DNA |
| 1467 | 39.4 | 2.7 | 192198 | 5 | AC147719 | AC147719 Gallus ga |
| 1468 | 39.4 | 2.7 | 194657 | 2 | AC110565 | AC110565 Mus muscu |
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| 1470 | 39.4 | 2.7 | 198056 | 2 | AC106280 | AC106280 Rattus no |
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| 1472 | 39.4 | 2.7 | 199554 | 10 | AL833778 | AL833778 Mouse DNA |
| 1473 | 39.4 | 2.7 | 199559 | 10 | AL954362 | AL954362 Mouse DNA |
| 1474 | 39.4 | 2.7 | 201201 | 2 | AC150433 | AC150433 Colobus g |
| 1475 | 39.4 | 2.7 | 203250 | 9 | AC007240 | AC007240 Homo sapi |
| 1476 | 39.4 | 2.7 | 204445 | 2 | AC126512 | AC126512 Rattus no |
| 1477 | 39.4 | 2.7 | 205171 | 9 | AC093562 | AC093562 Homo sapi |
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| 1480 | 39.4 | 2.7 | 209770 | 2 | AC140409 | AC140409 Mus muscu |
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| RESULT 1 | AX358856 | 1485 bp | DNA | linear | PAT 13-FEB-2000 |
| LOCUS | AX358856 | | | | |
| DEFINITION | Sequence 109 from Patent WO0193983. | | | | |
| ACCESSION | AX358856 | | | | |
| VERSION | AX358856.1 | | | | |
| KEYWORDS | Homo sapiens (human) | | | | |
| SOURCE | Homo sapiens | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watnabe,C.K. and Wood,W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent: WO 0193983-A 109 13-DEC-2001. | | | | |
| AUTHORS | 1 | | | | |
| TITLE | Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent: WO 0193983-A 109 13-DEC-2001. | | | | |
| JOURNAL | Genetech Inc. (US) | | | | |
| FEATURES | source | | | | |
| ORIGIN | 1..1485 | | | | |
| Query Match | 100.0%; | Score 1485; | DB 6; | Length 1485; | |
| Best Local Similarity | 100.0%; | Pred. No. 0; | | | |
| Matches 1485; | Conservative | 0; | Mismatches | 0; | Gaps 0; |

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Pol 13 Dec 2001

Pol - 2 June 2000

PRTS0015264

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LOCUS Sequence 109 from Patent WO0208288.
ACCESSION AX362349
VERSION AX362349.1 GI:18694632
KEYWORDS
SOURCE
ORGANISM
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Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Waranabe, C.K. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0208288-A 109 31-JAN-2002; *Pub*
Genentech, Inc. (US)
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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| | | | |
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| Db | 781 | TCGCCGCTCCCTGTGCAGAAAGGCGTGANATCAAAACAAAACCTAAGAGGAGGACAGGCGAC | 840 |
| Qy | 841 | GGCAGGAGAGGCTTCCAGCTGTGTTCCTCTCACTTGGAGAAACGACACTCTCATCTT | 900 |
| Db | 841 | GGCAGGAGAGGCTTCCAGCTGTGTTCCTCTCACTTGGAGAAACGACACTCTCATCTT | 900 |
| Qy | 901 | TCAGAAATCTCCAAAGCCAAAGTTCAGGCTCACTGACCTGAGCTCTACGAGAGACCCAGAC | 960 |
| Db | 901 | TCAGAAATCTCCAAAGCCAAAGTTCAGGCTCACTGACCTGAGCTCTACGAGAGACCCAGAC | 960 |
| Qy | 961 | CACCTGAGAAAGACCTTGGAGTGAAGGACAAGGCTGACAGGCGCTCTTTCGGGTTTCCTTGG | 1020 |
| Db | 961 | CACCTGAGAAAGACCTTGGAGTGAAGGACAAGGCTGACAGGCGCTCTTTCGGGTTTCCTTGG | 1020 |
| Qy | 1021 | ACAGTGCATAGGTTCCAGTGCCTGAGTGTCAACCCAGAGACAGAGCCACTCGGGGCCCGGCT | 1080 |
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| Db | 1441 | GTTCGTTGTGACCCCAATCTGCTTGAAGAAAAAATAAAAAAAAA | 1485 |

musculi

priority linkage prior to
bidding.

tebrata; Euteleostomi;
omnidae; Homo.

part
pd - 23 June 1990

| | | | |
|------------|--|-------------|------------------------|
| RESULT 5 | | | |
| AX697127 | | | |
| LOCUS | AX697127 | 1485 bp | DNA |
| DEFINITION | Sequence <u>195</u> from Patent WO0078961. | | linear PAT 02-APR-2003 |
| ACCESSION | AX697127 | | |
| VERSION | AX697127.1 | GI:29498088 | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | Homo sapiens (human) | | |
| | Homo sapiens | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| REFERENCE | 1 | | |
| AUTHORS | Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L., Eaton, D.D., Gao, W.Q., Pan, J., Boetsch, D., Fong, S., Goddard, A., Godowski, P.J., Gurney, A.L., Smith, V.V., Yumas, D., Wood, W.I., Grimaldi, C.J., Hillan, K.J., Peoni, N.F., Roy, M.A. and MacNamee, C.K. | | |
| TITLE | Secreted and transmembrane polypeptides and nucleic acids encoding the same | | |
| JOURNAL | Patent: WO 0078961-A 195 28-DEC-2000; | | |
| FEATURES | Genentech Inc. (US) | | |
| source | Location/Qualifiers 1..1485 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" | | |

linear PAT 02-APR-2003

unassigned
protein

pd - 23 June 1999

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 SOURCE Homo sapiens
 ORGANISM Homo sapiens
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 REVERSE AUTHORS
 Clark,H.F., Burney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.B.,
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
 Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
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 Steinson,J., Vagts,A., Vandien,R., Watanabe,C., Wiand,D., Woods,K.,
 Xie,M.H., Yamsura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
 Goddard,A., Wood,W.I. and Godowski,P.
 The Secretd Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secretd and Transmembrane Proteins:
 A Bioinformatics Assessment
 Genome Res. 13 (10), 2265-2270 (2003)
 JOURNAL PUMED 12975309
 REFERENCE 2 (bases 1 to 1485)
 AUTHORS Clark,H.F.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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| AUTHORS | | Hillman,J.L., Lal,P., Tang,Y.Tom., Yue,H., Au-Young,J., Corley,N.C., Guegler,K.J. and Baughn,M.R. | |
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